SOCIETY FOR PROGRESSIVE LEARNING & RESEARCH

ORGANISES

INTERNATIONAL CONFERENCE ON

APPLICATIONS AND INNOVATIONS OF SCIENCE INNOVATIONS OF SCIENCE AND TECHNOLOGY IN INDUSTRY

ICAISTI 2024

ABSTRACT BOOK

OCT. 5TH & 6TH 2024

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APPLICATIONS AND INNOVATIONS OF SCIENCE AND TECHNOLOGY IN INDUSTRY

(ICAISTI 2024)

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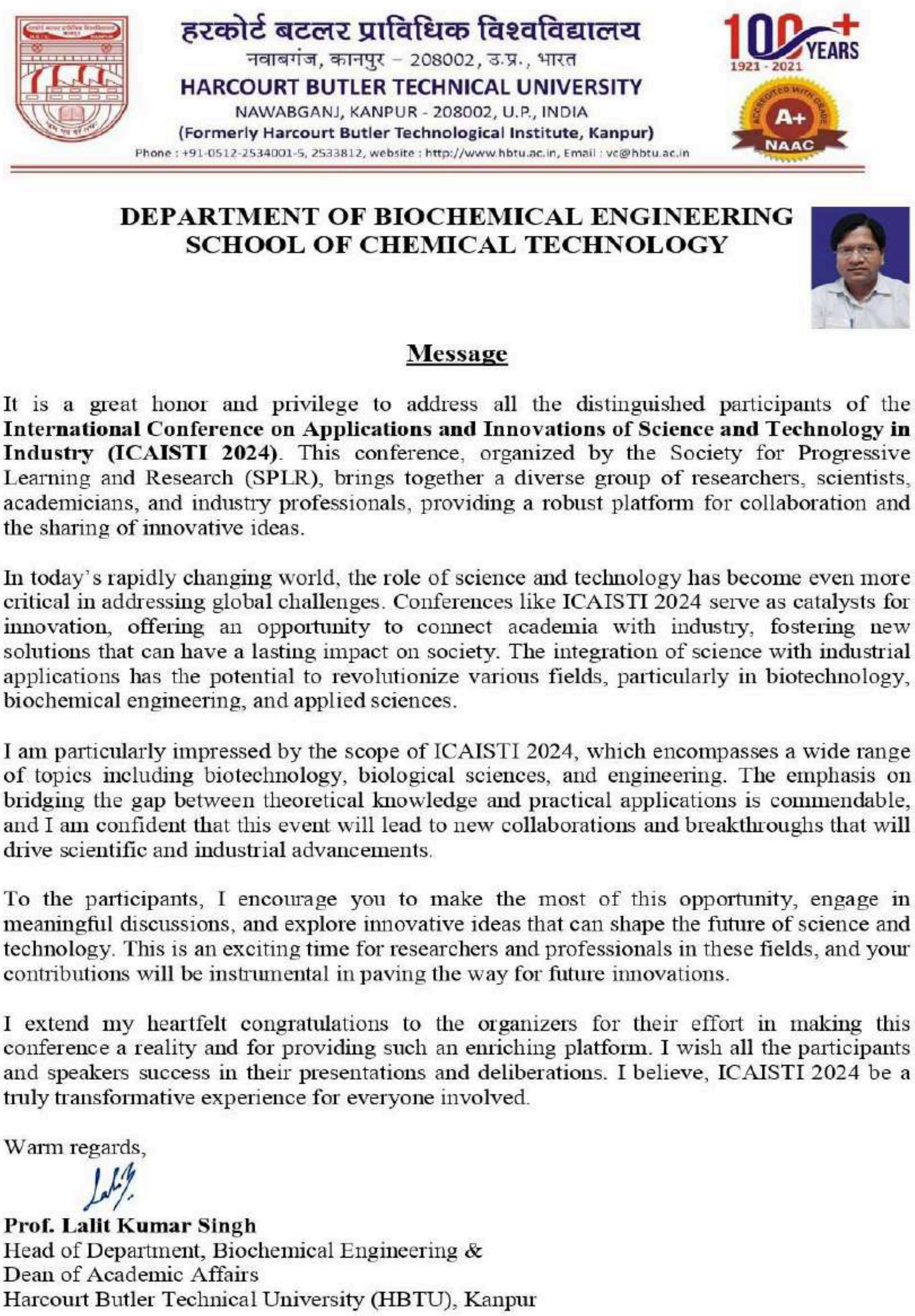
OCTOBER 5th & 6th, 2024

MESSAGES



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DEPARTMENT OF BIOCHEMICAL ENGINEERING
SCHOOL OF CHEMICAL TECHNOLOGY

Message

It is a great honor and privilege to address all the distinguished participants of the **International Conference on Applications and Innovations of Science and Technology in Industry (ICAISTI 2024)**. This conference, organized by the Society for Progressive Learning and Research (SPLR), brings together a diverse group of researchers, scientists, academicians, and industry professionals, providing a robust platform for collaboration and the sharing of innovative ideas.

In today's rapidly changing world, the role of science and technology has become even more critical in addressing global challenges. Conferences like ICAISTI 2024 serve as catalysts for innovation, offering an opportunity to connect academia with industry, fostering new solutions that can have a lasting impact on society. The integration of science with industrial applications has the potential to revolutionize various fields, particularly in biotechnology, biochemical engineering, and applied sciences.

I am particularly impressed by the scope of ICAISTI 2024, which encompasses a wide range of topics including biotechnology, biological sciences, and engineering. The emphasis on bridging the gap between theoretical knowledge and practical applications is commendable, and I am confident that this event will lead to new collaborations and breakthroughs that will drive scientific and industrial advancements.

To the participants, I encourage you to make the most of this opportunity, engage in meaningful discussions, and explore innovative ideas that can shape the future of science and technology. This is an exciting time for researchers and professionals in these fields, and your contributions will be instrumental in paving the way for future innovations.

I extend my heartfelt congratulations to the organizers for their effort in making this conference a reality and for providing such an enriching platform. I wish all the participants and speakers success in their presentations and deliberations. I believe, ICAISTI 2024 be a truly transformative experience for everyone involved.

Warm regards,

Prof. Lalit Kumar Singh
Head of Department, Biochemical Engineering &
Dean of Academic Affairs
Harcourt Butler Technical University (HBTU), Kanpur

Message from Mr. Dinesh Sharma

Vice President - Technical Sales (South Asia) - Food Division, Camlin Fine Sciences Ltd

I am pleased to extend my warm regards to the organizers and participants of the **International Conference on Applications and Innovations of Science and Technology in Industry (ICAISTI 2024)**. It is a privilege to be part of such an esteemed event that brings together thought leaders, scientists, and professionals to share their expertise and explore innovative applications of science in various industries.

At **Camlin Fine Sciences Ltd.**, we are committed to providing cutting-edge shelf life solutions to enhance food quality and safety across the globe. This conference is an ideal platform for exchanging ideas, discussing emerging trends, and fostering collaborations that drive innovation forward. The growing need for sustainable and efficient solutions in food science and technology cannot be overstated, and I am confident that ICAISTI 2024 will spark meaningful discussions that will contribute to the future of food innovation and other industrial advancements.

The importance of connecting academia, research, and industry to create actionable outcomes is paramount. I look forward to witnessing the outcomes of this event, and I extend my best wishes to all the participants for fruitful discussions and successful collaborations.

With warm regards,

Dinesh sharma

Dinesh Sharma
Vice President - Technical Sales (South Asia) - Food Division
Camlin Fine Sciences Ltd.

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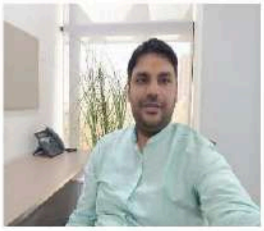

Message from Mr. Ajay Yadav

AGM - Technical Sales & Marketing Food Ingredients, Camlin Fine Sciences Ltd

I am honored to contribute a message for the **International Conference on Applications and Innovations of Science and Technology in Industry (ICAISTI 2024)** organized by the Society for Progressive Learning and Research (SPLR). This event represents a valuable opportunity for professionals from diverse fields to come together and explore innovative solutions that address industry challenges through scientific advancements.

As part of Camlin Fine Sciences Ltd., a company dedicated to providing shelf life solutions and food ingredients that enhance product quality, I truly believe that the intersection of science and industry is crucial for sustained growth. Conferences like ICAISTI 2024 help create a collaborative environment where scientists, researchers, and industry professionals can discuss breakthroughs, share knowledge, and drive forward the application of science in ways that benefit not only specific sectors but society as a whole.

In an age where industries must adapt to constant changes in technology and consumer demands, it's essential for research and development to focus on sustainable, efficient, and innovative solutions. I hope that the discussions and ideas exchanged during this conference will inspire new collaborations and pave the way for innovative products and processes that can shape the future of industry.

My best wishes to the organizing committee and all participants of ICAISTI 2024. I am confident that the insights gained through this conference will contribute significantly to the advancement of science and its application in industrial contexts.

Warm regards,
Ajay Yadav
Mr. Ajay Yadav
AGM - Technical Sales & Marketing Food Ingredients
Camlin Fine Sciences Ltd.

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- ***Mr. Harsh Bhaduria***
- ***Mr. Harsh Pandey***

Inaugural Keynote

- **Dr Lalit Kumar Singh,** HOI, Biochemical Engineering and Dean Academic Affairs, HBTU Kanpur, UP, India

Technical Session I

Keynote Lecture 1

- **Dr. Lalit Goswami,** Postdoctoral Researcher, Department of Civil Engineering, Kyung Hee University-Global Campus, South Korea

Industry Interactive Session

- **Dr. Neelam Lohiya,** Head: Business Development, Global Active Clay LLP, Ahmedabad Gujarat, India
- **Dr. Sneha Mishra**, Founder & Director, Skill Integrator Services India Pvt. Ltd. Gurgaon, Haryana, India

Technical Session II

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- **Dr. Protibha Nath Banerjee,** Associate Professor, Department of Chemistry, Pimpri Chinchwad University, Pune, Maharashtra, India

Keynote Lecture: 3

- **Dr. Dilfuza Jabborova,** HOD, Institute of Genetics and Plants Experimental Biology, Uzbekistan

Keynote Lecture: 4

- **Dr. Anshu Rastogi**, Research Scientist, Laboratory of Bioclimatology, Poznan University of Life Sciences, Poznań, Poland

Session Chairs and Judges

Oral Session I:

- **Dr. Naresh Kumar**, Assistant Professor, Deshbandhu College, University of Delhi, New Delhi, India
- **Dr. Madhulika Singh,** Assistant Professor, Department of Life Sciences and Biotechnology, Chhatrapati Shahu Ji Maharaj University, Kanpur, UP, India

Oral Session II:

- **Dr. Naveen Gaurav,** Associate Professor and Head, Department of Biotechnology, Shri Guru Ram Rai University, Dehradun, UK, India
- **Dr. Annu Mishra,** Senior Electrochemist, R&D, ASTAM Diagnostics Pvt.Ltd, Bhiwadi

Oral Session III:

- **Dr. Protibha Nath Banerjee,** Associate Professor, Department of Chemistry, Pimpri Chinchwad University, Pune, Maharashtra, India
- **Dr. Himani Kulshrestha,** Assistant Professor, Sharda university, Greater Noida, India

Oral Session IV:

- **Dr. Raj Kamal Kushwaha,** Assistant Professor, Department of Biochemical Engineering, Harcourt Butler Technical University, Kanpur, India.
- **Dr Manish Dwivedi,** Assistant Professor, Amity University Uttar Pradesh, Lucknow

About International Conference on Applications and Innovations of Science and Technology in Industry (ICAISTI-2024)

Society for Progressive Learning and Research (SPLR) has organized a two-day International Conference on "Applications and Innovations of Science and Technology in Industry (ICAISTI-2024)" in Online mode on October 5th & 6th, 2024. The basic aim of the present conference was to provide current updates of science and technology applications in industries.

The two-day International Conference "ICAISTI-2024" convened some of the brightest minds in the field, serving as a pivotal platform for scholars, researchers, and academic experts to converge and exchange cutting-edge insights. Against the backdrop of rapid advancements, the conference provided a forum to explore the latest breakthroughs, emerging technologies, and innovative applications shaping the landscape of biotechnology in industries. Through keynote speeches, scientists and teachers' expert talks and interactive oral presentations, participants delved into diverse topics ranging from waste-derived biochar, biorefinery for circular economy, beneficial role of plant growth promoting bacteria, importance of peatland, insect diversity, microbiome research, industry sectors quality control measures, developing stress models, osteoporotic changes in bone to Skills required for students to become Industry-ready.

With a focus on interdisciplinary collaboration and knowledge dissemination in the form of more than eighty oral presentations by delegates, the ICAISTI-2024 fostered a dynamic environment conducive to fostering new ideas, forging partnerships, and charting the course for the future of biotechnology, food technology and pharmaceutical industries.

About Society for Progressive Learning and Research (SPLR)

Society for Progressive Learning and Research (SPLR) stands as a foremost non-profit professional association, operating under the India Trust Act (1882), dedicated to fostering research, development, and the advancement of life sciences, social sciences, engineering and technology. Our organization's primary focus is to promote and facilitate research progress, prioritizing innovation, and nurturing a platform that supports the growth and evolution of these fields.

As one of the most promising and upcoming societies, we boast a global membership drawn from universities, industries, hospitals, research institutes, and educational institutions, positioning us as a diverse hub for professional expertise and collaborations worldwide. The Society serves as a charitable membership organization catering to researchers passionate about exploring new horizons in the form of collaborations and research.

Feel free to write back to join or to give your valuable suggestions, on sforplar@gmail.com or splrceo33@gmail.com.

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KEYNOTE LECTURES

Keynote Lecture: 01

Waste-derived Biochar for enhancing the Biological Treatment of Biomass Gasification Wastewater

Dr. Lalit Goswami
Department of Civil Engineering, College of Engineering, Kyung Hee University,
Yongin, Republic of Korea

Abstract

Wastewater from biomass gasification chiefly contains monocyclic (MAHs) and polycyclic aromatic hydrocarbons (PAHs) that are generated by wet scrubbing process of raw synthetic gas during its cleaning process. These MAHs and PAHs are well-known as toxic, mutagenic, and carcinogenic agents which need to be removed prior to their release into the environment. The present study evaluated the potential of an up-flow packed bed bioreactor (UFPBBR) with immobilized *Rhodococcus opacus* onto biochar loaded polyurethane foam (PUF) as the packing material for treating biomass gasification wastewater (BGWW). Initially, the chemical, physical, morphological, thermal, and magnetic properties of the cheaply derived biochar were initially characterized employing different techniques. UFPBBR was operated utilizing only PUF as the support material and a maximum COD removal of 81 ± 2.65% was achieved with 1820 mg L^{-1} of influent COD concentration and 24 h of HRT. Using biochar loaded PUF as the support material; more than 95 ± 1.27% of COD removal was attained under the same COD loading condition and HRT. Furthermore, the wastewater was detoxified to 96.2% demonstrating the ability of UFPBBR system using the novel biochar-based support material for biomass gasification wastewater treatment.

Keywords: Attached-growth bioreactor; bio-support material; *R. opacus*; up-flow packed bed bioreactor

Keynote Lecture: 02

Biorefinery for Circular Economy

Dr. Protibha Nath Banerjee
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Abstract

There is a pressing need to switch from fossil-based economy to bio-based economy as the fossil reserves are depleting very fast. Biorefinery is a process of converting bio-based feedstocks into chemical, fuels and energy while circular economy is a closed loop sustainability framework for production and consumption that keeps materials in circulation. When bio-based feedstocks are used for circular economy then it is called circular bio-economy. The main goal of the circular bio-economy is to reduce the waste and extend the life cycle of the product by systematic use of bioresources for economic development. Biorefinery is going to be a crucial game changer for circular bioeconomy as it has the capability of large-scale use of biomass for a sustainable and greener world. The concept of biorefinery for the circular economy will not only result in cost competitive products and reduce the emission of greenhouse gases (GHG's) but will also boost the socio-economic security of the rural people. The systematic approach of biorefinery processes will open the door for bio-based industries which in turn will have significant effect on circular bio-economy. Sugarcane biorefinery is one of the main focus of the government of India as it has the potentiality to meet the demand of the fuel, chemicals and products if proper biorefinery technology is developed. At present sugar industries in India produce nearly 100 million tonnes of bagasse per annum. This huge quantity of agricultural residue can be converted to a variety of chemicals, biofuels and bioenergy which can contribute significantly in circular bio-economy. At present the use of bagasse is restricted to generation of electricity by burning the bagasse which emits GHG and contributes significantly to global warming. Considering the potential of bagasse for the production of high-cost chemicals and fuels, the present production of electricity is not an economically viable valorisation process. But due to lack of availability of technology and economically viable biorefinery process the sugar industries are compelled to burn bagasse to generate electricity. The challenges with the existing biorefinery process technologies lie with the structural diversity and the recalcitrant nature of lignin – which is one of the important components of bagasse or any lignocellulosic biomasses. Recently few biorefinery processes has been developed using statistical and artificial intelligence-based process modeling tools which have a significant effect on process economies. Mathematical modeling using response surface methodology and artificial intelligence techniques like artificial neural network (ANN), fuzzy inference system (FIS) and genetic algorithm (GA) are very promising predictive modeling tools in the development of biorefinery processes. The artificial intelligence-based techniques reduce the need for time and resource consuming experimentation and have shown outstanding accuracy in predicting the optimal reaction conditions through pattern recognition of the various parameters involved in complex biorefinery processes. Although, lot of work has been done in the development of different biorefinery processes around the world, the concept of biorefinery is still at its infancy stage and needs continued efforts to build a robust and economically viable processes for actual realization of circular bio-economy.

Keynote Lecture: 03

Beneficial role of plant growth promoting bacteria on growth of ginger

***Dr. D. Jabborova*[1*] *and Dr. D. Kadirova*[2]
[1]Institute of Genetics and Plant Experimental Biology, Academy of Sciences of the Republic of Uzbekistan; dilfuzajabborova@yahoo.com,
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Abstract

Plant growth-promoting bacteria are of the importance of sustainable agricultural practices. Plant growth-promoting bacteria could improve germination, plant growth and yield either directly and indirectly. They are a secure and favorable alternative to chemical fertilizers as well as a beneficial option to decrease abiotic and biotic. The aim of this research was to study the effect of plant growth promoting bacteria on the growth and yield of ginger in Surkhandarya Region, Uzbekistan. For the first time in Uzbekistan, the ginger rhizome was cultivated to study the growth and yield in ginger. The effect of plant growth-promoting bacteria on the growth of ginger plant in the climatic conditions of SurkhandaryaRegion was analyzed in 90 and 180 days. It was found that *B. subtilis* IGPEB 1, *P. koreensis* IGPEB 17 and *B. endophyticus GPEB* 33 bacteria increased the plant height, leaf number, leaf length and leaf width of ginger. When the plant height of ginger was analyzed in 90 days, it was noted that *B. subtilis* IGPEB 1 strain increased the plant height of ginger by 20.3%, *P. koreensis* IGPEB 17 strain increased by 27.1%, and *B. endophyticus* IGPEB 33 strain increased by 33.9%. According to the results of the analysis at 180 days, it was noted that *B. subtilis* IGPEB 1 strain increased the plant height of ginger by 12%, *P. koreensis* IGPEB 17 strain by 14.7%, and *B. endophyticus* IGPEB 33 strain by 18.8% compared to the control.The effect of plant growth-promoting bacteria on the leaf length of ginger plant in the climatic conditions of SurkhandaryaRegion was analyzed in 90 and 180 days. It was found that *B. subtilis* IGPEB 1, *P. koreensis* IGPEB 17 and *B. endophyticus* IGPEB 33 strains increased the leaf length of ginger. When the leaf length of ginger was analyzed in 90 days, compared to the control, it was noted that *B. subtilis* IGPEB 1 strain increased the leaf length of ginger by 33.3%, *P. koreensis* IGPEB 17 strain by 35.7%, and *B. endophyticus* IGPEB 33 strain by 38%. In 180 days, *B. subtilis* IGPEB 1 strain increased the leaf length of ginger by 19.3%, *P. koreensis* IGPEB 17 strain by 21.8%, and *B. endophyticus* IGPEB 33 strain by 26%.The Potential Plant growth-promoting bacteria could be a frontier goal to achieve a positive effect on ginger and reduce the negative impact of mineral fertilizers on the sustainable agriculture.

Keywords: Plant growth-promoting bacteria, ginger, plant height, leaf length, sustainable agriculture

Keynote Lecture: 04

Peatland and its importance for our environment

Dr. Anshu Rastogi
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Abstract

Sun-Induced Fluorescence: A Novel Remote Sensing Tool for Enhanced Earth Observation

Sun-induced fluorescence (SIF) is an emerging tool for remote sensing, with the potential to significantly enhance Earth observation by directly linking to photosynthetic processes. This presentation focuses on SIF's application in monitoring peatland ecosystems, which store about one-third of global soil carbon and are highly sensitive to climate change. Using the Piccolo Doppio system, which includes hyperspectral and fluorescence measurements, we explore the seasonal dynamics of SIF in response to environmental changes such as warming and precipitation manipulation. The study demonstrates that SIF provides more accurate insights into peatland vegetation productivity and physiological status than traditional reflectance-based indices. This research has implications for understanding the impacts of climate change on carbon cycling and vegetation health. Furthermore, SIF's use in satellite missions, such as planned ESA's Fluorescence Explorer (FLEX), underlines its growing importance in environmental monitoring. This study contributes to advancing remote sensing methodologies and highlights the critical role of SIF in understanding complex ecosystems like peatlands.

Keywords: Sun-Induced Fluorescence, Remote Sensing, Peatlands, Vegetation, Climate Change

Industry Interaction

Skills Required for Students to become Industry-Ready

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Abstract

In today's rapidly evolving job market, students must possess a diverse skill set to thrive. Preparing students for industry readiness requires a comprehensive curriculum that equips them with a blend of technical skills, soft skills, and problem-solving abilities. Technical skills encompass domain-specific knowledge, programming proficiency, and the ability to utilize relevant tools and technologies. Soft skills, including communication, teamwork, adaptability, and critical thinking, are essential for effective collaboration and professional development. Additionally, fostering problem-solving skills empowers students to approach challenges with innovation and resilience. By cultivating a synergistic combination of technical, soft, and problem-solving skills, educational institutions can empower students to thrive in today's dynamic and competitive job market.

Keyword: skills, synergistic, technical, competitive, industry readiness

INVITED LECTURES

IL01:

Ayurvedic Approach to Pain Management

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Abstract:

Pain affects millions worldwide, and conventional treatments often focus on symptom suppression. Ayurveda offers a comprehensive approach to pain management, addressing physical, mental, and emotional well-being. This article explores Ayurvedic strategies for pain relief, including:

- Dietary modifications
- Herbal remedies (turmeric, ginger, boswellia)
- Panchakarma therapies (abhyanga, swedana, basti)
- Yoga and meditation
- Lifestyle modifications

Case studies demonstrate effective pain reduction using Ayurvedic approaches. By understanding individual constitutions and imbalances, Ayurveda provides personalized pain management solutions. This holistic approach offers a promising complementary or alternative therapy for pain sufferers.

Keywords: Ayurveda, pain management, holistic approach, natural remedies, complementary therapy.

IL02:

Environmentally Derived Bacteriophages can be a Potential Source to Combat Drug Resistance

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Abstract:

Bacteriologically confirmed treatment failures are now frequently reported due to the growing resistance against multiple drug classes, including commonly used β-lactams, macrolides, and fluoroquinolones. Hospital-acquired Gram-negative infections pose a significant challenge to patient safety. Studies indicate that 50-70% of all urinary tract infections (UTIs) are caused by multidrug-resistant (MDR) organisms, underscoring the urgent need for alternative therapies. Bacteriophages (viruses that infect bacteria), found abundantly in sewage treatment plants, ponds, lakes, and rivers, represent a unique class of naturally evolved recognition tools for bacteria. These phages are highly specific to their bacterial hosts, often targeting only a single species or strain. Decades before the development of antibiotics, phages were recognized as potential antibacterial agents, as they are major bacterial predators in nature. Given their ubiquity in natural environments, it is feasible to isolate bacteriophages for virtually any bacterial target. They are not only highly host-specific but also stable across a wide range of environmental conditions, making them a promising alternative to conventional antibiotic treatments. Moreover, phage cocktails—combinations of multiple phages—are being reported to exhibit broad-spectrum activity against many common pathogenic bacteria. Before being considered for therapeutic use, bacteriophages undergo a thorough process of isolation, physical and in-vitro characterization, cocktail formulation, purification, dosing, and in vivo testing. In addition, endolysins, phage-encoded hydrolytic proteins, can cause rapid lysis and bacterial cell death by degrading the peptidoglycan layer when applied as purified recombinant proteins.

Keywords: *Sewage water, Bacteriophage, Phage lysin, Peptidoglycan hydrolases, Gram negative bacteria, Antimicrobial resistance, MDR, Biomedical applications*

IL03:

Deciphering the Structural and functional properties of the copper transporters as a novel therapeutic target in *M. tuberculosis.*

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ABSTRACT

Tuberculosis is one of the severe infectious global diseases caused by *Mycobacterium tuberculosis* and become an epidemic for many years. After its infection, the human immune system induces macrophages and other granuloma cells to combat disease. Macrophagesfacilitate immunity viathe acquisition of Cu^+ inside the phagosome by exploiting certain transporters and further, neutralize MTB. Interestingly, *M. Tuberculosis* has developed a versatile Copper transporter system to avoid the toxic concentration of Cu^+ions inside the macrophages and thereby, MTB becomes capable to survive in the host system being in a dormant state for decades. Therefore, copper transporters could be a considerable drug target in *M. tuberculosis*and alteration in the activity of this protein can make MTB vulnerable to Cu toxicity in the host system. Several research-based findings on structural and biophysical properties have established Mycobacterial copper transporters as a promising drug target.

Keywords: *Mycobacterium tuberculosis*, copper transporters, MctB, therapeutics, Drug target.

IL04:

From Microbe to Market: Life Cycle Assessment of Sustainable Glucose Oxidase Production

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Abstract

This study presents a comprehensive life cycle assessment (LCA) of the microbial production of glucose oxidase enzyme (GOx), focusing on *Aspergillus niger* as the primary production organism. We evaluate the environmental impacts, resource consumption, and economic viability of GOx production using different carbon sources and fermentation strategies. The analysis encompasses strain development, media preparation, fermentation, downstream processing, and enzyme formulation. Our results indicate that the choice of carbon source and fermentation method significantly influences the overall sustainability of GOx production. Fed-batch fermentation using food industry by-products as substrates demonstrated the lowest global warming potential (GWP) at 3.8 kg CO2eq/kg GOx, compared to 5.2 kg CO2eq/kg GOx for batch fermentation with pure glucose. Optimization of the fed-batch process increased GOx yield by 28%, reaching 24.7 U/mL, while reducing water consumption by 18% compared to conventional batch methods. The cradle-to-gate analysis revealed that fermentation and downstream processing account for 65% and 25% of the total environmental impact, respectively. Energy consumption in these stages was identified as a hotspot, with potential for improvement through process intensification and renewable energy integration. A Monte Carlo simulation considering uncertainties in key parameters showed that the GWP could vary by ±12% (95% confidence interval). Economic assessment indicates a production cost of $87.3/kg GOx, with raw materials and energy contributing 40% and 35% to the total cost, respectively. Sensitivity analysis suggests that a 15% increase in fermentation productivity could reduce both environmental impact and production costs by approximately 10%. This LCA provides crucial insights for researchers and industry stakeholders to enhance the sustainability of microbial GOx production, highlighting opportunities for process optimization and resource efficiency improvements.

Keywords: Glucose Oxidase; Life Cycle Assessment, Enzyme Production; Fermentation; Environmental Impact; Resource Efficiency; Bioprocess Optimization; Sustainable Biotechnology; Industrial Enzymes

IL05:

Industry Sectors QA & QC: An Opportunity for Science and Technology

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Abstract

The industries are having various sectors for the science and technology students. In the current scenario, it is highly required to bridge a gap between the industries and the students of science and life sciences. Industries look for the industry-ready candidates, so it is required to guide and trained them as per the industry requirements. The various sectors of industries for science and life science students are marketing, resarrch, production and quality assurance and quality control (QA&QC). The QA&QC sectors are the booming industry for science and life science students in various fields like FMCG, chemical, food, pharmaceutical, pathology, plant, animal, microbiology, environment etc. The products developed in industries required to get tested based on quality and thus need QA&QC. The QA&QC in various field need recognition of accreditation bodies like National Accreditation Board for Testing and Calibration Laboratories (NABL), specifically for the Testing and Calibration Laboratories (ISO/IEC 17025), and Medical Testing Laboratories (ISO 15189). To work in the various disciplines of QA&QC like biological, chemical, diagnostic radiology QA testing and forensic many talented and trained candidates are required from science, life science and biotechnology area. These disciplines include various groups such as air, water, food and agriculture, drug and pharmaceuticals, pathology and many more. It is highly required to provide information, knowledge, and training to the students so that they are aware, acquainted and ready to work in the different QA&QC sectors. The current lecture will provide insight for the opportunity for science and technology students, so that get will get awareness about this sector and will get to know how they can utilize their learning and potential with full zeal.

Keywords: science, life science, biotechnology, QA, QC, industry, microbiology, NAB

Flash Talks

FT01:

Developing chronic predictable and unexpected stress models to simulate depression like cognitive impairments

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Abstract

Stress is defined as a state of threatened homeostasis, which can be of physical and/or psychological nature. Physiological and psychological responses to stress are mediated by the Hypothalamic-Pituitary-Adrenal (HPA), sympathetic (adrenergic) and brain monoaminergic systems. The duration and nature of an applied stressor are important determinants whether adaptation to the stress response acts as being protective or damaging.We aimed to develop stress models which differ in intensity, duration, and predictability of stressors namely chronic stress (CS) and chronic unpredictable stress (CUS) to explore the stress induction and/or adaptation, so that such models can simulate depression like cognitive impairments. Developing such models are vital for studying the biological basis of stress-induction and examining depression like changes.Adult male Sprague-Dawley (SD) rats, weighing 180-220 g were used in the study.Chronic stress (CS) is a homotypic model in which rats were subjected to immobilization stress for 150 minutes daily for a period of seven days, whereas Chronic unpredictable stress (CUS) is a heterotypic model in which rats were subjected to different type of stressors mild and severe intensity every day in an unpredictable manner, for a period of seven days. To examine stress-induction, plasma corticosterone levels was examined, and its levels were estimated by HPLC-UV detector. The results were analysed by One Way Anona followed by Newman-Keuls post hoc test.Exposure of CUS caused a significant (426.40 ±27.22 ng/ml, $P<0.001$) increase in the plasma corticosterone level as compared to the non-stress control group (223.36 ±68 ng/ml), while no significant ($P>0.05$) change was observed in the CS group (242.34 ±10.75 ng/ml).In CS group, the level of corticosterone was not significantly increased, which could be due to the adaptation against the repeated stress and depletion of reserve glucocorticoid stores in the adrenals. Interestingly, CUS model the corticosterone level was significantly increased. The different corticosterone response among the two chronic models (CS and CUS), could be explained on the difference in the functionality state of HPA-axis feedback mechanism. It can be proposed that the unpredictability of stressors in CUS group may cause desensitization or deregulation of HPA-axis feedback mechanism. This study extrapolates that the modern lifestyle, with its constant stressors and new difficulties, may cause a variety of neurological and cognitive deficits if it is not managed appropriately.

Keywords: Chronic stress, corticosterone, depression, HPA-axis, stress

FT02:

Secondary osteoporosis: histomorphometric and histopathological changes in bone

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Abstract

Secondary osteoporosis is defined as micro-damage at ultra- and micro-structural level due tounderlying disorder and/ or medication affecting bone mass and quality. In our lab, we arestudying histomorphometric and histopathological changes in bone in polycystic ovariansyndrome (PCOS) and diabetic mouse models. Micro-computed tomography was used tostudy histomorphometric changes in bone and haematoxylin-eosin staining of decalcifiedbone was done to study histopathological changes. Our findings report that femur trabaecularparameters viz., BMD, BV/TV, Tb.N, Tb.Th, Conn. Dn., DA, were lowered whereas SMI,Tb.Pf., and Tb. Sp. were increased in both PCOS and diabetic mice. BMD of femur corticalwas unchanged in PCOS as well as in diabetic group; B.Ar., Cs.Th., M.M.I., and T.Arwerereduced in diabetic group whereas the same parameters were unchanged in PCOS group. Ourfindings suggest that bone micro-architecture was significantly negatively altered in PCOSand diabetic groups when compared with control. The severity of damage was more indiabetic group as damage was covering the cortical zone along with trabaecular zone offemur.

Keywords: bone, osteoporosis, secondary, histomorphometric, micro-architecture

FT03:

In silico Approach to Predict Structural and Functional Impact of OXP3 G52V Polymorphism on its Protein

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Abstract

The FOXP3 gene codes for a transcription factor that is believed to be crucial for the development and function of regulatory T cells (Tregs), which play a role in regulating T cell activation and are therefore vital for maintaining immune homeostasis. FOXP3 polymorphisms, common in the general population, have been studied for many complex human diseases. A malfunction in the FOXP3 gene product can lead to a deficiency of Tregs, resulting in autoimmune diseases. On the other hand, high levels of Tregs have been reported in the peripheral blood, lymph nodes, and tumour tissues of patients with various cancers. The rs17847095 C>A polymorphism of the FOXP3 gene results in the substitution of Glycine (G) for Valine (V) at the 52 position of its protein. In the present study, it has been hypothesized that this amino acid substitution might alter the structure and function of its protein. To achieve the aim, the protein sequence of the human FOXP3 gene was retrieved from the NCBI Protein database. To check the effect of G52V polymorphism on the structure, and function/ disease association of FOXP3 protein different web server-based tools including SIFT, PhD-SNP, SNAP, Meta-SNP, PolyPhen-2, MutPred2, I-Mutant2, and ConSurf were used. This amino acid substitution was found to be deleterious for the functioning of FOXP3 protein by SIFT (score 0.014) and possibly damaging by PolyPhen-2 (score 0.437). However, as per analysis with I-Mutant2 presence of V amino acid at position 52 of FOXP3 protein was found to increase its stability (DDG -0.66 Kcal/mol) at 25^{o}C and pH 7.0. The G52V substitution was found as a disease-causing variant through PhD-SNP (score 0.638), SNAP (score 0.665) and Meta-SNP (score 0.559) analyses. The degree of evolutionary conservation of these amino acids in protein was found to be variable (score 1) when the protein sequence was checked with the ConSurf web server which measures the degree of evolutionary conservation of an amino acid in a protein. The loss/gain of structural and functional properties with this substitution was non-pathogenic as calculated by Mut-Pred-2 with a score of 0.249. Our result suggests that the G52V polymorphism of FOXP3 might affect the structure, stability, and functioning of its protein and needs to be validated through wet lab-based studies.

Keywords: FOXP3, Polymorphism, Structure, Function, *Insilico*

FT04:

A transcriptomic analysis of immune cell infiltration in endometriosis using CIBERSORT tool

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(AIB Comunication No. AIB/RA/2024/579)

Abstract

Endometriosis is an inflammatory disease, involving immune cell infiltration and production of inflammatory mediators. In the current investigation, gene expression data was obtained from the dataset GSE7305. CIBERSORTx tool was employed to inspect the differences in infiltration of the 22 types of immune cells in tissue samples with endometriosis and normal healthy tissue samples in the GSE7305 dataset. The expression matrix of immune cell types was deconvoluted by using the CIBERSORTx tool, using the LM22 as the reference, 500 permutations, and $P < 0.05$. The infiltration of T cells gamma delta, macrophages M2, B cells naïve, T cells CD4 memory resting cells, macrophages M0, plasma cells, T cells CD8 and mast cells activated was higher in the samples with endometriosis while NK cells resting, NK cells activated, dendritic cells resting, dendritic cells activated, T cells regulatory (Tregs), and T cells follicular helper were more expressed in the healthy normal endometrial tissue. Specifically, M2 macrophages are shown to be elevated in endometrial lesions and thus may be important in the development and recurrence of endometriosis. These findings thus indicate a dysregulation of the immune system in endometriosis which may contribute to disease progression and so targeted therapeutic approaches may be developed to modulate the immune response and alleviate the symptoms of endometriosis.

Keywords: Endometriosis, CIBERSORT x, GSE7305.

FT05:

Treatment of tuberculosis: a comprehensive analysis

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Abstract

It is an in-complexity assessment of a worldwide substantial infectious disease, tuberculosis (TB). It covers the treatment part of Tuberculosis with attention to its successes and shortcomings. The chapter observes this complex connection between *Mycobacterium tuberculosis* and the human host. It defines how consequences are as the action in terms of treatment. It introduces the current therapeutic regimen strategies; the recurring emphasis is on targeted involvement and public health efforts. Also, the chapter covers upcoming attempts in TB research, that will further increase in better treatment regimens. These incorporate vaccines; and different emerging new drugs (containing an expedition for unique representatives). Despite two eras of exaggerated exploration to recognize and treat tuberculosis disease, natural worries remain and creel advancement. Though, outstanding collective creativities comprise the academic world, the drug industry, and different organizations, the drug entrant channel is encouraging. This outstanding accomplishment occurs with the fundamental experiment of highlighting multidrug treatments for scientific testing and restoring test proposals to speed up regimen improvement and take advantage of drug discovery innovations. Furthermost required are indicators of movement from dormant infection to lively pulmonary illness, indicators of drug retort and forecasters of reversion, and in vitro paraphernalia to reveal synergies that translate clinically and animal models to reliably assess the treatment shortening probability of novel treatments. In this chapter, the benefits and challenges of treatment regimens and treatment periods against personalized remedies based on disease difficulty and host and pathogen types, believing systematic and prepared perceptions.

Keywords: Tuberculosis, Treatment, Multidrug resistance, *Mycobacterium Tuberculosis*

FT06:

Studies on Insect Diversity in Sri Vijay Vidyalaya College of Arts and Science College Campus, Dharmapuri, Tamil Nadu, India.

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Abstract

A study on the status and diversity of Insects at SVVCAS College Campus, Dharmapuri, Tamil Nadu, India was conducted from June 2023 to February 2024. 96 species comprising 59 families and 13 orders were recorded on college campuses during the present study. The study can be used constructively in planning the sustainability of both man and the environment. The different insect orders identified during the brief study have only highlighted the potential magnitude of biodiversity on the college campus. Insects for over half of all living organisms have a vital role in the ecosystem by influencing the diversity abundance and distribution of plant communities. Among the recorded in our campus area insects are edible insects 23.95%, pollinating insects 21.87%, Harmful insects 27.08%, medicinal insects 8.33%, and predator insects 18.75%. It was recorded that urbanization and climate conditions are found to be significant factors in determining the distribution of insects in the preferred study area.

Keywords: Insect, Diversity, Edible, Pollinating, Distribution.

FT07:

Integrated Farming System: A Sustainable Approach

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Abstract

An Integrated Farming System (IFS) is a holistic approach to agriculture that combines various agricultural practices to create a sustainable and productive farming ecosystem. This chapter explores IFS's principles, benefits, challenges, andfuture prospects, emphasizing its role in enhancing food security, environmental sustainability, and economic viability for smallholder farmers. Key features of IFS include crop-livestock integration, where livestock manure serves as a natural fertilizer, and agroforestry, which helps in nutrient cycling and carbon sequestration. Aquaculture and renewable energy sources like biogas and solar power further support the system's sustainability by reducing dependency on external inputs. Integrating different farming enterprises allows for the diversification of income streams, improving farm resilience and reducing the risk from market or climatic fluctuations. This system focuses on recycling resources within the farm reducing waste and improving efficiency.

FT08:

Unraveling Gene Expression Alterations in Alzheimer's Disease: An RNA-Seq Analysis of Neural Tissue

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Abstract

Alzheimer’s disease (AD) is a neurodegenerative disorder characterized by cognitive decline, memory loss, and neuronal dysfunction. To gain deeper insights into the molecular mechanisms underlying AD, RNA sequencing (RNA-Seq) data from the European Nucleotide Archive (ENA) under project accession number PRJNA123456 focusing on hippocampal tissue samples from AD patients and healthy controls. Raw RNA-Seq data were processed using the FASTQC tool for quality control, followed by trimming of low-quality reads with Trimmomatic. The cleaned reads were then aligned to the human reference genome (GRCh38) using STAR aligner. Differential gene expression analysis was conducted with DESeq2, identifying 1,200 differentially expressed genes (DEGs), with 680 genes upregulated and 520 downregulated in AD samples. Upregulated genes were enriched in inflammatory and immune response pathways, including TYROBP and TREM2, which are known to be involved in microglial activation. Downregulated genes were predominantly linked to synaptic transmission and neuroplasticity, including GRIN2B and GABRB1. Pathway enrichment was assessed using Gene Ontology (GO) and KEGG pathway analysis, revealing disruptions in oxidative stress response, lipid metabolism, and mitochondrial function. Network analysis with Cytoscape identified hub genes such as APP, PSEN1, and CLU, central to AD-related pathways and potential therapeutic targets. Non-coding RNA alterations, including microRNAs and long non-coding RNAs, were also identified, indicating a broader regulatory role in AD pathology. This study provides valuable insights into the transcriptomic changes in AD, highlighting key genes and pathways implicated in disease progression. The identified DEGs and pathways offer potential biomarkers for early diagnosis and therapeutic targets.

Keywords: Alzheimer’s disease, RNA-Seq, Differential gene expression, KEGG pathway, transcriptomic analysis

ORAL PRESENTATIONS

OP01

Assessment of genomic fidelity by using RAPD markers of Vitexnegundo L., an important Indian medicinal plant

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Abstract

The straightforward method known as Random Amplified Polymorphic DNA (RAPD) can be used to evaluate genotoxicity because it uses a small amount of DNA for PCR amplification. The investigation that assessed the efficacy of RAPD in detecting genetic integrity and geneflow in V. negundo explants treated with various plant growth regulators. Steroids, flavonoids, lignans, and terpenoids found in Vitex negundo, an Indian medicinal plant, can be utilized as precursors for industrial manufacture. To evaluate the genetic integrity of Vitex negundo, an effective marker technique that includes Random Amplified Polymorphic DNA (RAPD) was utilized. In this study, RAPD has been performed with in vitro plantlets of Vitex negundo and mother plant and correlated the presence of genomic integrity of the in vitro raised plantlets. Various growth regulators such as 6-benzylaminopurine (BAP), di-phenyl urea (DPU), thidizuron (TDZ) and meta-topolin (mT) were added to in vitro plantlets and grown on MS medium. Thirty-one of the 150 unique bands produced by six of the thirteen RAPD primers were polymorphic, with a mean of 5.16 polymorphic bands for each primer. The amplicons ranged in size from 100 to 1500 base pairs, with a maximum of 32 fragments amplified and an average of 25 fragments per primer. With a mean of 16.6, the polymorphism percentage ranges from 12.9 to 22.5. For RAPD primers, the PIC values varied from 0.11 to 0.63. According to the study, RAPD markers assess genomic integrity of Vitex negundo. All in vitro grown plantlets treated with various plant growth regulators were categorized as BAP, DPU, TDZ, and mT by the UPGMA cluster analysis and this pattern of clustering is also supported by the principal component analysis. The molecular marker technique was helpful in determining high levels of genetic fidelity and in estimating the genetic relationships between mother plant V. negundo accessions and in vitro-raised plantlets treated with various plant growth regulators.

Keywords: Genetic fidelity, Molecular marker, RAPD, Vitex negundo, Polymorphism, plant growth regulators, clustering, analysis.

OP02

Zerovalent Iron Nanoparticles Synthesized from Plant Extracts for Heavy Metal Removal

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Abstract

Groundwater is frequently contaminated with heavy metals, which poses a risk to human and ecological health. Iron nanoparticles (nFe) are very effective at extracting heavy metals from aqueous solutions due to their huge specific surface area. But as the conventional reductive synthesis of nFe is somewhat costly and frequently results in secondary contamination, a low-cost green synthetic technique utilizing plant extracts needs to be developed. Over the last few years, research has been conducted on nanoscale metallic iron (nZVI) as a potential novel solution for water contaminated with heavy metals. The type of heavy metal and its thermodynamic characteristics determine the removal processes. The reduction process removes a metal whose redox potential is more negative or near to the reduction potential of Fe(0), while precipitation, complexation, or other sorption processes mediate the removal of the other metals. Because of its greater reactivity than micro zero valent iron, cost-effectiveness, and capacity to treat a wide spectrum of contaminants, nano zero valent iron(nZVI) has recently attracted interest as a remediation technique for contaminated land and groundwater. According to recent studies, nZVI may effectively remediate inorganic pollutants including Ni2+, PO43-, Co2+, and Cu2+ as well as organic pollutants such azo dyes, halogenated organic compounds, and pharmaceutical waste.

Keywords: Adsorption; Biomolecules; Green Synthesis; Zero-valent iron

OP03

Phytocompounds to regulate the MDR *A. baumannii* infection: An *In-silico* strategy

Sukriti Singh[1], **Jyotsna Agarwal[3]**, **Anupam Das**, **Mala Trivedi[1]**, **Manish Dwivedi[1,2]**
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Abstract

Many major multidrug-resistant (MDR) infections are caused by bacteria belonging to the & quot; ESKAPE & quot; group, which includes *A. baumannii*. Particularly in hospital settings, the organism has produced variants resistant to both single and multiple medications due to its rapid adaptability to environmental signals. Using an in silico subtractive genomics technique and considering the Omp33-36 porin as a potential therapeutic target, we have established in this work the regulatory potential of phytocompounds of selected plants against *A. baumannii*. Following the extraction and preparation of the target receptor protein (Omp33–36), the putative ligands from three plants—*Andrographis paniculata, Cascabela thevetia*, and *Prosopis cineraria*—were assessed for their potential to treat infectious illnesses in light of previous research. The IMPPAT database was initially used to identify seventy possible phytocompounds from the chosen plants. A phytocompound & its potential as a treatment was assessed utilizing physio-chemical characterizations using ADMET prediction and toxicity assessment using ProTox prediction. Furthermore, using Autodock Vina, interaction experiments of 15 out of 70 compounds with the target Omp33-36 protein utilizing PDB id 6GIE were carried out. After careful consideration, seven compounds with the highest binding affinities—this ranged from -7.2 Kcal/mol to -7.9 Kcal/mol—were selected. Molecular dynamics (MD) simulations using the Amber 20 program were performed. Partial charges were calculated and the receptor protein and docked ligands were optimized using GAUSSIAN 09. RMSD analysis revealed few aberrant interactions for complexes comprising Tamarixetin and Quercitin. Wogonin showed instability all through the simulation, while Prosogerin A showed stability for 160 ns until significant divergence. Based on RMSF analysis, all complexes showed similar atomic variations, however Quercitin and Tamarixetin showed continuous fluctuations after initial residues. Greater oscillations were observed for Wogonin. It is possible to determine each complex & its stability and binding affinity by calculating its binding free energy. The two medications with the most consistent interactions, Quercitin and Tamarixetin, showed promise as A. baumannii therapy leads.

Keywords- *A.baumannii*, Omp 33-36, phytocompounds, binding energy, therapy leads.

OP04

The Future of Dairy: Cellular Agriculture's Impact on Milk and Dairy Products

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Abstract

Cellular agriculture is an emerging technology that enables the production of animal-derived products, such as milk, without the need for livestock. By utilizing cells containing specific genetic codes or engineered microbes in controlled environments like fermenters or bioreactors, cellular agriculture replicates essential molecules found in traditional animal products. This process, known as protein-based engineering, has been widely applied in fields such as insulin production. It offers a more sustainable, ethical, and scalable method for manufacturing milk and other animal-based products for mass consumption. The benefits of cellular agriculture extend far beyond efficiency. Environmentally, it significantly reduces greenhouse gas emissions, land use, and water consumption compared to conventional livestock farming. Cellular agriculture also represents a humane alternative by sparing animals from the often-harsh conditions of industrial farming. Additionally, for human health, products developed through cellular agriculture can be precisely engineered to be free from pathogens, antibiotics, and hormones, offering safer and potentially healthier options for consumers. In terms of food justice, it has the potential to make nutritious animal-derived products more accessible to populations affected by food insecurity. Furthermore, cellular agriculture is designed to replicate the taste, texture, and nutritional profile of conventional animal products, ensuring that consumers experience no compromise in flavor or quality. Cellular agriculture holds immense promises addressing many of the environmental, ethical, and health challenges associated with traditional food systems. With further advancements, this technology could pave the way for a more equitable and sustainable food future, reducing the need for intensive animal farming while providing high-quality, animal-based products to a growing global population.

Keywords: cellular agriculture, sustainable, genetic codes, animal-based, protein-based Engineering

OP05

Screening and Evaluation of Anti-Cancer Potential of *Withania somnifera* Phytochemical through *In-silico* study

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Abstract

Ashwagandha (*Withania somnifera*) is one of the most used medicinal plants in Ayurvedic system of medicine and has been subjected to a plethora of investigations in relation to its pharmacological properties, including anti-tumor effects. The objective of this study is to assess the anti-cancer efficacy of *Withania somnifera* using biomolecular screening in *in-silico* methods. *In-silico* targeting was used to evaluate the major bioactive metabolites of *Withania somnifera* such as withanolide and alkaloid against molecular targets associated with cancer diseases. The molecular docking analysis of the phytochemicals was performed to estimate their binding modes and their likelihood of interacting with the specific proteins associated with cancer, like p53, HER2, and EGFR. Outcome obtained from these computational models showed that within these phytochemicals, withanolide A and withanolide D has a potent binding affinity of -9.1 and -8.5 to these targets hence supporting the evidence for the apoptosis inducing activity, anti-angiogenic property and cell cycle modulator of cancer cells. These results of in-silico screening imply that *Withania somnifera* possesses substantial anti-cancer potentiality because of its phytochemical constituent, which has the potency to act directly on the carcinoma cells and to combat those bacteria also which lead to the commencement of carcinogenic process. Further experimental studies, in *in-silico* analyses are warranted to confirm these findings and explore the herb's therapeutic potential in cancer treatment.

Keywords: Ashwagandha, cancer, bioactive compounds, apoptosis, bacterial infection

OP06

Role Played by Th2 type Interleukins in IgE mediated Asthma and TheirAssociation with Transfluthrin Mosquito Repellent as a Risk Modifier

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Abstract

Introduction/Objective: Mosquito repellents contain Transfluthrin (TFT), which is one of the most frequently used in-house to prevent mosquito-borne diseases, such as dengue and malaria, which are most common in India. Type 2 helper T cells (Th2) play a triggering role in the activation/recruitment of IgE antibody-producing B cells. Exposure to TFT is responsible for a shift of Th2 balance in the immune system towards the pre-allergic Th2 response. Th2 secrete Interleukin (IL-4, IL-5, IL-13) and regulate IgE and eosinophil-mediated responses. So, in this study, we have hypothesized that children's exposure to TFT-based mosquito repellants may trigger childhood asthma and follow the Th2 pathway by influencing the levels of IL-4, IL-5, and IL-13 and their association with TFT and IgE levels. Methods: TFT +ve (n=47) and TFT -ve (n=33) were recruited and IgE was estimated using a Beckman Coulter analyzer (AU480). The serum TLF levels were measured using a gas chromatography triple-quadrupole mass spectroscopy. IL-4, IL-5, and IL-13 were measured byusing Sandwich ELISA method. Results: TFT +ve asthmatic children had significantly increased IgE (1.6-fold), IL-4 (1.8-fold),IL-5 (2.3-fold), and IL-13 (3.7-fold) levels than TFT -ve asthmatic children ($p<0.0001$). TFT was significantly higher in asthmatic children (1.38±0.91 vs. control 0.69±0.41µg/L,$p<0.0001$). FEV1(L) and FEVI/FVC ratio were significantly reduced in TFT +ve asthmatic children ($p<0.05$). TFT levels were correlated with IL-4 ($r=0.542$; $p<0.0001$), IL-5 ($r=0.493$; $p<0.0001$), and IL-13 ($r=0.355$; $p<0.0001$). IgE levels were also correlated with IL-4 ($r=0.879$; $p<0.0001$), IL-5 ($r=0.981$; $p<0.0001$), and IL-13 ($r=0.795$; $p<0.0001$). Conclusion: TFT increases the risk of asthma by triggering the interleukins of Th2 pathwayof allergic asthma and also influences the IgE level.

Keywords: Transfluthrin, IgE, IL-4, IL-5, IL-13, Th2, TFT

OP07

Integrative Approach to Assessing the Anticancer Potential of Leaf Extractson Breast Cancer Cell Lines: Insights from In Silico and In Vitro Studies

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Abstract

Natural compounds are gaining attention as promising alternatives in cancer therapy due to their potential for targeted treatments with fewer side effects compared to conventional drugs. This study investigates the anticancer potential of leaf extracts against breast cancer, with a specific focus on the Luminal A subtype, a hormone-driven form that presents unique therapeutic challenges. While natural compounds have been widely explored in cancer research, there remains a gap in understanding their efficacy and mechanisms against specific breast cancer subtypes, particularly Luminal A. Addressing this gap is crucial for advancing safer, targeted therapeutic options that may complement or replace traditional cancer treatments. The aim of this study is to evaluate the anticancer properties of leaf extracts on Luminal A breast cancer cell lines, using a combination of in silico computational modeling and in vitro experimentation. By utilizing molecular docking and dynamic simulations, bioactive compounds within the extracts are screened for their potential to inhibit key proteins involved in cancer cell proliferation and survival. This integrative approach is followed by biological validation through in vitro assays. Preliminary results suggest that the leaf extracts contain potent compounds capable of selectively targeting breast cancer cells, particularly within the Luminal A subtype. These findings provide a strong basis for further exploration, including testing in animal models and deeper investigations into the molecular mechanisms of action. This research contributes to the growing field of natural therapeutics for cancer, offering theoretical insights into the use of bioactive compounds for breast cancer treatment. It also presents practical implications for developing safer, natural alternatives to conventional therapies, with the potential for future clinical application.

Keywords: Cancer therapy, luminal A subtype, breast cancer, phytochemicals, natural compounds

OP08

Different Phytohormones and their combinations response on the regeneration potential in the nodal explant of *Rosa hybrida* L.

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Abstract

This study investigates the impact of diverse phytohormone compositions and concentrations on the growth regeneration of *Rosa hybrida* L. nodal explants for micropropagation. Nodal explants were cultivated on five distinct MS media incorporating varying levels and combinations of Indole Butyric Acid (IBA), Benzyl Aminopurine (BAP), and Naphthalene Acetic Acid (NAA). Treatments included A-1 (IBA 400 ppm, BAP 125 ppm), A-2 (IBA 650 ppm, BAP 175ppm), A-3 (IBA 900 ppm, BAP 225 ppm), B-1 (BAP 900 ppm, NAA 90 ppm), and B-2 (BAP 450 ppm, NAA 45 ppm). Under optimized culture conditions, explants were monitored for growth and contamination over 30 days. Results analysis revealed that the A-2 hormone combination exhibited the highest regeneration potential in *Rosa hybrida* L. nodal explants among the five treatments (A-1, A-2, A-3, B-1, & B-2). This suggests that the specific concentration of IBA and BAP in A-2 treatment significantly influenced the regenerative capacity of the nodal explants. These findings contribute valuable insights into optimizing micropropagation protocols for *Rosa hybrida* L., offering potential applications in large-scale production and conservation efforts.

Keywords: Nodal explant; Micropropagation; phytohormones; Indole butyric acid; Benzyl Aminopurine ; Naphthalene acetic acid.

OP09

Niobium Mxene-Enhanced Quartz Crystal Microbalance (QCM) Based Piezoelectric biosensing for Cardiac Troponin I Point-of-Care Diagnosis

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Abstract

The increased need for oxygen in the cardiac muscle due to the rupture or destruction of atherosclerotic plaques is known as myocardial infarction (MI), a cardiovascular illness. The death rates linked to MI are continuously rising on a global scale. Due to a number of limitations with traditional diagnostic biomarkers used in clinical settings for MI diagnosis, researchers are searching for quick, accurate, and extremely sensitive biosensor platforms and technologies. The methods currently employed for the detection of cardiac troponin I (CTnI) are inadequate for point-of-care testing (POCT), clinical diagnosis, and screening. Therefore, to increase the signal and offer an oriented immobilization surface, we developed and assessed a QCM-based immunosensor by modifying its surface with Niobium MXene (Nb_4C_3). 2D nanomaterials such as Nb MXene, are used in sensor applications because of their distinctive characteristics, which include high hydrophilicity, strong metallic conductivity, and ease of functionalization. Anti-CTnI antibodies were immobilized utilizing NHS/EDC chemistry after coating Nb_4C_3 on the gold electrode surface. The homogenous distribution of Nb_4C_3 with high density and purity on the surface was validated by FTIR, XRD, BET and RAMAN. The immunosensor demonstrated strong cTnI recognition following antibody immobilization, within concentration range of 2 ng/mL-100 ng/mL. The developed sensor further exhibited a LoD and sensitivity of 0.16 ng/mL and 0.37 Hz/ng/mL respectively. The proposed biosensor utilizes the unique features of quartz crystal microbalance (QCM) technology to overcome the drawbacks of existing diagnostic techniques, such as low sensitivity and time-consuming. A low limit of detection (LoD), rapid output, excellent sensitivity, and specificity are attributes that make the biosensor ideal for clinical applications.

Keywords: Myocardial infarction (MI), Cardiac troponin I (CTnI), Point-of-care testing (POCT), Niobium MXene (Nb_4C_3), Quartz crystal microbalance (QCM), Piezoelectric biosensing

OP10

Investigating the efficacy of natural bioactive compounds against NLRP3 inflammasome mediated oral carcinogenesis: An *in silico* approach

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Abstract

Inflammation has been reported to play an important part in the development of tumor and carcinogenesis. Among the different types of pattern recognition receptors (PRRs), NLRP3 has been shown to play a key role in inflammation mediated progression of different types of cancer, including oral cancer. In this work, *in silico* analysis and drug screening using natural compounds has been performed to assess the effectiveness of the selected compounds against NLRP3, in order to develop novel anti-oral cancer treatment strategies. Seven bioactive compounds of *Withania somnifera* (Ashwagandha), i.e., Withaferin A, Withanone, Withanolide A, Withanolide D, Withanolide E, Withanoside IV, and Withanoside VI, were selected based on their biomedical and anticancer properties from previous research works. In order to determine the drug-likeness of these compounds the SwissADME tool was utilized, which predicts the ADME parameters of such compounds. It was found that five of these compounds, i.e., Withaferin A, Withanone, Withanolide A, Withanolide D, and Withanolide E, can act as potential drug molecules, as these had 0 Lipinski violations, whereas two compounds, i.e., Withanoside IV and Withanoside VI, will not be suitable drug molecules, as these had 3 Lipinski violations (MW>500, N or O>10, NH or OH>5). The five compounds were then analyzed further by docking them against the target NLRP3 protein using PyRx software. All the five compounds showed good or minimum binding energy/affinity with NLRP3, with binding affinity values (in kcal/mol) as: Withaferin A (-9.8), Withanone (-9.1), Withanolide A (-9.5), Withanolide D (-9.2), and Withanolide E (-8.3). This study therefore concludes that the five natural bioactive compounds from *Withania somnifera* (Ashwagandha), i.e., Withaferin A, Withanone, Withanolide A, Withanolide D, and Withanolide E, demonstrate significant promise as potential drug leads against NLRP3 inflammasome facilitated oral cancer.

Keywords: NLRP3, Oral Cancer, *in silico*

OP11

Synergism between coliphage ASEC2201 and various antibiotics of different generation

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Abstract

With the growing investment of 22 billion $ per year in America alone, multi-drug resistance has become a major problem for clinicians. The use of bacteriophages is an attractive approach to overcome the problem of drug resistance in several pathogens that cause fatal diseases. This study aimed to isolate lytic bacteriophages from sewage water using clinical strains of *Escherichia coli.* Sewage water sample collected from Bharwara Sewage Treatment Plant (BSTP), Lucknow and later physio-chemically characterized. *E. coli* samples used in this study were aseptically collected from Ram Manohar Lohia Institute of Medical Sciences, Lucknow. Isolated coliphage had been amplified and tested *in vitro* for lytic activity against these MDR. In vitro analysis of the antibiotic susceptibility test suggested that for some of the antibiotics, no zone of inhibition was observed against the clinical isolates of *E. coli*, *Bacillus* and *Staphylococcus.* The synergistic results showed promising results while using ASEC2201 with different antibiotics such as cefepime 30 mcg for *E. coli*, cefadroxil 30 mcg for *Bacillus* and Imipenem, cilastin 10 mcg for *Staphylococcus* with a clear zone of inhibition observed 10 mm, 12 mm, 15 mm. However, more study is needed for phage therapy to be an ideal alternative and potential therapeutic option to combat the problem of drug resistance in case of fatal pathogenic infections.

Keywords: Bacteriophage, Antimicrobial resistance, Drug resistance, Protein, Synergistic effects

OP12

Antimicrobial Properties of Rose Plant Extracts Against Antibiotic Resistant Bacterial Strains

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Abstract

The growing concern regarding the emergence of antibiotic-resistant bacterial strains has ledto an increased interest in exploring alternative sources of antimicrobial agents. This study aimed to evaluate the antimicrobial property of the rose plant (Rosa spp.) against a specific bacterial strain. A bacterial strain was isolated and identified using standard microbiological techniques. Extracts from parts of the rose plant flower were prepared using various solvents (hexane, distilled water and ethyl acetate). The antimicrobial activity of the rose plant extracts was assessed using a well diffusion method. The zones of inhibition were measured. reliance on conventional antibiotics. The rising concerns regarding antibiotic resistance have necessitated the search for alternative sources of antimicrobial agents, and plants have long been recognized as valuable reservoirs of bioactive compounds. The rose plant extracts were tested against the bacterial strain using standard microbiological methods. the mechanism of action of the active components will be elucidated to better understand their mode of inhibition against the bacterial strain. These findings could contribute to the development of novel antimicrobial agents derived from the rose plant, potentially providing alternative treatment options against antibiotic-resistant bacteria. This study demonstrates the potential antimicrobial activity of rose plant extracts against a selected bacterial strain. The results highlight the importance of exploring natural sources for novel antimicrobial agents and emphasize the significance of plant-based therapeutics in the fight against antibiotic resistance. These findings indicate that the rose plant possesses promising antimicrobial potential against the bacterial strain under investigation. Further investigations are warranted to fully harness the antimicrobial potential of the rose plant and its bioactive constituents.

OP13

Extraction and Characterization of *Xanthomonas citri* from Citrus Canker Lesions on Lemon Trees

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Abstract

Citrus canker, caused by *Xanthomonas citri*pv. citri, is a devastating bacterial disease affecting citrus plants worldwide, particularly lemon trees. This study focuses on the extraction and characterization of *X. citri* from infected lemon tree leaves, a crucial step in disease diagnosis, epidemiological research, and development of control measures. The extraction method involved collecting symptomatic leaves with typical canker lesions, surface sterilization, and crushing in sterile saline solution. Successive dilutions were plated on nutrient agar and selective media (tryptic soya broth and agar) designed for *Xanthomonas* species. After incubation, distinctive yellow, mucoid colonies were identified using morphological criteria. The retrieved bacterial isolates were evaluated for virulence by inoculating healthy lemon leaves, which subsequently developed typical canker symptoms, confirming pathogenicity. This research highlights the importance of accurate pathogen extraction for effective disease management and control. Understanding *X. citri*'s biology and behavior in its natural habitat is crucial for developing resistant citrus varieties and implementing targeted strategies to prevent citrus canker spread. The extraction technique described here facilitates disease detection in various citrus crops, enabling timely management measures and improved tracking of disease progression across different geographic locations. In conclusion, the successful extraction and identification of *X. citri* from citrus canker-infected leaves contribute significantly to advancing citrus canker research and enhancing disease management strategies in citrus-producing regions worldwide.

Keywords: Citrus canker, *Xanthomonas citri*, virulence, pathogenicity, epidemiology, lemon trees, disease management

OP14

Anticancer potential of cisplatin and mangiferin in combination on osteosarcoma cell line.

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Abstract

Osteosarcoma, a prevalent primary bone malignancy affecting young adults, is primarily treated with surgery and high-dose chemotherapy. While traditional agents like cisplatin, doxorubicin, and ifosfamide show promise, they often face limitations due to drug resistance and adverse effects. Recently, innovative treatment strategies have emerged, including combination therapy, immunotherapy, hormone therapy, and stem cell therapy, offering renewed hope for improved patient outcomes and enhanced treatment efficacy. In this preclinical study, combination of mangiferin and cisplatin has been investigated for the treatment of osteosarcoma in vitro. To evaluate the anti-cancer potential of mangiferin and cisplatin in combination anti-proliferative potential of the combination on MG-63 cells were analyzed using MTT assay and apoptosis assay. Combination of cisplatin and mangiferin displayed inhibition of cell proliferation in the combination group which was significantly high when compared with that of single drug groups. In conclusion, mangiferin is cytotoxic to MG-63 cells in vitro and potentially enhances the cytotoxicity of cisplatin synergistically in osteosarcoma.

OP15

Gut Microbiota's Role in Cardiovascular Disease: Mechanisms of Dysbiosis and Therapeutic Insights

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Abstract

The gut microbiota, a complex ecosystem of microorganisms in the human gastrointestinal tract, plays a crucial role in various physiological functions, including metabolism, immune modulation, and maintenance of intestinal homeostasis. An imbalance in gut microbiota, known as dysbiosis, is linked to the onset and progression of numerous diseases, especially cardiovascular diseases (CVDs). Cardiovascular diseases (CVDs) encompass a range of disorders of the heart and blood vessels, often leading to severe and life-threatening conditions such as myocardial infarction, stroke, hypertension, and atherosclerosis. This review offers a comprehensive overview of the types of microorganisms in the gut (such as lactobacillus, clostridium, bifidobacterium, etc.), their role in health and disease, and how changes in their levels can contribute to the development and progression of cardiovascular conditions. The review also highlights the mechanisms through which dysbiosis contributes to CVDs, including the disruption of the gut barrier integrity leading to a "leaky gut", systemic inflammation, and the release of harmful metabolites such as trimethylamine-N-oxide (TMAO) and short-chain fatty acids (SCFAs) into the systemic circulation. The study emphasizes potential therapeutic approaches targeting gut microbiota to manage and reduce the risk of cardiovascular diseases.

Keywords: Gut microbiota, Dysbiosis, Cardiovascular Diseases (CVDs), Leaky Gut, TMAO

OP16

Revolutionizing Bioavailability: Next-Gen Drug Delivery Solutions

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Abstract

The advancement of pharmaceutical sciences has led to the development of innovative drug delivery systems aimed at overcoming the challenges associated with low bioavailability of drugs. This review paper comprehensively explores the recent advancements in novel drug delivery systems designed to enhance the bioavailability of various therapeutic agents. The focus is primarily on strategies such as nanoparticles, liposomes, micelles, nanocrystals, and solid dispersions, which offer unique approaches to improve the solubility, stability, and targeted delivery of poorly water-soluble drugs. The paper critically analyzes the formulation techniques and the impact of these novel delivery systems on drug absorption and distribution in the body. Additionally, the review discusses the potential applications of these technologies in the treatment of various diseases, emphasizing the significance of personalized medicine and tailored drug delivery approaches. It also aims to provide a comprehensive overview of the current state of research in the realm of novel drug delivery systems, offering valuable insights for researchers, practitioners, and policymakers in the pharmaceutical industry and academia.

OP17

Exploring Phytochemicals as Potential Therapeutics for Frontotemporal Dementia

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Abstract

A neurodegenerative condition known as frontotemporal dementia (FTD) is characterized by the gradual degeneration of the brain's frontal and temporal lobes, which results in severe behavioural and cognitive abnormalities. There is still a lack of effective treatment alternatives, which makes novel strategies to address FTD at the molecular level necessary. Known for their wide range of bioactive characteristics, phytochemicals have drawn interest due to their neuroprotective benefits. This work focuses on using in silico docking method, to predict and assess phytochemicals as possible therapeutics for FTD. An assortment of phytochemicals was tested against important protein targets connected to the mechanism of FTD. To predict the binding affinity and interaction patterns of these chemicals, auto-docking simulations were carried out using auto-docking software CB-Dock2. The findings showed several substantial binding affinities and advantageous interaction patterns with disease- associated proteins in numerous viable candidates. Interestingly, substances like ladostigil, Luteolin, Triterpenoids, Lycopene, Spicatoside and Withanolides have shown promise in stabilizing protein conformations and preventing aggregation a distinctive feature of familial thyroid disease (FTD). Current research highlights the possibilities for treating neurodegenerative diseases by acting as a first step toward creating innovative, plant-derived therapies for FTD.

Result: Molecular docking studies were performed to evaluate the binding affinities of various compounds with the 6T4B protein. The Vina scores indicated that Withanolide A exhibited the strongest binding affinity (-8.1), followed by Spicastoside (-7.6) and Luteolin (-7.4). Other compounds, such as Triterpenoid (-7.1), Lycopene (-6.3), and Ladosteil (-5.8), also showed moderate binding affinities. These results suggest that Withanolide A and Spicasoside could be promising candidates for further investigation in therapeutic applications involving the 6T4B protein.

Keywords: Frontotemporal, Dementia, FTD, Phytochemicals, Docking

OP18

Impact of Letrozole-Induced Polycystic Ovary Syndrome on Bone Histopathology in Mice

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Abstract

Polycystic ovary syndrome (PCOS) predominantly causes adverse effect on overall health of women, leading to reproductive and metabolic dysfunction. This study aims to evaluate the effect of PCOS on bone histopathology in mice additionally demonstrating that letrozole only induces polycystic ovaries with no sign of toxicity in the organs. Female BALB/c mice were divided into two groups: a control group and a PCOS group, which received letrozole (6 mg/kg b.w./day) in 0.9% NaCl orally for 21 days to induce PCOS. Presence of polycystic ovaries, organ safety evaluation and effect of PCOS on bone histopathology was done using hematoxylin-eosin staining. The control group exhibited a normal estrous cycle with all phases, while the PCOS group showed diestrus phase, characteristic of PCOS. Histological analysis revealed that control ovaries had numerous corpus luteum and follicles at various stages, whereas PCOS ovaries exhibited an increased number of immature and atretic follicles, along with multiple cystic follicles. Liver and kidney analyses showed no signs of toxicity, with normal hepatocyte morphology and no structural changes in glomeruli or renal tubules. Thus, letrozole effectively induces PCOS without adverse effects on these organs. H&E staining of femur bone indicated that the PCOS group had thinner and more scattered trabecular bone, with a decreased number of trabeculae and widened trabecular gaps compared to the control group. Our result suggests that PCOS has an adverse effect on trabecular bone health.

Keywords: PCOS, Bone, Histology, letrozole, Trabecular bone.

OP19

Investigating Protein-Protein Interactions in Apoptosis Pathways of Cancer Cells for Targeted Therapeutic Approaches

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Abstract

Apoptosis, or programmed cell death, is an essential physiological process that maintains cellular homeostasis and eliminates damaged or dysfunctional cells. In cancer, the dysregulation of apoptotic pathways allows malignant cells to evade death, contributing to tumor progression and resistance to conventional therapies. The intricate mechanisms underlying apoptosis in cancer cells is vital for developing targeted therapeutic strategies that can effectively induce cell death in tumors while minimizing harm to healthy tissues. Understanding the molecular interactions that govern apoptosis is crucial for identifying potential therapeutic targets. This study aims to elucidate the protein-protein interactions (PPIs) involved in the regulation of apoptosis pathways in cancer cells using the STRING database. By leveraging the STRING database, we will map and analyze the interactions of key proteins implicated in apoptosis pathways. Our study will focus on identifying high-confidence interaction networks, functional enrichments, and potential druggable targets that could potentially restore apoptosis in cancer cells. The selected proteins are BCL-2, BAX, BAK, CASP3, CASP9, SMAC. Our Analysis revealed that the P53 signaling pathway was enriched significantly in the four investigated proteins as a common pathway. In addition, clusters associated with apoptosis and TRAIL signaling were common in the three investigated tissues. However, there were many more clusters made associated to cancer. Insights gained from this analysis may serve as a foundation for developing targeted cancer therapies.

Keywords: Apoptosis, programmed cell death, protein-protein interactions (PPIs), functional enrichments.

OP20

Identification of antibody-based biomarkers for myositis

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Abstract

Myositis is among one of the rare autoimmune diseases characterized by inflammation and weakness of the skeletal muscles which can also involve internal organs such as the lungs, heart, and esophagus. Approximately 1.2 to 19 per million individuals are diagnosed with myositis per year. Polymyositis (PM), Dermatomyositis (DM), Juvenile myositis (JDM) and Anti-synthetase syndrome (ASS) are some of the different kinds of myositis. It develops gradually where muscle weakness and soreness are common symptoms along with distinctive skin rashes seen on face, eyelids, knuckles and chest in case of dermatomyositis. Females are more susceptible to the disease than males by approximately 2:1 ratio. The disease generally occurs between the ages of 40-60 years. However, JDM may also occur between 5-15 years. Being an autoimmune disease, different kinds of myositis have been found to be associated with Myositis Specific Autoantibodies (MSA) and Myositis Associated Antibodies (MAA). The present study aims to identify diagnostic MSAs which may serve as biomarkers for specific types of myositis. For this, demographic and clinical data from 100 patients of myositis after informed consent were collected. Thereafter, data was analyzed through Microsoft excel to identify and associate MSAs with different types of myositis in the study population. Results showed that Anti RO52 is the most prevalent MSA in overall myositis population (n=100). For PM and ASS, anti RO52 is the most predominant MSA (23.5% and 40% respectively). However, in patients with PM, melanoma differentiation-associated protein 5 (MDA5) is equally prevalent with anti-RO52 (23.5%). Anti-transcription intermediary factor 1 gamma (anti-TIF-1g) was found to be the most predominant (14.28%) MSA for DM. The analysis suggests that the occurrence of anti-TIF-1g in serum may indicate that the patient is suffering from DM. Similarly, prevalence of anti-RO-52 may indicate ASS. High amounts of anti-MDA5 and anti-RO52 in serum may suggest the possibility of PM. Identifying specific type of antibody may serve as biomarkers for a particular type of myositis which will ease the diagnosis and treatment process for the disease.

Keywords: Myositis, polymyositis, dermatomyositis, anti-synthetase syndrome, myositis specific antibody

OP21

Exhaustive Review on Vaccine Drug Delivery Systems

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Abstract

Vaccines are the preparations given to patients to evoke immune responses leading to the production of antibodies (humoral) or cell-mediated responses that will combat infectious agents or noninfectious conditions such as malignancies. Alarming safety profile of live vaccines, weak immunogenicity of sub-unit vaccines and immunization, failure due to poor patient compliance to booster doses which should potentiate prime doses are few strong reasons, which necessitated the development of new generation of prophylactic and therapeutic vaccines to promote effective immunization. Attempts are being made to deliver vaccines through carriers as they control the spatial and temporal presentation of antigens to the immune system thus leading to their sustained release and targeting. Hence, lower doses of weak immunogens can be effectively directed to stimulate immune responses and eliminate the need for the administration of prime and booster doses as a part of conventional vaccination regimen. This paper reviews carrier systems such as liposomes, microspheres, nanoparticles, dendrimers, micellar systems, ISCOMs, plant-derived viruses which are now being investigated and developed as vaccine delivery systems. This report also describes various aspects of “needle-free technologies” used to administer the vaccine delivery systems through different routes into the human body.

Keywords: Edible vaccines, micro needles, microparticulate, needle-free delivery.

OP22

New potential target for computational analysis-based therapy in *Alzheimer Disease*

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Abstract

Alzheimer's Disease is characterized as a Neurodegenerative disorder. It is a form of dementia. Dementia is characterized as a decline in cognitive abilities which mainly affects a person's thinking abilities or to perform daily activities. Alzheimer disease generally occurs at old age that is at 60 yr and according to survey Alzheimer disease occurs mostly in males than in females. Prevention of Alzheimer's Disease is very crucial for public health. With increasing days Alzheimer Disease's impact on people and society is becoming more prevalent. Since no cure or prevention of Alzheimer's disease exists yet, researchers suggest that if people modify their lifestyle, they can significantly reduce the risk of disease or can delay the onset of Alzheimer's Disease. In India 2019, there are approx. 3.69 million active cases of Alzheimer Disease are reported. In March 2015, 4.3% Alzheimer Disease are reported in India. The late stage of Alzheimer's Disease is severe as reported. It was ranked as the seventh leading cause of death in the US. Alzheimer Disease is common among older adults. Some research projects investigated two types of biomarkers used for the diagnosis of Alzheimer Disease include: Blood based Protein and Lipid Biomarkers from which they investigated the enzyme responsible for beta Amyloid generation. In the past 30 years, it has been observed that the main cause of Alzheimer Disease is the accumulation of abnormally folded proteins which leads to neuronal death. Features which have been discovered for Alzheimer Disease were Neurofibrillary tangles (NFTs) and Amyloid plaques. Therefore, the main cause of AD is the Neurofibrillary cascade and Amyloid cascades. In recent discoveries along with the amyloid hypothesis, the glymphatic system hypothesis and the dopaminergic system are also involved.

Keywords: Alzheimer Disease, Amyloid plaques, Acetylcholinesterase, Dementia, Tau, NFTs.

OP23

Advancements in Neuropathic Pain Management: Combining DrugTherapy and Exercise for Diabetic Neuropathy

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Abstract

Neuropathic pain (NP) is a complex condition resulting from damage to the somatosensory nervous system, frequently associated with diseases such as diabetes, HIV/AIDS, multiple sclerosis, and cancer. Unlike pain from external injuries, NP arises from internal nerve disruptions affecting both the Peripheral Nervous System (PNS) and Central Nervous System (CNS). Common symptoms include pain, numbness, tingling, and muscle weakness, with variations depending on the neuropathy type (e.g., mononeuropathy, polyneuropathy). NP can develop through mechanisms like metabolic dysfunction, infections, trauma, and autoimmune disorders, leading to abnormal nerve signaling. For instance, diabetic neuropathy is caused by hyperglycemia-induced nerve damage, while HIV-associated neuropathy involves peripheral nerve inflammation. Treatment remains challenging, with first-line options such as tricyclic antidepressants, serotonin-norepinephrine reuptake inhibitors, and gabapentinoids often providing partial relief. Advanced therapies, including neurostimulation and targeted drug delivery, offer alternatives for cases resistant to conventional treatments. This paper highlights the innovative approach of combining drug therapy with exercise for diabetic neuropathy, representing a promising advancement in treatment strategies.

Keywords: Somatosensory Nervous System, Neuropathic Pain, Combination Drug Therapy, Diabetic Neuropathy, Peripheral Nerve Damage

OP24

Investigating the Synergistic Effects of Honey on Healing and Antibacterial Activity in Burn Wounds Infected with Pseudomonas aeruginosa

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Abstract

Honey has been widely studied for its antimicrobial properties, particularly in wound care, due to its rich composition and ability to inhibit microbial growth. Honey's antibacterial activity is primarily due to its low pH, high sugar concentration, hydrogen peroxide production, and the presence of bioactive compounds like flavonoids and phenolic acids. These components work synergistically to create an environment hostile to bacterial growth. In this study, honey was used to investigate its efficacy against *Pseudomonas aeruginosa*, a common and opportunistic pathogen frequently associated with burn wound infections. *Pseudomonas* is known for its antibiotic resistance, making alternative treatments crucial, especially in burn patients where infections can lead to complications such as delayed healing, sepsis, and increased mortality. Previous research studies has demonstrated the effectiveness of honey against Pseudomonas aeruginosa in wound infections. Honey's antibacterial effects are mediated by hydrogen peroxide production and other phytochemical components that inhibit bacterial growth and biofilm formation. Honey's ability to disrupt *Pseudomonas* biofilm formation, which is critical in chronic wound infections. In this experiment, *Pseudomonas* cultures were treated with honey using the agar well diffusion method.

Keywords: Antimicrobial, honey, bioactive compounds, *Pseudomonas aeruginosa,* biofilm formation, wound infection.

OP25

Role of Filarial Heat Shock Proteins in Disease Progression

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Abstract

Lymphatic filariasis, a debilitating disease caused by parasitic nematodes, poses a significant global health burden. Despite decades of research and control efforts, the parasite's ability to evade the host's immune response remains a challenge. Heat shock proteins (HSPs), essential molecular chaperones, play a crucial role in parasite survival and virulence. This study aims to explore the potential of targeting filarial Heat Shock Proteins as a novel chemotherapeutic approach. The research involved a comprehensive literature review focusing on filarial biology, HSPs, and their role in parasitic infections. Specific areas of interest included the expression and function of Heat Shock Proteins in filarial parasites, their role in immune evasion, and the potential for developing HSP-targeting drugs. Additionally, the study investigated the feasibility of using nutraceuticals as a delivery mechanism for these drugs, aiming to improve drug bioavailability and reduce side effects. The review revealed that filarial parasites express various Heat Shock Proteins, including HSP70, HSP90, and small HSPs. These proteins are involved in a wide range of cellular processes, including protein folding, stress response, and immune evasion. Targeting Heat Shock Proteins could disrupt these essential functions, leading to parasite death or reduced virulence. Furthermore, the study identified potential nutraceuticals that could be used to deliver HSP-targeting drugs, such as curcumin and resveratrol. These compounds have been shown to have anti-parasitic properties and could enhance the efficacy of HSP-targeting therapies. In conclusion, this study highlights the potential of targeting filarial Heat Shock Proteins as a novel therapeutic approach for lymphatic filariasis. By disrupting essential cellular functions, HSP-targeting drugs could impair parasite survival and reduce disease progression. The use of nutraceuticals as delivery mechanisms offers promising avenues for improving drug efficacy and safety. Further research is needed to develop and evaluate HSP-targeting drugs in clinical trials.

Keywords: filariasis, parasites, nematodes, disease, chemotherapeutic

OP26

In silico identification of novel cutinase homologs for PET hydrolysis from phylum Actinomycetota

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Abstract

Plastic pollution is the most concerning problem of today's world, a sustainable method is needed to deal with. Microbial or enzymatic degradation can be a most promising approach, there have been many enzymes reported for hydrolysis of plastic, cutinase is one of them which can degrade polyethylene terephthalate (PET). Microbes from phylum Actinomycetota are widely reported for producing PET degrading cutinase and other cutinase like enzymes. In our study we selected 6 PET degrading cutinases from Actinomycetota as reference and explored other enzymes from this phylum for hydrolysis activity against PET. We got 131 homologs from BLASTp. Different computational tools were used to study domains, evolutionary and phylogenetic relationships, physiochemical, structural and functional properties. 51 proteins were found to have instability index less than 40 which ensures their stability, hydrophobic nature of proteins was determined by analyzing GRAVY index, 122 proteins fell into the high aliphatic index range (71.13- 143.54) which indicate their thermostability, since thermostability is a crucial parameter of PET degrading enzymes thus it supports our study, non-polar amino acids were found to be present in major portion in which alanine is predominant with average of 10 %. Secondary structure analysis was done using SOPMA tool that revealed major contribution of random coils. 3D homologous structures of most suitable enzymes were predicted and validated structures were selected for molecular docking. On the basis of mentioned *in silico* studies we found novel PET degrading enzymes from Actinomycetota.

Keywords: Biodegradation, plastic, PET, cutinase, sustainability, environment, computational analysis.

OP27

Advancing Pain Management: Integrating Mechanisms, Pathways, and Nutritional Approaches for Acute, Chronic, and Neuropathic Pain

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Abstract

Pain is a complex phenomenon involving persistent or recurring discomfort often unrelated to visible tissue damage. It serves as a critical warning system but becomes problematic when it transitions to chronic pain, which persists beyond the expected healing period and is commonly associated with conditions like arthritis and diabetes. This poster explores the intricate mechanisms of pain, highlighting advances in understanding both biological and psychological dimensions. Biologically, pain perception is influenced by genetics, nervous system function, immune responses, and endocrine factors. Pain signals start with peripheral nociceptors detecting noxious stimuli, which are transmitted via A and C fibers to the spinal cord's dorsal horn. These signals then ascend through second-order neurons to the thalamus and somatosensory cortex, where they are perceived as pain, primarily mediated by excitatory neurotransmitters such as glutamate and substance P. The descending pain pathway, originating in the brainstem, modulates this experience through neurotransmitters like serotonin, norepinephrine, and endogenous opioids, which can inhibit or enhance pain signals. Effective pain management requires a comprehensive understanding of these pathways, as dysregulation can contribute to chronic pain. Psychological factors, including anxiety and stress, can exacerbate pain, while resilience and coping strategies can aid in management. Recent research also emphasizes the role of nutritional interventions in pain management, providing new avenues for enhancing patient outcomes. This aims to integrate insights into pain mechanisms with practical approaches, including pharmacological treatments, psychological therapies, and nutritional strategies, to offer a holistic approach to improving patient care and quality of life.

Keywords: Chronic Pain, Pain Pathways, Nociception, Neurotransmitters, Multidisciplinary Treatment

OP28

Association of Elevated Arsenic and Nickel Levels with ER Stress Genes regulation and consequent Insulin Resistance in Type 2 Diabetes Mellitus Patients

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Abstract

The increasing global prevalence of type 2 diabetes mellitus (T2DM) necessitates investigating its complex etiology. This study aimed to explore the relationship between exposure to toxic metals, expression of endoplasmic reticulum stress response (ERSR) genes, and various biochemical parameters, including glycated hemoglobin (HbA1c), insulin resistance (HOMA-IR)/sensitivity (QUICKI), lipid profile, and estimated glomerular filtration rate (eGFR) in T2DM patients. T2DM patients and control subjects matched for age, gender, and lifestyle factors. Biochemical parameters, toxic metal levels, and ERSR gene expression were analyzed using inductively coupled plasma mass spectrometry (ICPMS) and quantitative reverse transcription PCR (qRT-PCR), respectively. T2DM patients exhibiting dysregulated lipid profiles and significantly higher fasting blood sugar (FBS), HbA1c, and insulin levels (all $p<0.0001$). The insulin sensitivity was lower in T2DM patients (0.32±0.09) than in the control group (0.35±0.02, $p=0.02$). Insulin resistance was significantly higher in the T2DM group (5.38±3.15) than in the control group (1.98±0.86, $p=0.0001$). Nickel (4.75±2.45 ppb, $p<0.0001$) and arsenic (1.85±1.78 ppb, $p<0.0001$) levels were significantly elevated in T2DM patients. There was significant upregulation of ER stress genes: GRP78, CHOP, IRE1, ATF4, ATF6, and XBP1 (all $p< 0.0001$), while PERK was significantly downregulated (0.68-fold, $p<0.0001$). Nickel levels were positively correlated with HOMA-IR ($r=0.49$, $p<0.0001$) and HbA1c ($r=0.35$, $p=0.002$). Arsenic levels were correlated with insulin ($r=0.34$, $p<0.0001$), insulin resistance ($r=0.51$, $p<0.0001$), HbA1c ($r=0.53$, $p<0.0001$), Arsenic levels ($\beta=0.37$, $p<0.001$), XBP1 ($\beta=0.36$, $p<0.0001$) independently associated with HbA1c. This study has revealed a significant association between arsenic exposure and the upregulation of XBP1 at the onset of T2DM. The overexpression of XBP1 and high levels of arsenic were independently associated with HbA1c and insulin resistance.

Keywords: T2DM, Toxic Metals, Endoplasmic Reticulum Stress Response (ERSR), Insulin Sensitivity/Resistance, Gene Expression.

OP29

In silico analysis of Fkbp4 as a stage specific marker to differentiate subtypes of Testis Germ Cell Tumor (TGCT).

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Abstract

Testis Germ Cell Tumor (TGCT) is a most common type of testicular malignancy (95%), manifesting mostly in adult men. In recent studies, TGCT have been characterized by aneuploidy, less alteration in genome and low levels of methylation, apart from pathological characterization. Expression of Cancer- Testis (CT) genes in TGCT have also been observed in tumors arising from non-germ cells. In our study, datasets from Genotype Tissue Expression (GTEx), The Cancer Genome Atlas (TCGA), Gene Expression Profiling Interactive Analysis (GEPIA) showed that expression of Fkbp4 in TGCT showed significant difference as compared to the normal testis tissues. FKBP4 belongs to families of peptidyl proline cis-trans isomerase (PPIase), which catalyses the cis-trans isomerization in peptide bonds which comes before proline. PPIases are engaged in numerous cellular processes, and when these processes go awry, can cause both neoplastic and degenerative disorders. Fkbp4 expression increases along with successive stages of the TGCT. The correlation of FKBP4 with other biomarkers (SALL4, NANOG, SOX2, FKBP4, SOX17 and KIT) of TGCT was also studied. Analysis showed the increased hazard ratio (HR) in case of overall survival (OS) as compared to the disease-free survival (DFS) in TGCT patients. Furthermore, gene ontology enrichment analysis was performed with upregulated genes in TGCT using DAVID tools. To decipher the pathway regulating the proliferation of TGCT, FKBP4 interaction analysis was conducted using STRING, which shows the interaction with known biomarkers of TGCT. All this dataset of expression profile, correlation, and interaction analysis of FKBP4 in TGCTs significantly represents FKBP4 as a potential biomarker for TGCTs.

Keywords: TGCT, FKBP4, GTEx, TCGA, GEPIA, PPIases

OP30

Exploring the Potential of Banana Pseudostem Extract as a Bioactive Agent: MIC and Antimicrobial Efficacy

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Abstract

Banana pseudostems have a complex chemical composition that makes them valuable for various applications. They primarily consist of cellulose (approximately 31-35%), hemicellulose (14-18%), and lignin (15-18%), along with pectins, waxes, and other organic compounds. This high cellulose content, combined with the presence of minerals like potassium, calcium, and magnesium, makes pseudostems an excellent candidate for "best out of waste" initiatives. After harvesting bananas, the pseudostems are often left as agricultural waste, but their fibrous nature and chemical makeup allow for innovative recycling. As per study banana pseudostem is a potent source of phytochemicals that includes flavonoids, phenols and antioxidants. The LC-MS (Liquid chromatography – mass spectroscopy) report tells the abundance of 6 – (Gamma, Gamma – Dimethylallylamino) Purine Riboside from positive mode and 2´ – Deoxyinosine from negative mode. This study investigates the antibacterial potential of banana pseudostem extracts using the Minimum Inhibitory Concentration (MIC) method. The methanolic extract of banana pseudostem was prepared and the antibacterial activity was evaluated against a range of pathogenic bacteria. The findings of the study suggest that banana pseudostem extracts possess promising antibacterial properties, potentially offering a natural alternative to synthetic antibiotics. Further research is warranted to isolate and characterize the active compounds responsible for this antibacterial activity, as well as to explore potential applications in medicine and food preservation.

Keywords: Agricultural waste, phytochemicals, MIC, antibacterial, synthetic antibiotics, medicine, food preservation.

OP31

Gene Therapy for Neurodegenerative Diseases

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Abstract

Gene therapy has the potential to provide therapeutic benefits for neurodegenerative illnesses by addressing pathogenic processes, protecting neurons, and managing symptoms. By focusing on the causes and signs of neurodegenerative diseases, gene therapy can help patients with these conditions. Success requires an understanding of the precise gene activity and the causes of disease. Making sure genes are delivered precisely and don't seep into other places is a difficulty. The most recent technology for accurate vector distribution is called interventional MRI-guided convection-enhanced delivery (iMRI-CED). This approach may hasten the creation of effective preclinical therapies for conditions including Alzheimer's, Parkinson's, and Huntington's. AAV-based gene treatments have shown promise in treating neurological illnesses, according to research. Adeno-associated virus (AAV) is a member of the Parvoviridae family and is favored for gene therapy due to its low immunogenicity profile, lack of disease-causing potential, and non-replicating nature AAV delivery is safe, even though some clinical trials have failed.

Keywords: gene therapy, neurodegenerative diseases, vectors, interventional MRI, AAV, Alzheimer’s disease, Parkinson’s disease, Huntington’s disease

OP32

TLR4 +896 A>G gene polymorphism and the risk of oral cancer

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Abstract

Oral cancer is heterogeneous cancer occurring in different parts of the head and neck area, including lips, cheeks, the palate, and salivary gland. Various etiological factors like tobacco smoking, alcohol consumption, and HPV infection are causative of oral cancer. The innate immune system's primary component is the pattern recognition receptor (PRR) family, including Toll like receptors (TLRs). TLRs detect invading pathogens and initiate an immediate immune response to them, followed by a long-lasting adaptive immune response. Activation of TLRs leads to the synthesis of pro-inflammatory cytokines and chemokines and the expression of co-stimulatory molecules. TLRs specifically recognizes bacterial lipopolysaccharide, along with several other components of pathogens and endogenous molecules produced during abnormal situations, such as tissue damage. The activation of TLR has been connected to the cancer invasion. Single-nucleotide polymorphism (SNP) has been identified in TLR4(rs4986790) by an A to G substitution at nucleotide position +896 resulting in an amino acid substitution A299G in the third exon of the TLR-4. The aim of this study was to evaluate the association between TLR4 +896A>G gene polymorphisms and risk of oral cancer. Single nucleotide polymorphism TLR4 gene was performed in oral cancer patients (n=30) and healthy controls (n=45) by PCR-RFLP method**.** The isolated DNA is amplified by PCR and the PCR products are digested using restriction endonuclease *NcoI*. The digested products were run on a 2% agarose gel and identified after staining with ethidium bromide (0.5 µg/ml). The distribution of genotype frequencies revealed that the heterozygous AG genotype (AG: 30% in oral cancer patients vs AG: 2.2% in control group, $p < 0.05$) had significant association with the risk of oral cancer while the homozygous wild (AA) and mutant (GG) genotype was not significantly associated with the disease.

Keywords: TLR4, SNP, PCR-RFLP, oral cancer.

OP33

Production of bioactive phytochemicals from in vitro regenerated callus of *Terminalia arjuna* (Roxb.) Wright and Arn.

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Abstract

Terminalia arjuna, a deciduous tree from the Indian subcontinent, is known for its cardioprotective properties due to presence of several bioactive compounds like flavonoids, tannins, and saponins. The increasing demand on plant based natural products has focused attention on in vitro plant materials as potential factories for secondary phytochemical products. This study aimed to examine the accumulation of bioactive compounds in callus culture. The culture was initiated on MS medium (Murashige and Skoog, 1962) supplemented with growth regulators. The impact of two plant growth regulators, 2,4-Dichlorophenoxyacetic acid (2,4-D) and Indole-3-butyric acid (IBA), were studied separately and synergistically on in vitro callus induction from leaf tissues of T. arjuna. Of the different concentrations of 2,4-D (0.0, 0.1, 1.0, 5.0, 10.0 mg/L) and IBA (0.0, 1.0, 5.0, 10.0 mg/L) tested alone, maximum percent response for callus induction in medium having 2,4-D was recorded at 5.0 mg/L and for IBA it was at 1.0 mg/L. Among the interactions of 1.0 mg/LIBA with various concentrations of 2,4-D (0.0, 0.1, 1.0, 5.0, 10.0 mg/L), maximum percent response for callus induction was obtained on medium having 5.0mg/L 2,4-D and 1.0mg/lIBA. The callus obtained on medium having 5.0mg/L 2,4-D and 1.0mg/l IBA was used for phytochemical extraction with different solvents (Methanol, Ethanol, Petroleum ether and Butanol). Methanol was recorded as the best solvent for phytochemical extraction. The extracted phytochemical showed presence of phenolic, flavonoid, saponin, tannin, and antioxidant activity. This study showed that the in vitro regenerated callus of T. arjuna is a source of various bioactive compounds that can be exploited for commercialization.

OP34

Effect of Salt stress on growth of different varieties of Pigeon Pea (*Cajanus cajan*)

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Abstract

Growth responses of leguminous plants to salinity vary considerably among species. Pigeon pea (*Cajanus cajan* (L.) Millsp.) is a sub-tropical crop, grown worldwide particularly in South Asia for edible and fodder purposes, while little is known about its salinity tolerance. In order to investigate the effect of salinity, plants were established at six different levels of salt concentrations i.e. 0mM, 25mM, 50mM, 75mM, 100mM NaCl. Plant growth was measured using Plant height, fresh and dry weight, shoot length (SL), root length (RL) in different varieties IPA-203, IPA-1502, PARAS, UPAS-120, PUSA-991, PUSA-992, BAHAR in Pigeon Pea. It can be concluded from above experiments that Pigeon pea varieties Paras, Pusa -992, Upas-120 are more sensitive varieties while Bahar, Pusa -991, IPA-1502, IPA-203 are more tolerant varieties.

Keywords: Fodder, Saline agriculture, Salt-tolerant, Salt-sensitive, salt stress.

OP35

Comparative Analysis of Antifungal Drug Efficacy and Resistance in *Candida auris*: In Silico Approaches

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Abstract

Candida auris is a multidrug-resistant yeast-like fungus that exhibits cross-resistance to various antifungal drugs, including azoles, polyenes, and echinocandins. This project report highlights the resistance mechanism of C. Auris, which involves the ERG11 gene, a key discovery in understanding its drug resistance. This gene encodes sterol 14-alpha demethylase, which is at the core of the resistance mechanism of C. auris. ERG11 mutations result in biofilm formation in the presence of drugs, which makes the antifungal agents less effective. Molecular docking studies using the software CB-Dock2 will now target sterol 14-alpha demethylase as the receptor and analyze its interactions with around 60 ligands that belong to the major classes of antifungal drugs. It has been seen that Ravuconazole, a molecule with the molecular formula of C22H17F2N5OS, proved to show better docking scores with docking in multiple binding sites i.e., C2 and C1 with docking score –10.2 and –10.1 respectively and could possibly be a therapeutic agent against C. auris. This fits very well with the fact that the approach used in this work is molecular docking, is very comprehensive and makes the unravelling of the hitherto unclear mechanisms of drug resistance in C. auris possible. Indeed, with the identification of Ravuconazole as a promising lead compound, future possibilities for the realization of novel and potent drugs against this menacing pathogen will significantly contribute toward further studies and clinical efforts in fungal infection treatment.

Keywords: Candida auris, CB Dock2, ERG11, sterol 14-alpha demethylase, and Ravuconazole.

OP36

Repurposing of Drugs for Autism Spectrum Disorder

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Abstract

Autism Spectrum Disorder (ASD) is a complex neurodevelopmental condition marked by challenges in social interaction, communication, and behavior. It encompasses a wide range of symptoms and severity levels, making it a "spectrum" disorder. While there is no cure for ASD, various treatment options, including behavioral therapies and medications, can help manage symptoms and improve quality of life. Social communication difficulties, repetitive behaviors, variability in functioning characterize ASD. The protein 7C7I of Ras Subfamily GTPases with the SPN Domain of Autism-associated SHANK3 is responsible for ASD and ligand Clonidine or Risperidone can be used and after docking using CB-Dock we can find the affinity between that protein and ligand. Molecular docking allows researchers to predict how potential drug candidates interact with specific biological targets, enhancing the efficiency of identifying effective treatments. In this current study, four proteins of ASD that is Shank3/ Prosap2, Neuroligin-3, Neuroligin-4, X-Linked, Lysine Specific Demethylase 1 (Lsd1) were used for docking with ligands Clonidine and Risperidone. Docking result shows that clonidine gives result -6.3, -5.7, -7.2, -6.7 and risperidone gives -9.6, -8.9, -9.4 and -13 with earlier mentioned proteins respectively. This research shows that protein Shank3 and Neuroligin-4 binds with risperidone better.

Keywords: Autism Spectrum Disorder, ASD, molecular docking, SHANK3, clonidine

OP37

Understanding Vascular Dementia and Molecular Targets

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Abstract

Vascular dementia is a type of dementia arising from cerebrovascular diseases that lead to impaired blood flow to the brain, resulting in cognitive decline. The cognitive decline in vascular dementia correlates with cerebrovascular events like strokes or microvascular lesions, particularly those responsible for memory, attention and executive function. It can develop suddenly after a stroke or gradually over time, depending on the severity and location of the vascular injury. Early diagnosis and intervention are crucial in managing the disease and improving the quality of life for patients. Current treatments focus on managing the underlying vascular conditions and symptoms as no cure exists for vascular dementia. Key proteins involved in vascular function, inflammation and neurodegeneration such as amyloid precursor protein (APP) and vascular endothelial growth factor (VEGF) and tau, with ligands that modulate their function, potentially altering disease progression. Ligands target proteins which involved in endothelial dysfunction, blood-brain barrier permeability and neuronal damage which are central to vascular dementia. By regulating these interactions, protein-ligand docking allows the identification of therapeutic compounds that inhibit disease-related proteins to slow or prevent cognitive decline. Understanding the dynamics of protein-ligand interactions could aid in the development of drugs aimed at preventing or mitigating the effects of vascular dementia. For protein-ligand interaction, we have taken three proteins 4RWF, 6WTS and 6V2E and ligand 2-((1-Benzylpiperidin-4-methyl)-5,6-dimethoxy-2,3-dihydro-1H-inden-1-one Aricept (donepezil), notice that interaction with 6V2E with vina score -9.8 with high negative value. Concluded that more negative value indicates stronger predicted binding at affinity. It helps to predict how well a small molecule (ligand) binds to a target protein, which is an important factor in drug design.

Keywords: Vascular dementia, Blood-brain barrier, Amyloid precursor protein, Vascular endothelial dysfunction, Microvascular lesions

OP38

Living on the Edge: Exploring the Industrial Benefits of Extremophilicn Organisms

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Abstract

Extremophiles are living organisms that can thrive in environments that are inhospitable to other organisms. Because of their harsh living environments, extremophiles exhibit distinct features in their morphology, structure, physiology, biochemistry, molecular evolution process, and other areas. In comparison to ordinary microbes, extremophiles exhibit enhanced growth and synthesis capabilities in severe environments, so enabling unsterilized fermentation processes and consequently improving low-cost manufacturing efficiency. The advent of the genomic age has made it possible to harness the biodiversity found in harsh environments and produce resilient microbial systems and enzymes under extreme pressure and temperature. It has been discovered that extremozymes are biocatalysts and they synthesize unique enzymes that can be used in a variety of industries, including food, cosmetics, chemical, and pharmaceutical industries. This review presents a detailed examination of existing knowledge about extremophiles and their distinctive enzymes, emphasizing their exceptional adaptations and investigating their prospective applications in biotechnology.

Keywords: Extremophiles, Industrial biotechnology, Biocatalysts, Extremozymes

OP39

Eco-Saviors: Microbial Solutions for Pesticide Biodegradation

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Abstract

The widespread application of pesticides in agriculture has resulted in significant damage of the environment, endangering both human health and ecosystems. Through biodegradation, microorganisms such as bacteria, fungi, and algae present a viable and environmentally sustainable way to reduce pesticide contamination. These microorganisms have metabolic pathways that allow them to detoxify and metabolize a variety of pesticides, changing dangerous substances into less hazardous or non-toxic forms. Microbial degradation of pesticides encourages the repair of contaminated sites while also lessening the persistence of pesticides in soil and water. The efficiency of microbial breakdown depends on numerous factors, including the chemical composition of pesticides, ambient circumstances, and the microbial species involved. The variety of microorganisms involved in pesticide breakdown and their mode of action are discussed in this paper along with their role in environment. Technological developments in biotechnology and genetic engineering have significantly improved microorganisms' capacity to more efficiently degrade persistent insecticides.

Keywords: Biopesticides, biodegradation, microbial communities, detoxification

OP40

Isolation and Characterization of Cadmium tolerant Plant growth promoting Rhizobacteria

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Abstract

Heavy metal contamination is major environmental issues which directly obstruct the global plant production. Among metals, cadmium is the topmost toxic heavy metal possess threat to food chain safety and human health. Prior causes of cadmium stocking in the soil are mining, industrial emissions, burning of fossil fuels and others. Their uptake in plants resists them by inhibiting the fixation of carbon and photosynthetic activities. Therefore, the present study was carried out to isolate, identify, and characterize the Cd-resistant bacteria stains from the contaminated soils of agricultural fields near thermal power of Tanda Ambedkar Nagar, Uttar Pradesh. Twenty-one bacterial strains were isolated and were screened for Cd resistance. The tolerant strains RRS-1, RRS-2, RRS-4, RRS-5, RRS-6, RRS-7 and SRL-3 were grown on Nutrient Agar plate supplemented with Cd as Cadmium chloride stock ranging between 50 µg /ml to 1000 µg /ml. The results showed that the strains RRS-1, RRS-2, and RRS-4 are capable to grow invitro up to 1000 µg Cd/ ml, whereas RRS-5, RRS-6, RRS-7 and SRL-3 can grow up to 600 µg Cd /ml. Based on morphological, biochemical, and molecular characteristics RRS-1, RRS-4 and RRS-6 was identified as Pseudomonas aeruginosa B77, Pseudomonas aeruginosa CS-17 and Pseudomonas aeruginosa CM5d respectively. This strain also showed plant growth-promoting (PGP) characteristics such as the production of Siderophore, IAA, HCN, Ammonia, Phosphate solubilization etc. On conducting a pot trial experiment, RRS-4 found to be effective in enhancing the growth with *Vigna radiata* (moong bean) plant with respect to untreated control under cadmium stress. Thus, RRS-4 inoculation protects moong plants from the detrimental effects of cadmium stress. PGP traits of isolated Cd resistant rhizobacterial strain indicated the strains could be useful as potential Phyto stimulators, biofertilizers, and stress ameliorators in achieving sustainable agriculture. The identified Cd-resistant bacterial strain may be used to develop bacterial consortia for the remediation of heavy metal contaminated soil.

Keywords: PGPR, Heavy metal, rhizobacteria, Pseudomonas, Cadmium

OP41

Proteomic Analysis of Cognitive Deficit Proteins and Functional Enrichment

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Abstract

Cognitive deficit proteins are proteins that, when dysfunctional or deficient, are associated with impairments in cognitive functions such as memory, attention, learning, and executive function. These proteins play crucial roles in brain development, synaptic function, neurotransmission, and cellular processes that support cognitive abilities. Here we have made use of 25 Human cognitive deficit proteins like, Zinc finger protein 41, Thiamine pyrophophokinase 1, DNA-binding protein SATB1, D-amino-acid oxidase, etc. This study used the STRING (Search Tool for the Retrieval of Interacting Genes/Proteins) database to perform a proteomic analysis of key proteins implicated in cognitive deficits, such as Amyloid-beta (Aβ), Tau, BDNF, and FMRP. Proteins involved in cognitive deficit-related proteins were identified through literature review and experimental data using Uniprot Database. STRING database was used to generate a comprehensive protein-protein interaction (PPI) network. Interaction sources such as experimental data, co-expression analysis, and text mining are used to construct and refine the network, with confidence scores set to prioritize high-quality interactions. The resulting PPI network highlights known and predicted interactions, clustering functionally related proteins into distinct subnetworks associated with cognitive processes, such as synaptic plasticity and neurodegeneration. Result shows the Protein-protein interaction between proteins of cognitive deficits, for the fragile X syndrome and autistic disorder for the biological process of regulation of synaptic depression. This research gives us insights into the cognitive deficits and their functional enrichments.

Keywords: Cognitive Deficit, Functional Enrichment, STRING DB, Amyloid-betaM, Pathway analysis

OP42

Effect of *Mentha spicata*, *Coriandrum sativum* and *Citrus limon* Plant Extracts on the Bacterial Strain

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Abstract

Plant extracts are tested for their ability to prevent the growth of pathogenic germs by using a variety of plants to test their antimicrobial activity. Usually, this procedure begins with gathering different plant parts, such leaves, stems, roots, or seeds. To extract the active chemicals, these materials are then dried, crushed, and put through an extraction process employing solvents such as ethanol, methanol, or water. By creating wells on agar medium plates, filling them with plant extracts, and measuring the zone of inhibition surrounding each well, the extracts are tested against various bacterial and fungus strains. This process is known as the agar diffusion assay. The minimum inhibitory concentration (MIC) of the extract needed to stop microbial growth can be found using the broth dilution assay, among other techniques. This project involves the study of antimicrobial activity of different medicinal plants on bacterial isolate (*Pseudomonas putida*). Methodology used is the antimicrobial susceptibility test with the help of agar well diffusion method, different medicinal plant extracts of different concentration were prepared and tested for the bacteria. Zone of inhibition is noted calculating the result in the end by the inhibition readings. Extracts prepared of the plants having medicinal properties and different dilutions were taken to analyze that on which concentration the medicinal properties are acting best on the isolate. Plant selected for the study are Mentha spicata, Coriandrum sativum, Citrus limon leaves of them are procured, dried under the sun then crushed and then the extract prepared of different dilutions. The objective for this project is to see the effect of medicinal plants extracts on bacterial isolates. This work involves the collection of different medicinal plants and selecting bacterial isolate for antimicrobial testing. As a result, among the three plant extracts used, Mint plant showed the maximum zone of inhibition. The concentration on which it showed maximum inhibition is 20mg/ml.

Keywords: antimicrobial, Minimum Inhibitory Capacity, *Pseudomonas putida*, plant, extract.

OP43

Ecotoxicological Perspectives of Micro & Nano Plastics (Mnps) on Human Cardiovascular System

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Abstract

Plastics are quintessential and chronic substances utilized in everyday existence that may be fragmented into Microplastics (MPs) and Nano plastics (NPs), which are unexpectedly arising environmental pollution, having a chief ecotoxicological challenge to humans and lots of other biotas, especially aquatic animals. Its exposure is unavoidable for its pervasiveness inside the environment. The physical and chemical compositions of MNPs majorly decide their ecotoxicological dangers. The perseverance of the latest manufacture and waste dealing with practices will probably cause massive amount, about 12 billion tons of waste in the environment by 2050. It perceives several cardiac toxicities including impairment of cardiac capabilities, aberrant heart charge, pericardial swelling, myocardial fibrosis etc. but, comprehensive understanding approximately the exposure routes and poisonous outcomes of MPs/NPs on health continues to be now not absolutely regarded. Right here this evaluation makes a specialty of the capability exposure routes, human health effects, and toxicity response of MPs/NPs on humans, through reviewing the literature on research conducted specifically in vitro and in vivo experiments. The contemporary literature evaluation has highlighted ingestion, inhalation, and dermal contacts as most important exposure routes of MPs/NPs. in addition, oxidative strain, cytotoxicity, DNA damage, infection, immune response, neurotoxicity, metabolic disruption, etc. worried structures, as critical fitness consequences. The findings discovered polystyrene form of MNP, which triggered cardiac fibrosis through Wnt/β-catenin signaling pathway in addition to oxidative stress influence the myocardium apoptosis. There are various several parameters for analysis such as left ventricular ejection fraction, cardiac magnetic resonance and echocardiography & even, new paths for cardiovascular investigation on MNP are counselled so that it will permit for greater accurate threat assessment..

Keywords: MNPs, environmental exposure, CVS, contaminants, echocardiography.

OP44

Biochar Assisted Adsorbent for Sustainable Management of Industrial Wastewater

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Abstract

Industrial wastewater contains significant amounts of heavy metals, endocrine disrupting compounds (EDCs), organic compounds and trace metals, all of which have direct or indirect disastrous effects on the environment. Although the effluent released into water bodies are treated, it often still contains non-biodegradable components. This abstract focuses mainly on Endocrine Disrupting Chemicals (EDCs) that interfere with the endocrine systems of both wildlife and humans, leading to reproductive issues, developmental problems, and changes in behavior. Additionally, these can accumulate in the ecosystem through food chain, causing biomagnification. Biochar, pyrogenic carbon, has shown tremendous potential to treat industrially generated wastewater. Biochar production uses biomass to create carbon rich material by heating it in the absence of oxygen. Biomass for biochar includes agricultural waste. Instead of burning this biomass which releases hazardous pollutants into the atmosphere -causing air pollution, respiratory diseases and global warming- can be converted into biochar. Since biochar is produced in oxygen-limited conditions, it sequesters carbon dioxide from the environment, helping to reduce pollution. Additionally, biochar valorizes waste biomass and can be further enhanced through various modification techniques -acid based, clay mineral modification, alkali based, metal oxides and metal salts modification to improve its ability to adsorb and manage industrial wastewater. It holds promise as a circular economic solution and a sustainable development method. In industrial processes, biochar can replace conventional materials for absorbing chemicals and contaminants, thus reducing the environmental impact.

Keywords: Biochar; Industrial wastewater; Mitigation; EDCs; Adsorbent.

OP45

Bioprocessing waste to utilizing as a feedstock for the Bioethanol Production

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Abstract

Waste to wealth should be the slogan for the coming future. The recent developments and research have contributed majorly to generating a huge amount of waste. Now it is a need to utilize the waste to convert it into valuable products. Bioethanol, a renewable and environmentally friendly alternative to fossil fuels, holds significant promise in mitigating climate change and reducing dependency on non-renewable resources. The utilization of *Saccharomyces cerevisiae*, a widely studied yeast species, offers advantages in terms of efficiency and scalability in ethanol fermentation processes. It is required to optimize the various parameters for the feasibility of bioethanol production from waste or cheaper sources using *Saccharomyces cerevisiae*. The current paper explores the various waste materials such as fruit waste, agricultural residues (sugarcane baggase) were used as potential and cheaper feedstock for bioethanol production. The semi solid state fermentation was performed for the production of Bioethanol and recovery was done by distillation process. The maximum bioethanol was estimated to be 0.08 mg/ml in Sugarcane baggase feedstock after 72 hr incubation period. The waste can be promising feedstock for the production of valuable bioethanol and the process can be optimized to enhance ethanol yield and productivity. The findings contribute to the advancement of sustainable bioenergy production by offering insights into cost-effective and environmentally friendly methods for bioethanol generation.

Keywords: Bioethanol, agricultural, waste, *Saccharomyces cerevisiae,* renewable

OP46

Cellulase Enzymes: Structure, Function, and Their Expanding Role in Industrial Applications

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Abstract

An enzyme called cellulase reduces cellulose, a complex carbohydrate found in plant cell walls, to smaller sugar molecules like glucose. Cellulase shows significant potential in various vital industries, including food processing, textiles, pulp and paper, agriculture, animal feed, bioethanol, and wine and brewery. Because of its great industrial potential, research institutions and industrial organizations have identified cellulases as a likely research topic. The current state of cellulase production knowledge has received a lot of attention in cellulase research these days, especially in terms of enhancing the process economics of diverse industries. These abstract addresses the structure and function of cellulase enzymes, their production methods, the factors that affect their activity, and their importance in industrial applications. It also focuses on the future advancements in cellulase technology, essential for realizing their full industrial and economic potential in our rapidly changing world.

Keywords: Cellulose, Carbohydrates, Cellulase, Industries, Economic importance

OP47

Innovative Approaches to E-Waste Valorization: A Path to Sustainability

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Abstract

The rapid increase in electronic waste (e-waste) presents major environmental, economic, and health challenges worldwide. E-waste valorization involves transforming discarded electronics into valuable resources through recycling, precious metal recovery, and repurposing components. This approach not only reduces the environmental harm caused by e-waste but also offers a sustainable method for reclaiming essential materials such as gold, silver, copper, and rare earth elements. Advances in technologies like hydrometallurgy, pyrometallurgy, and bioleaching have enhanced material recovery rates while lowering energy use. Additionally, the application of artificial intelligence (AI) and machine learning (ML) in e-waste sorting and recycling processes improves material separation, minimizes errors, and boosts overall efficiency. This paper explores the latest advancements in e-waste valorization, with a focus on innovative technologies, economic viability, and environmental advantages. By embracing a circular economy model and encouraging technological progress, e-waste valorization can turn a growing global issue into an opportunity for resource recovery and sustainable development.

OP48

Screening and identification of microbes and their gene and protein for biodegradation of plastic through in silico study

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Abstract

Plastics are so common in modern life; their persistence in ecosystems has made them a serious environmental concern. Plastics are non-biodegradable polymers that are built in landfills and the ocean, causing pollution and endangering human health and wildlife. Degradation of plastic is crucial to reducing these environmental effects. Degradation can effectively minimize waste volume, restricts the production of microplastics, and stops hazardous chemical leaching. The current work focuses on in silico study to examine microorganisms and their genes having potential for the degradation of plastics. The data was collected through literature search, NCBI. The proteins of these genes were identified using Uniprot tool. The genes identified were cutL1, cutL2, and PaCLE1 with the responsible protein Cutinase 1 and Cutinase-like enzyme. The microorganisms identified were *Aspergillus oryzae* and *Pseudozyma antarctica* (Yeast) (*Candida Antarctica*). BLASTp tool was used to search homologous protein and various microorganisms responsible for degradation of plastics. The phylogenetic analysis of identified gene was done using Cluster omega tool. The current study helps to identify various microorganisms and their protein that can effectively degrade plastics. These microorganisms were used further for in vitro analysis for the plastic degradation. The identified gene will be further utilized for developing genetically modified organisms that can be more potential for the biodegradation of plastic and can also help in figuring out quick and effective method. This study can be very helpful in finding a way to solve the problem and maintain the sustainable environment.

Keywords: Plastic degradation, Environment, Micro plastics, Plastic degrading gene, GMO

OP49

The Role of Microbes in Bioremediation: Cleaning Up Environmental Contaminants

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Abstract

Microorganisms play a highly important role in bioremediation-a friendly, low-cost process that involves using living organisms to break down or neutralize a wide array of environmental pollutants including heavy metals, petroleum hydrocarbons, pesticides, and organic pollutants. Bacteria, fungi, and other microbes possess special metabolic capabilities that enable them to convert toxic substances into nontoxic or even benign products thus aiding in the restoration of polluted environments. Key microbial processes involved in effective bioremediation include biodegradation, bioaccumulation, and biosorption. Biodegradation is the microbial degradation of complex contaminants into harmless forms. Bioaccumulation is the taking up of pollutants by microbes and their concentration in the cells, while biosorption describes the adherence of microorganisms to a cell wall and removal of a contaminant from the environment. More advanced genetic engineering developments have improved the efficacy of bioremediation. For example, several strains have been engineered with particular metabolic characteristics to target particularly persistent or highly hazardous pollutants that would not be biodegraded by natural strains. In addition, the microbial consortia that involve several microbial species with complementary capabilities have been shown to make a difference in improving bioremediation performance under varied and challenging conditions. All these innovations stretched the application of bioremediation to large-scale environmental management, addressing pollution in soil, water, and air.

OP50

In-silico screening and identification of genes and proteins of microbes responsible for effective degradation of dyes

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Abstract

Dye pollution from various industrial processes poses significant environmental challenges, necessitating the development of effective bioremediation strategies. Microbial degradation of dyes represents a promising approach, with specific genes playing crucial roles in this process. Understanding these genes can enhance our ability to design effective bioremediation systems. This study aims to identify and characterize the gene responsible for dye degradation in microbes and to elucidate its role and mechanisms in the biotransformation of synthetic dyes. In current research dye degrading microbes were selected with respective gene and protein sequence from literature search and various databases. The BLAST and BLASTp of searched gene and protein was done for the homologous search of gene and protein. During search 38 genes were identified for dye degradation in various microbes, out of these 25 genes belong to different microbes (20 bacteria, 1yeast, 2 white rod fungi, 1 round worm and 1protozoan parasite). The 7 dye degradable genes were screened on the basis of unique protein responsible for bioremediation of dyes. These identified genes as a key player for specific dyes degradation were ATG2, CrnA, AzoR, Trm2, dyp, lac and VP2. Functional analysis revealed that these genes encode different type of proteins such as Autophagy related protein 2, Creatinine amidohydrolase, Triphenylmethane reductase, dioxygenase, reductase dye decolorizing peroxidase etc. The genes and proteins screened for effective bioremediation of various dyes belong to microbes were *Saccharomyces cerevisiae* (strain ATCC 204508 / S288c) (Baker's yeast), *Pseudomonas putida, Comamonas testosterone, Mycobacterium tuberculosis* (strain ATCC 25618 / H37Rv), Pseudomonas sp. MDB-1, *Phlebia radiata* (White-rot fungus). These findings provide valuable insights into the molecular mechanisms underlying dye degradation and offers potential avenues for engineering microbial strains with enhanced bioremediation capabilities. Future research should focus on exploring the gene's potential in broader environmental contexts and optimizing its application in industrial settings.

Keywords: Dyes, microbes, biodegradation, gene, protein, BLAST

OP51

Unlocking Lignocellulosic Biomass: Pretreatment Strategies for Sugarcane Bagasse

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Abstract

Pretreatment of sugarcane bagasse is a crucial initial step in transforming this lignocellulosic biomass into value-added products like biofuels, chemicals, and bioproducts. Sugarcane bagasse, a fibrous by-product of juice extraction, contains cellulose, hemicellulose, and lignin, forming a recalcitrant structure that impedes enzymatic hydrolysis required for releasing fermentable sugars. Effective pretreatment is essential for disrupting this structure, enhancing cellulose and hemicellulose accessibility to enzymes or microorganisms. The main objectives of pretreatment are to increase the porosity of the biomass, reduce cellulose crystallinity, and modify or remove lignin. These changes facilitate the conversion of polysaccharides into fermentable sugars, which can be further used for bioethanol production and other bio-based applications. Pretreatment methods are classified into physical, chemical, biological, and physicochemical approaches. Physical methods, such as milling and grinding, reduce particle size and increase surface area. Chemical methods, including acid, alkaline, and solvent treatments, target the solubilization of hemicellulose and lignin removal. Biological pretreatment leverages microorganisms to selectively degrade lignin, while physicochemical techniques, such as steam explosion and ammonia fiber expansion, combine both physical and chemical effects to break down biomass. Despite the potential of pretreatment in advancing bioethanol production, biogas generation, and bio-based polymer synthesis, challenges remain, including high operational costs, the formation of inhibitory byproducts, incomplete lignin removal, and environmental concerns. Addressing these challenges is essential to improve the efficiency and scalability of pretreatment processes for sustainable bio-based product development.

Keywords: biofuels, cellulose, enzymatic hydrolysis, lignin removal, polymer synthesis

OP52

Impact of environmental toxic metal exposure on the risk of chronic kidney disease of unknown etiology (CKDu)

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Abstract

A major outbreak of chronic kidney disease of unknown etiology (CKDu) has been observed in arid regions of India (North India, Maharashtra, and South India). It predominantly affects male agricultural workers. The exposure and subsequent bioaccumulation of toxic metals, can lead to kidney failure. This study aims to investigate the correlation between the bioaccumulation of toxic metals and the prevalence of CKDu in north Indian population. The study involved 311 subjects (211 CKDu cases and 100 normal controls). The diagnosis of CKDu was confirmed following KDIGO guidelines. Toxic metals, including lead (Pb), arsenic (As), lithium (Li), cadmium (Cd), and mercury (Hg), were quantified using inductively coupled plasma-mass spectrometry (ICP-MS). Additionally, urea and creatinine levels were measured using a Beckman Coulter analyzer, and the eGFR was calculated by the CKD-EPI eGFR equation. The results showed that all the studied toxic metals were significantly higher in the CKDu group than in the control group. Pblevels (3.27 ± 3.61 µg/L vs. 0.50 ± 0.27 µg/L; $p < 0.0001$), As (6.22 ± 6.06 µg/L vs. 1.94 ± 1.023µg/L; $p < 0.0001$), Li (16.82 ± 31.92 µg/L vs. 1.26 ± 0.97 µg/L; $p = 0.0001$), Cd (4.88 ± 4.48 µg/Lvs. 0.12 ± 0.27 µg/L; $p < 0.0001$), and Hg (22.77 ± 18.56 µg/L vs. 15.44 ± 9.17 µg/L; $p = 0.0024$)were significantly higher in the CKDu group when compared to their respective control. Furthermore, the kidney injury biomarkers- urea and creatinine were positively correlated with arsenic ($r = 0.311$, $p = 0.007$; $r = 0.363$, $p = 0.018$), cadmium ($r = 0.612$, $p < 0.0001$; $r = 0.632$, $p< 0.0001$), and lead ($r = 0.313$, $p < 0.0001$; $r = 0.331$, $p < 0.0001$), respectively. The study indicates a significant correlation between elevated levels of toxic metals and the prevalence of CKDu, suggesting that bioaccumulation of these metals could be a key factor in the disease's etiology.

Keywords: CKDu, Toxic Metals, ICPMS, eGFR, CKD-EPI

OP53

Industrial Applications of *Linum usitatissimum*: Advancements in Agroinformatics, Biotechnology, and Sustainable Engineering

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Abstract

Linum usitatissimum (flax), a versatile crop known primarily for its fiber and oil, has gained significant attention in agroinformatics and related industries due to its wide range of applications. The integration of agroinformatics—applying data-driven technologies in agriculture—with linum cultivation presents opportunities for optimizing its industrial potential. This chapter explores the emerging roles of linum in sectors such as bioinformatics, precision agriculture, and environmental monitoring. By utilizing genomic and phenotypic data, agroinformatics enables enhanced breeding programs that optimize linum's fiber quality, oil content, and disease resistance. Beyond agriculture, linum's derivatives—such as flaxseed oil and fiber—have found utility in biotechnology, bio-composites, nutraceuticals, and cosmetics. The development of eco-friendly bio-composites for automotive and construction industries has opened new avenues for linum in sustainable engineering. Moreover, in environmental applications, linum-based products are used for soil remediation and as bio-adsorbents for pollution control. In this chapter, we discuss the intersection of linum cultivation with agroinformatics, focusing on advances in data-driven farming and industrial uses across various fields. The convergence of technology and natural resources in the case of linum highlights its role in promoting sustainability and innovation in modern agriculture and industrial applications.

Keywords: Flaxseed, bioinformatics, bio-composites, soil remediation, breeding optimization

OP54

Impact of biofertilizer on sustainable Agriculture

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Abstract

The escalating demand for food, alongside environmental degradation from chemical fertilizers, has prompted a transition toward sustainable agricultural practices. Biofertilizers, composed of beneficial microorganisms such as bacteria, fungi, and algae, present a viable solution to enhance soil fertility and support plant growth while mitigating the negative impacts of synthetic fertilizers. These microorganisms play a crucial role in fixing atmospheric nitrogen, solubilizing phosphorus, and decomposing organic matter, thereby promoting healthy nutrient cycles. Review indicates that the application of biofertilizers can significantly increase crop yields— demonstrated by yield enhancements of 10-30% in rice, wheat, and legume systems. Additionally, biofertilizers contribute to improved soil organic carbon, microbial biomass, and enzymatic activity, fostering long-term agricultural sustainability. By preventing nutrient runoff into water bodies and reducing greenhouse gas emissions, biofertilizers also mitigate environmental pollution associated with conventional fertilization practices. Despite these advantages, several challenges hinder the widespread adoption of biofertilizers, including limited farmer awareness, variable product quality, and concerns over storage and shelf life. Addressing these issues through targeted research, enhanced product formulations, and educational initiatives is critical for promoting biofertilizers as integral to sustainable agriculture. Ultimately, by reducing dependence on synthetic inputs and fostering ecological balance, biofertilizers offer a pathway to a resilient agricultural future, ensuring food security and environmental conservation for generations to come. Their role in sustainable farming practices exemplifies the potential of biofertilizers to harmonize productivity with ecological health, making them a vital component of modern agricultural systems.

Keywords: biofertilizers, sustainable agriculture, soil fertility, crop yield, environmental conservation, ecological balance.

OP55

Harnessing biosynthesised Ni/Ni(OH)$_2$ film for exploration of liquified petroleum gas sensor: A preliminary study

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Abstract

The physicochemical properties of the metal nanoparticle are completely different from that of the bulk material due to a high surface to volume ratio, which is critical in their biological activities. This study has been aimed at using Nickel/nickel hydroxide nanoparticles to fabricate a responsive Liquified Petroleum Gas (LPG) sensor to operate at ambient temperature. Green synthesis process was employed to generate Ni/Ni(OH)$_2$ nanoparticles. Characterization and optimization of Nickel nanoparticles was carried out following standard protocol using X-ray diffraction (XRD), Fourier-Transform Infrared Spectroscopy (FTIR), Transmission Electron Microscopy (TEM), Scanning Electron Microscopy (SEM), and UV-visible spectroscopy. Recovered nanoparticles were found to be round and size ranges from 20-30 nm. Films were made using the spin-coating approach, and Nickel/nickel hydroxide thin film sensing features were investigated. Ni/Ni(OH)2 NPs thin film were found to be highly useful for detecting LPG below the lowest explosion limit (0.5-2.0 vol%). At 2.0 vol%, the highest observed sensor response was ~3.96 (linear fit), with response and recovery times of 8 second and 9 second, respectively, for 0.5 vol%. Results are adequate for further investigations and development of a commercial LPG sensor to operate at room temperature.

Keywords: Gas sensor, Liquified petroleum gas, Nanoparticles, Ni/Ni(OH)$_2$ NPs.

OP56

Kinetic Study to Optimize the Decolorization of Dyes using Fungus

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Abstract

For industries, it is essential to decolorize the dye effluents which they are releasing in the environment to reduce the pollutants. The dyes are frequently used in food, textiles, paper, leather, and various other industries on a large scale. These dyes are commonly used for colorant, straining in laboratories, and various other purposes. The dyes cause hazardous impacts on the surroundings, and also, it's hard to degrade and reduce the level of effluents, due to their complex structures. Our motive of current study was to decolorize dyes using *Aspergillus niger* through the submerged fermentation process. Two different dyes selected for decolorization studies were methyl orange and methyl red. The kinetic study was performed on two different concentrations (50 ppm and 100 ppm,) of both the dyes. The color degradation was observed in both dyes at different concentrations. The maximum color decolorization observed in methyl orange was 100% in 50 ppm at 120 hrs, whereas methyl red was showing 75.07% in 100 ppm at 168 hrs incubation. The decolorization was also observed in high dye concentrations in a sample which was the promising result. The continuous decrease in dye concentration can further lead to complete 100% decolorization of methyl orange and methyl red if they are kept for a long incubation time. The protein concentration was also observed in all sets of experiments, which indicates the production of the same valuable product during the process of dye decolorization process. These results conclude that the kinetic study of dyes can help to explore solutions for the dye decolorization as well as degradation released from the industrial effluents.

Keywords: Dye, decolorization, kinetics, effluent, methyl orange, methyl red.

OP57

Screening and identification of bacterial genes responsible for biodegradation of oil spills using *In-silico* tool

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Abstract

Oil spills are one of the most prevalent forms of environmental contamination because they not only damage the water but also the land and air around them. When oil enters the water, it blocks sunlight, which affects plants and animals that rely on light to grow and survive. It can also harm the balance of the entire ecosystem. Tiny marine creatures can be poisoned by chemicals in oil, and when larger animals eat them, the toxins travel up the food chain affecting many species including humans. In addition to harming wildlife, oil spills can hurt local communities by affecting fishing, tourism and the livelihoods of people who depend on clean water and beaches. Hydrocarbons which are major components of oil are highly poisonous and bioaccumulative posing serious environmental and human health risks. Biodegradation which is driven by microorganisms offers a natural and affordable way to clean up areas polluted by oil. The purpose of this study is to screen and identify bacterial genes that are responsible for hydrocarbon biodegradation in oil spills. The genes and the microbes were searched through literature search. The protein responsible for biodegradation of the gene was searched through the Uniprot database. The genes screened for the biodegradation of oil spills are fleQ, gdhBdszC, alkB1, and gyrB in bacteria *Pseudomonas aeruginosa, Acinetobacter calcoaceticus*, *Rhodococcus erythropolis, Alcanivorax borkumensis* and *Micrococcus luteus* respectively. The protein of above gene was Transcriptional regulator FleQ, Quinoprotein glucose dehydrogenase B, Dibenzothiophene monooxygenase, Alkane 1-monooxygenase 1 and DNA gyrase subunit B These identified genes and protein that can be further used as a key for the more effective bioremediation for the cleaning up oil spills.

Keywords: oil spill, hydrocarbon, biodegradation, bioaccumulation, microbes.

OP58

Application of Biotechnology in Clinical Diagnosis

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Abstract

Biotechnology has revolutionized the field of clinical diagnosis, enhancing the accuracy and speed of disease detection. This abstract explores the various applications of biotechnological techniques in diagnosing health conditions, including genetic disorders, infectious diseases, and cancers. Key methods such as polymerase chain reaction (PCR), enzyme-linked immunosorbent assay (ELISA), and next-generation sequencing (NGS) are discussed. PCR allows for the rapid amplification of specific DNA sequences, making it a vital tool for detecting pathogens and genetic mutations. ELISA offers a reliable approach for identifying antibodies and antigens in samples, crucial for diagnosing viral infections. NGS has transformed our understanding of genetic diseases by enabling comprehensive genomic profiling, facilitating personalized medicine. The integration of these biotechnological advancements not only improves diagnostic accuracy but also reduces turnaround times, allowing for timely interventions. Furthermore, the use of biotechnology in point-of-care testing is enhancing accessibility to diagnostic services, particularly in resource-limited settings. This abstract aims to highlight the transformative role of biotechnology in clinical diagnostics, discussing current trends and future prospects. By fostering collaboration between researchers and healthcare providers, we can continue to innovate and improve patient outcomes.

Keywords: Biotechnology, clinical diagnosis, PCR, ELISA, Next Generation Sequencing, personalized medicine, infectious diseases.

OP59

Comparative Study of Growth and Cadmium Accumulation, in Tolerant and Sensitive Cultivars of Chickpea (Cicer *arietinum L.)*

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Abstract

Cadmium (Cd) is a TM ranked seven among the top 20 pollutants due to its high toxicity and solubility in water, taken up by the plants and affects their growth and metabolism. Trace metals (TM) contamination is a severe problem in the environment and produces an adverse effect on the productivity of crops. In this study, we estimate the growth, Cd accumulation and tolerance capacities of four chickpea (Cicer *arietinum* L.) cultivators (IPC-K-13-163, GNG-1581, IPC-11-112, IPC-K-09-145) subjected to four concentration (0 µM ,25 µM, 50 µM, 75 µM and 100 µM) in hydroponic condition. Higher accumulation of cadmium is observed in IPC-11-112, IPC-K-09-145 as compared in GNG-1581, IPC-K-13-163 at concentration of 100µm measured by AAS spectrophotometry. This means that IPC-K-13-163, GNG-1581 shows best tolerance as compared with other two varieties. We also evaluated the growth of some cultivars of chickpea i.e. IPC-05l.-62, ICCV-1205, IPC-K-13-.163, GNG-1581, IPC-11-112, IPC-K-09-145 at 0µM, 25µM, 50µM, 75 µM and 100µM Cd concentration. The toxicity of Cd reduced the plant height and fresh and dry biomass in all cultivars. The maximum reduction of root, shoot, and leave length was observed at 100 µM of Cd. It was observed that in different chickpea varieties IPC-K-13-163, GNG-1581 exhibited better performance as compared with other two varieties.

Keywords: chickpea, cadmium, physiological response, tolerance, sensitive, contamination

OP60

Sustainable Bio-Based Plastics from Agricultural Waste

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Abstract

This research explores the potential of agricultural waste to produce sustainable bio-based plastics. By leveraging biorefineries, synthetic biology, and advanced polymerization techniques, we aim to create high-performance materials that reduce reliance on fossil fuels and minimize environmental impact. The project focuses on developing biodegradable packaging materials, automotive components, textiles, and consumer goods made from bio-based plastics. Rigorous testing and life cycle assessments will ensure the sustainability and viability of these materials. The development of bio-based plastics offers a promising solution to the pressing challenges of plastic pollution and resource depletion, promoting a more sustainable future.

OP61

Food Adulteration: Impacts, Detection, and Regulation

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Abstract

Food adulteration poses a significant public health threat, particularly in developing countries, characterized by the intentional degradation of food quality through the addition of inferior substances or the removal of valuable ingredients for economic gain. Common adulterants, including chemical dyes and artificial preservatives, pose severe health risks, leading to gastrointestinal diseases, organ damage, and long-term consequences such as cancer. Advances in detection methods—such as chromatography, spectroscopy, and DNA-based techniques—have improved the ability to identify even trace amounts of these harmful contaminants. Regulatory bodies, including the Food Safety and Standards Authority of India (FSSAI) and the World Health Organization (WHO), have implemented strict guidelines to monitor food quality. However, gaps in regulations, coupled with limited consumer awareness, continue to facilitate the sale of adulterated food products. To combat this issue, it is essential to raise public awareness and educate consumers on simple home testing methods while advocating for stricter law enforcement. Collaboration between government agencies and the food industry is vital for enhancing food safety from production to consumption. By fostering awareness and implementing effective regulatory measures, stakeholders can significantly mitigate the prevalence of food adulteration, thereby protecting public health and ensuring the integrity of the food supply chain.

Keywords: food adulteration, public health, detection methods, regulatory bodies, consumer awareness, food safety.

OP62

Isolation of Streptococcus from Throat Sample

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Abstract

Streptococci are catalase-negative, nonmotile, gram-positive, non-spore-forming cocci that grow in chains or pairs. Cultures that are older could become less Gram-positive. While certain streptococci are obligate (strict) anaerobes, the majority are facultative anaerobes. Most need blood agar (enriched media). Group A Gram-positive streptococcus is a type of bacteria that grows in chains and has a remarkable history of altering the course of disease. It possesses a multitude of virulence factors that aid in tissue adhesion, tissue damage, and the development of autoimmune problems. One of the main microbiological procedures for detecting infections like strep throat is the isolation of Streptococcus from a throat sample. Because blood agar media may sustain the development of Streptococcus species and exhibit hemolytic properties—two essential diagnostic features—it is frequently employed for this purpose. Patients' throat swabs are obtained, and sheep's blood is then streaked onto blood agar plates. To promote bacterial growth, the plates are incubated for 24 to 48 hours at 35 to 37°C. Blood agar media is essential for the proper diagnosis and treatment of streptococcal infections because it offers a differential medium that helps identify Streptococcus based on hemolytic activity. Following incubation, the plates were checked for hemolytic patterns and bacterial growth. For identification, colonies with distinguishing characteristics were further put through biochemical testing and Gram staining. After isolation, further biochemical tests, such as catalase, are conducted to confirm the specific species. The study's findings proved that the blood agar medium is a useful tool for separating different streptococcal species from throat samples. Identification of streptococci, such as *S. pyogenes*, yielded important data for infection diagnosis and management.

Keywords: Streptococci, blood agar, isolation, hemolytic properties, diagnosis, throat swabs, infection.

OP63

Transesterification of non-edible oils for the production of Biodiesel

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Abstract

In the current era even after so much research on biodiesel, still the problem related to the fast depletion of fossil fuels remains unsolved. Global energy consumption is rising every day, which emphasizes on finding more and effective feedstocks for biodiesel production that can be promising sustainable energy sources. The current study explores the production of biodiesel using Refined cooking oil, Sesame oil, and Mahua oil as feedstocks. The Transesterification process was done to convert selected oil into biodiesel. For the Transesterification process, the methanol and oil ratio were 6:1 and the catalyst concentration used was 0.5% and 1% w/v of the oil sample. The analytical tests, including specific gravity, acid value, and moisture content, were performed to evaluate the quality of both the feedstocks and the biodiesel produced. The results indicated that refined cooking oil and sesame oil were showing promising results as feedstock with 91% and 88% yield respectively. However, Mahua oil posed challenges due to its high acid value, which can hinder the biodiesel production process by promoting soap formation. To address this issue, pretreatment of mahua oil was done before the transesterification process to improve biodiesel yield and efficiency. Overall, the study highlights the viability of refined cooking oil and sesame oil for biodiesel production and the need for further research to optimize the use of high-acid feedstocks like Mahua oil in biodiesel manufacturing. In conclusion, this study demonstrates the potential of biodiesel production from diverse feedstocks, highlighting refined cooking oil and sesame oil as promising sources, while emphasizing the need for further research to optimize the use of high-acid value oils like Mahua. These studies lead to explore new feedstocks as an alternative source to non-renewable sources. The fossil fuels are a threat to ecological balance and energy security.

Keywords: Biodiesel, Transesterification, feedstock, renewable energy, fossil fuel

OP64

Isolation and Functional analysis of Microbial Flora from Wastewater Sample of Kathauta Lake

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Abstract

Water plays a vital role in sustaining the livelihood of the people. With an ever-increasing population, the demand of water resources has increased manifold to cater the demand from agriculture, industry and domestic activities. In Lucknow city, Kathauta Lake is a major source for drinking water for around 40% of Lucknow City. The resources are depleting at a faster pace particularly in urban sprawl. Hence, it becomes essential to manage and utilize natural resources more efficiently. Microbial communities play a crucial role in maintaining environmental health, particularly in waste degradation and bioremediation. This study investigated the diversity and functional potential of microbes isolated from Kathauta Lake. Microorganisms were isolated using culture-dependent techniques and tested for their functional analysis. Alpha and beta diversity indices were employed to assess microbial community richness and composition, respectively. Different functional analyses were performed to explore the metabolic potential of the isolates. Our findings revealed a diverse microbial community in water samples from the bank and center of the lake, with distinct compositions. Notably, isolates from the bank side displayed a higher abundance of taxa known for xenobiotic degradation, suggesting adaptation to pollutants. Functional analysis identified whether the isolates were capable of degrading dye, heavy metals, lactose and starch. These results highlight the potential of these microbial communities for bioremediation applications. This study underscores the importance of exploring microbial diversity and unravelling their functional potential for developing sustainable strategies in bioremediation and biotechnology. After testing two promising isolates were considered for characterization; Named SB5 (Isolate from Bank Sample) and SC5 (Isolate from Centre Sample). Sample SB was a white, filamentous, rod shaped, gram negative and citrate positive colony. It tested positive for starch utilization and mercury and copper degradation. The sample SC was white, filamentous, cocci and gram and citrate positive in nature. It tested negative for antibiotic properties and metal degradation.

Keywords: microflora, bioremediation, metabolic, functional analysis, pollutants

OP65

Taxonomic and Functional Metagenomic Analysis of Gut Microbiome in Parkinson's Disease

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Abstract

Parkinson's disease is a neurodegenerative disorder increasingly linked to alterations in the gut microbiome. This study employs metagenomics to investigate the role of gut microbiota in the progression and onset of Parkinson's disease by analyzing the genetic material from gut microbes. Significant differences have been determined between groups at the taxonomic and functional level. The data was downloaded from ENA using accession number: PRJNA1096686 and performed quality control with FastQC and Trim Galore. FASTQ sequences were filtered to FASTA format, and VSeach Dereplication was applied to remove redundancy. Taxonomic profiling was performed using MetaPhlAn2. Krona pie charts and GraPhlAn were used to visualize community structures. Functional analysis of the sequences was performed using SortMeRNA and HUMAnN2, providing the results generated from both MetaPhlAn2 and HUMAnN2 analyses. In this disease, some bacteria were identified to be most prominently related to the condition. The bacteria included *Eubacterium rectale, Stenotrophomonas maltophilia, Bifidobacterium longum,* and *Bacteroides vulgatus*. Such results emphasize microbial imbalances, indicating that gut dysbiosis plays a significant role in the progression of Parkinson's disease. This analysis enhances our understanding of how the microbial ecosystem influences neuroinflammation and gut permeability, which may ultimately lead to new strategies for managing Parkinson's disease in light of innovations brought about by metagenomics.

Keywords: Parkinson’s disease, Metagenomics analysis, Taxonomic analysis, and Functional analysis.

OP66

In silico analysis of fungal gene and protein responsible for biodegradation of oil spills

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Abstract

Oil spills problem is a huge environmental issue, inflicting broad harm to ecosystems, wildlife, and human health while also having considerable economic consequences. These spills contaminate marine and coastal areas, alter food chains, and have long-term environmental issues. There is growing interest in bioremediation, a natural technique that breaks down hydrocarbons present in oil using microorganisms. In current studies fungi and their genes were searched through literature search and NCBI databases. The protein responsible for biodegradation of oil spill was searched through the UniProt database. Fungi show great potential for oil spill bioremediation due to their ability to create enzymes that help in breakdown of hydrocarbons. The fungal species identified for the effective oil biodegrading were *Aspergillus candidus, Aspergillus niger, Aspergillus ficuum*, and *Aspergillus flavips* and their respective genes were cfoL, lacA, inu2, and ffsA. The enzyme/protein responsible for the biodegradation of oil spills identified were Acetolactate synthase catalytic subunit, mitochondrial, Beta-galactosidase A, Extracellular endo-inulinase inu2, Polyketide synthase-non ribosomal peptide synthetase ffsA. These identified funguses can be utilized for the biodegradation of oil spills and many more fungal species can be searched through these identified genes. Fungal gene-based bioremediation has a high potential for increasing efficiency and sustainability of oil spill cleanup. This approach, which takes advantage of fungi's inherent metabolic processes, presents a viable alternative to conventional approaches for addressing environmental damage caused by oil spills and aiding in the restoration of impacted ecosystems.

Keywords: bioremediation, hydrocarbon, oil spills, fungus, *Aspergillus*.

OP67

Microbial Limit Test on cosmetic products (non-sterile)

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Abstract

A cosmetic product is any material or combination that is meant to be applied to the exterior of the body, the teeth, or the mucous membranes of the mouth in order to clean, scent, alter, preserve, or otherwise improve them. From a microbiological perspective, cosmetics are divided into two categories: 1) sterile products and 2) non-sterile goods. The term "sterilized" describes products that have been produced under aseptic conditions and are devoid of any microorganisms; non-sterile products, on the other hand, were not produced under aseptic conditions and therefore contain microorganisms; legal authorities have defined microbial limit ranges for these products. Among the most commonly used cosmetic contaminants, there are spore-forming bacteria, molds, yeasts and bacteria This study includes Microbial limit test (MLT) which is a test to determine the number, and the type of microorganisms present in non-sterile products. The purpose of Microbial limit test is to ensure the quality and safety of product by checking for presence of harmful bacteria, fungi, or other microbes. Two brands of moisturizer and compact powder each were taken randomly. Their bacterial and fungal loads as well as types were evaluated by Microbial limit test. There are two main parts of MLT: the first is the total aerobic microbial count (TAMC) which measures the total number of viable aerobic bacteria and fungi in the product using methods such as plate count. The second is the test for specified microorganisms (TSM) using selective media and biochemical tests. All the products were contaminated to varying degrees. Different types of microorganisms were found in the cosmetic products which could be harmful if not present in the right quantity. This test has been useful and appropriate to compare the quality of cosmetic products and to check the health effects of these products if they meet the standards for microbial limits.

Keywords: cosmetic, non- sterile, microbial limit test, quality.

OP68

Advance approaches for biodegradation of Plastics: an effective and supportive tool for its Reuse and Recycle

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Abstract

The most frequent plastic used worldwide is polythene. Polythene accounts for the greatest portion (64%), of all the plastic garbage produced. The growing amount of plastic garbage is being reusing and recycling using a variety of techniques and approaches. Though lots of efforts are in process to reutilize and recycle the polythene, still there is high need to reduce plastic, specifically by breaking down the polythene into smaller compounds. These breakdown compounds can be better utilized for the various usages. Bioremediation is thought to be the most extensively used and environmentally benign approach. Polyethylene Terephthalate (PET) breaks down into terephthalic acid (TPA) and ethylene glycol (EG) by *Ideonella sakaiensis* due to the enzymes like PETase and MHETase. TPA is further processed for the production of alkyd resins, that is chief ingredients in paints, coatings, and varnishes. The ethylene glycol (EG) is used in the manufacture of adhesives. Similarly, *Pseudomonas putida*, *Brevibacillus borstelensis* and *Fusarium redolens* help in the breakdown of polyethylene and convert it in fine micro-particles which can be utilized as an additive, binder, hence enhancing the flexibility, strength to asphalt for road development that can withstand with temperature fluctuations so as to reduce the road damage. Ascomycota, Amycolatopsis help in degradation of Polylactic Acids (PLA) into lactic acids and other smaller polymers that can be used in various industries such as food industries. The various studies show that various bacteria and fungus can perform in degradation of polyethylene. Still much more study is required to screen and identify various microbes that have potential for plastic degradation. Also, the consortia and genetically engineered microorganisms can be developed for the degradation of polythene. These discoveries can be used more widely and commercially by enhancing degrading capacity through evaluation of the ideal circumstances through microbial activity.

Keywords: Polythene, garbage, biodegradation, consortia, genetically engineered microorganism

OP69

Production and characterization of phytase producing bacteria

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Abstract

Introduction: Phytase is an enzyme that makes the phosphorus from phytin available for animal digestion. Up to now, phytase has been mainly used as a dietary supplement for swine and poultry. As phytase is increasingly used in animal feeds, science and technology related to this enzyme are rapidly evolving. The benefits of phytase are its double effects on reducing the use of expensive inorganic phosphorus in animal diets and the environment pollution from excessive manure phosphorus runoff.

Methods: The present study deal with isolating and identifying phytase–producing bacteria from various soil samples which include sewage sites, rhizospheric soils and other habitats of the soil. Subsequently, serial dilution, colonial streak technique, initial screening, subsequent screening, the media optimization for pH, temperature, carbon sources, nitrogen sources, optimum growth conditions, crude enzyme extraction and dialysis for the purification process were performed. This enzyme's pH and optimal temperatures were determined during its characterization.

Results: Serial dilution of the sample reduced bacterial count, and colonial streaking at 37°C led to the identification of 18 distinct colonies. Positive phytase producers were initially screened using selective agar with sodium phytate, identified by clear hydrolysis zones. These colonies were further tested in nutrient broth with sodium phytate, confirming phytase production. Media optimization revealed optimal growth at pH 7 and 37°C, with maltose and beef extract as the best carbon and nitrogen sources. Crude enzyme was extracted using ammonium sulfate precipitation and purified by dialysis. Phytase was characterized, with optimal activity at 37°C. CuSO4 and MgSO4 acted as activators, while EDTA and EtBr were inhibitors of the enzyme.

Conclusion: The possibility that certain bacteria can serve as sources of phytase in various industrial and farming sectors is central to this approach.

OP70

Sustainable Organic Waste Management and Future Directions for Environmental Protection and Techno-Economic Perspectives

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Abstract

The rapid growth of global population, urbanization, and economic development has led to a substantial increase in the generation of organic and solid waste, posing significant environmental and socioeconomic challenges. Annually, billions of tons of waste are produced, necessitating sustainable management approaches. Composting has emerged as an effective and eco-friendly solution for treating organic waste, converting it into nutrient-rich compost, which can be used in agriculture to improve soil health, productivity, and sustainability. This review addresses the optimization of composting processes, highlighting recent innovations such as microbial inoculants and in-vessel composting that enhance efficiency and compost quality. It emphasizes the benefits of recycling organic waste into valuable soil amendments, reducing the reliance on chemical fertilizers and mitigating the negative impacts of improper waste disposal. However, challenges such as managing contaminants, ensuring compost safety, and addressing socioeconomic barriers remain critical. The study also discusses the European Union's Circular Economy Action Plan, which promotes the use of organic fertilizers like compost, underscoring the economic and environmental advantages of adopting these technologies. Composting not only recycles essential nutrients but also improves soil structure, restores organic carbon, and reduces environmental impacts. This review provides a comprehensive overview of the composting process, its benefits for agriculture, and the potential for scaling up composting technologies as a sustainable waste management strategy globally.

Keywords: organic waste management, composting, sustainable agriculture, circular economy, nutrient recycling, soil fertility.

OP71

Methods for Degradation of Phenolic Pollutants: A Review

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Abstract

Significant volumes of phenolic pollutants have been released into rivers as a result of the industrial sectors' explosive expansion, which has raised serious environmental concerns in recent years. One major difficulty that still exists is the degradation of phenolic contaminants in water systems. The environment, other living things, and human health are all at risk from these toxic pollutants. Researchers have investigated a potentially effective strategy for degrading phenolic contaminants. That is the biodegradation of phenolic pollutants. This technique is a viable and efficient way to get rid of harmful contaminants from aquatic ecosystems. Other techniques for dealing with phenolic chemicals are membrane filtration, chlorination, and oxidation. These methods have the potential to convert phenolic contaminants into less harmful materials. This particular review looks at all of the different techniques used to break down phenolic pollutants into less toxic compounds. It offers a thorough evaluation of all feasible methods.

Keywords: Degradation, Bioremediation, phenolic pollutants, Wastewater treatment, environment

OP72

Screening and Evaluation of Anti-Cancer Potential of *Allium sativum* Phytochemical through *In-silico* study

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Abstract

The numerous health benefits of garlic are widely known anticancer effects of garlic are probably most noticeable. Observations over the past years have shown that the consumption of garlic in the diet provides strong protection against cancer risk. This food spice is famous mainly for its medical healing qualities and it has been used in the cure of cancer and microbial infections. The aim of current *in-silico* analysis was to study the anticancer properties of phytochemicals present in *Allium sativum* (garlic). Molecular docking analyses were performed to study the binding abilities and energies of these phytochemicals of garlic against the cancer-causing protein to inhibit the growth of cancer cells. Bioactive compounds identified in garlic, for the prediction of the anticancer potential through molecular docking were allicin, diallyl disulfide, ajoene, thiamine and protopine all exhibiting significant anticancer properties. Among these Protopine demonstrated the highest binding affinity to TP53 target with the binding energy of -9.1 kcal/mol, which can be argued out as strong enough to kill cells growing abnormally in cancerous growth. This work is pertinent to understanding the therapeutic potential of *Allium sativum* and calls for continued research on enhancing this plant as a potential candidate for an anticancer application and also this anticancer agent could be investigated further through *in-vitro* studies for the development of new medications. More such studies are required to analyze antibacterial, antifungal, antioxidant, anti-inflammatory, properties of garlic through *in-silico* and *in-vitro* tools. Together these findings highlight the therapeutic potential of *Allium sativum* as a natural anticancer and antibacterial agent.

Keywords: Carcinogenesis, garlic, docking, phytochemicals, anticancerous.

OP73

Advances in Pectinase Production and Applications: Enhancing Industrial Processes through Sustainable Practices

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Abstract

The conversion of agricultural waste into valuable products is gaining attention in the context of sustainable development. Pectinase, a crucial enzyme for degrading pectin, plays a significant role in numerous industries, including fruit juice clarification, textile processing, and biofuel production. As a biocatalyst, pectinase facilitates the breakdown of complex polysaccharides in plant cell walls, offering a green and cost-effective alternative to chemical processing methods. The utilization of microbial strains such as *Aspergillus niger* and *Bacillus subtilis* for pectinase production has shown advantages in terms of enzyme yield, activity, and scalability. Various studies have explored the use of various agricultural residues, including fruit peels and sugar beet pulp, as cost-efficient substrates for pectinase production through solid-state fermentation (SSF) processes. The optimization of various fermentation parameters, such as pH, temperature, and incubation time are critical for enhancing enzyme yield and activity. There is a need to optimize the production of pectinase under various optimization conditions, with a focus on maximizing enzyme output and industrial applicability. The findings highlight the potential of waste-derived pectinase for industrial applications, contributing to the advancement of environmentally sustainable technologies. By utilizing low-cost feedstocks and optimizing production techniques, pectinase-based processes can offer eco-friendly solutions for various sectors, including biofuel production, textile processing, and food industries.

Keywords: Pectinase, agricultural waste, *Aspergillus niger*, *Bacillus subtilis*, biofuel, solid-state fermentation

OP74

In-silico analysis to find the biocontrol against Rice Blast disease of *Oryza sativa*

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Abstract

It is of paramount importance to raise both productivity and quality of *Oryza sativa*, which is the staple crop around the world to safeguard food security and economic development. The discoveries in computational biology have led to more research in agriculture. The fast methods of *in silico* techniques have helped in improving crop quality and quantity. The current *in-silico* study was carried out to identify a stable biocontrol agent against the virulence mechanisms of the fungus responsible for the Rice Blast disease of *Oryza sativa*. The genes and proteins of screened bacteria and fungus causing Rice Blast disease were screened through literature search, NCBI and Uniprot databases. The bacteria, gene and protein searched against the fungus were *Streptomyces griseus,* strB1 and Inosamine-phosphate amidinotransferase 1 (IPAT). The homologous search of protein IPAT was done using the BLASTp tool. The various homologous microbes were observed through the BLASTp result such as *Streptomyces sp., Actinokineospora spheciospongiae, Nocardia sp. NPDC046473, Umezawaea sp., Catenulispora sp. GP43, Actinomycetota bacterium, Micromonospora sp. WMMD882, Amycolatopsis sp. H6, Herbidospora mongoliensis, Actinoplanes sp., Micromonospora halophytica.* The PDB structure of fungus and identified bacteria was downloaded in the PDB file from the PDB database. The protein-protein molecular docking analysis was done through the HDOCK and ClusPro tool. The highest molecular docking score was observed at 6.765kal/mol for fungus causing disease against Inosamine-phosphate amidinotransferase (IPAT) using the HDock server. *Streptomyces griseus* and other homologous bacteria can be used as a biocontrol against rice blast disease. This interaction may be significant in the context of rice blast disease. Future research should concentrate on investigating the synergistic effects of multiple treatments and verifying these in silico results through field trials. All things considered, this work lays the groundwork for improving chemical treatments to raise *Oryza sativa* productivity and for analyzing bacterial strains as a biocontrol against rice blast disease, both of which support sustainable agriculture and food security.

Keywords: *Oryza sativa,* docking, *in silico,* biocontrol, rice blast disease, bacteria

OP75

Enhanced Sensitivity of Hydrogen Gas Sensor Using Palladium-Graphene Oxide (PdGO) Nanocomposite

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Abstract

Hydrogen is a sustainable carbon-free energy source for future power generation, however, its properties like explosive, colorless and odorless nature make its detection more challenging. Palladium (Pd) is known to absorb 1000 times hydrogen as compared to its own volume at room temperature and 1 atm pressure, due to which it plays a key role in the hydrogen storage and sensing. However, the major drawback of Pd is the incomplete desorption of hydrogen from its lattice. To overcome this limitation, Pd is modified with various nanomaterials to enhance its hydrogen absorption-desorption characteristics. The modification of Pd with 2- dimensional (2D) nanomaterials facilitate migration of hydrogen molecules from its lattice to the surface of the nanomaterial, allowing complete desorption of hydrogen. In this work, PdGO (synthesized using a simple chemical reduction method) thin films were formed on SiO_2/Si substrates (1x1 cm^2) using spin coating. The synthesized PdGO thin films were characterized using XRD, XPS, FTIR, SEM and EDS analysis. The samples were tested for H_2 gas sensing by varying parameters such as temperature, concentrations of GO, and concentrations of H_2 gas. At an optimized temperature of 150°C, PdGO-200 (with 200 mg GO) demonstrated the highest response of 32.2% at 100 ppm of H_2 exposure. The limit of detection (LoD) was found to be 12 ppm. The selectivity of PdGO-200 was found to be the best for hydrogen among other gasses (NO_2, H_2S, CO, and NH_3).

Keywords: Hydrogen; Sensing; Palladium; Graphene oxide.

OP76

Multi-Omics Techniques for Investigating Oral Cancer Biomarkers

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Abstract

Oral cancer is a prevalent and aggressive malignancy with complex molecular underpinnings that involve genetic, epigenetic, proteomic, and metabolic changes. Multi-omics techniques have emerged as a transformative approach for unraveling the intricate biological mechanisms driving oral cancer and identifying robust biomarkers for early detection, prognosis, and treatment. By integrating data from genomics, transcriptomics, proteomics, and metabolomics, multi-omics approaches provide a comprehensive view of the molecular alterations involved in oral cancer progression. This integrative approach improves our understanding of the disease's molecular basis and offers new opportunities for targeted therapeutic interventions. This review highlights recent advancements in multi-omics research, emphasizing its pivotal role in the discovery of reliable biomarkers that can improve clinical outcomes for oral cancer patients.

OP77

Exploring Phytochemicals for Therapeutic Applications in Wilson's Disease: A Computational Approach

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ABSTRACT

Wilson's disease (WD) is a rare genetic ailment caused by mutations in the ATP7B gene that cause an excessive buildup of copper in numerous tissues, including the brain and liver. Overconsumption of copper induces oxidative stress and cellular damage, which can have serious effects on the liver and nervous system. There are drawbacks to current treatments, such chelation therapy, such as toxicity and adverse effects. With their reputation for being chelating and antioxidants, phytochemicals present a viable substitute for therapeutic intervention in WD. Using in silico molecular docking techniques, this study investigates the potential of phytochemicals as therapeutic agents against Wilson's illness. Important phytochemicals from medicinal plants were chosen because of their proven antioxidant and metal-chelating properties. These chemicals' molecular interactions and binding affinity were assessed by autodocking with the ATP7B protein and other target proteins involved in copper metabolism. Auto-docking simulations were carried out utilizing auto-docking software which was CB-Dock2. The results demonstrated a number of significant binding affinities and beneficial interaction patterns with disease-associated proteins in a large number of strong candidates. It's interesting to note that compounds like withanolides, luteolin, ladostigil, lycopene, spiactioside, and triterpenoids have demonstrated potential in stabilizing protein. The findings pave the way for further in vitro and in vivo studies to validate the efficacy of these compounds and potentially lead to the development of novel therapeutic agents with fewer side effects.

RESULTS: In the present study, protein 7XUM was docked against six phytocompounds:
Luteolin, Spicatoside, Triterpenoid, Lycopene, Withanolide A, and Ladostigil. The binding affinities of the chemicals varied, as assessed with AutoDock software (CB-Dock2). Withanolide A had the most significant interaction with the protein, rating -10.8, followed by triterpenoid at -10.0. Spicatoside also demonstrated high binding, with values of -9.7 and -9.1 in multiple regions. Lycopene and luteolin demonstrated relatively small affinities, scoring - 8.7 and -8.3, respectively. Ladostigil had the weakest interaction, rating -7.3. Overall, withanolide A and triterpenoid emerged as the most promising options for protein inhibition.

Keywords: Wilson's disease, phytochemicals, molecular docking, copper metabolism, drug discovery

OP78

Molecular Docking study of Biocontrol agents against Fungus causing Disease in Wheat

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Abstract

Wheat (*Triticum aestivum*) is one of the most important staple crops worldwide, yet its production and quality are frequently jeopardized by fungal diseases, particularly yellow stem rust caused by *Puccinia graminis*. These fungal pathogens pose a serious threat to wheat crops, often leading to reduced yields and significant financial losses, which in turn affect global food security. While chemical control strategies have been commonly employed to manage these diseases, they present challenges, such as environmental harm and the growing issue of pathogens developing resistance to these treatments. The current in-silico study was carried out to identify stable biocontrol agents against the virulence mechanisms of the fungus responsible for the yellow stem rust disease of wheat. The bacteria against the fungus were searched through literature review as *Bacillus subtilis*. The genes and proteins of screened bacteria and responsible fungus for wheat disease were searched through literature search, NCBI and Uniprot databases. The PDB structure of fungus and identified bacteria was downloaded in the PDB file from the PDB database. The protein-protein molecular docking analysis was done through the ZDOCK tool. The BLASTp of the identified bacteria was also done to screen the homologous bacterial strains. The literature search reveals that *Puccinia graminis*, is the causative agent of yellow stem rust of *Triticum aestivum*. The ZDOCK results revealed that *Bacillus subtilis* showed the highest molecular docking interaction (-1.235 kcal/mol) against the fungus *Puccinia graminis*. *Bacillus polymyxa* and *Bacillus megaterium* as a result of homologous search were also showing promising results. This computational study provides a foundation for future experimental validation and the formulation of *Bacillus subtilis*-based biocontrol approaches in wheat farming. It emphasizes the potential of *Bacillus subtilis* to improve wheat health and productivity by reducing the impact of this major plant pathogen.

Keywords: *Triticum aestivum*, fungal disease, Bacillus sp, pathogen, biocontrol, BLAST

OP79

Comparative Molecular Docking Studies of Guava leaves extract with drugs against bacteria that causes Endodontic infections

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ABSTRACT

Enterococci are common bacteria that inhabit the gastrointestinal tract, oral cavity, and vagina of humans and animals. One of the most prevalent species is *Enterococcus faecalis*, or *E. faecalis*. It is one of the species that may be responsible for endodontic treatment failure and plays a significant role in infections of the human oral cavity. Oral conditions like caries, endodontic infections, periodontitis, and peri-implantitis all are caused by *E. faecalis*, the most common enterococcus in humans. The plant Guava (*Psidium guajava*) is a very common tropical tree in India and has an enormous amount of therapeutic potential. Its anti-inflammatory, antibacterial, antioxidant, antidiarrheal, and antimutagenic qualities have long been recognized. Antibacterial activity of guava has been demonstrated against both Gram-positive and Gram-negative microorganisms. Guaijaverin from guava leaves contains bacteriostatic properties that prevent *Streptococcus mutans* and *Staphylococcus aureus* from growing and may be used as an antiplaque agent. This study aims to compare the antimicrobial efficacy of natural extracts such as guava leaf extract and Chlorhexidine against *Enterococcus faecalis* in endodontitis.

In this study we have selected five compounds from guava leaves and five medicines used to treat endodontosis. Cytotoxity level is also checked using in-silico tools. Molecular docking studies and cytotoxicity studies on these active compounds and medicines against the surface protein of *Enterococcus faecalis* reveal that the antibacterial activity can be modulated by the presence of natural extracts comparatively better than some medicines available to treat endodontic infections.

OP80

Bioreactor Designs for Microbial Dye Degradation: From Laboratory to Industrial ScaleOptimization

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Abstract

As textile and dye industries continue to contribute significantly to environmental pollution, the need for effective, scalable solutions to degrade synthetic dyes becomes critical. The use of microbial consortia in bioreactors presents a promising method for the bioremediation of these pollutants. This chapter explores various types of bioreactors and their designs suitable for microbial dye degradation at different scales, including laboratory, pilot, and industrial stages. The chapter begins by discussing laboratory-scale bioreactors, including simple batch and continuous systems, which are ideal for controlled, small-scale experiments to optimize microbial growth and degradation efficiency. Various bioreactor configurations, such as stirred-tank, airlift, and packed-bed reactors, are analyzed based on their suitability for testing microbial activity under different conditions. Special focus is given to parameters such as oxygen transfer, pH control, and nutrient flow, which influence dye degradation rates. Transitioning to the pilot scale, the chapter covers semi-continuous and hybrid bioreactors designed to bridge the gap between laboratory success and industrial implementation. Key challenges such as scale-up kinetics, mass transfer limitations, and operational stability are addressed. Finally, industrial-scale bioreactor designs are discussed, focusing on high-efficiency reactors like fluidized bed, membrane bioreactors, and trickling filters. These designs are optimized for large-volume treatment with sustainable operational costs and maximized dye degradation efficiency. By comparing each stage, the chapter provides a comprehensive guide for researchers and engineers to select and design bioreactors that align with their degradation goals and operational requirements.

Keywords: synthetic dyes, laboratory-scale bioreactors, packed-bed reactors, hybrid, bioreactors, scale-up kinetics

OP81

Curcumin Inhibits Coronavirus E484k Mutated Spike Protein: An *In-Silico* Approach

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Abstract

The COVID-19 disease has wreaked havoc over the planet. Unfortunately, developing a therapeutic medicine or vaccine that effectively treats the virus due to mutation is difficult. The disease initiates when viral spike protein binds with the human ACE2 receptor. Of all the viral spike proteins associated with COVID-19, E484K is the most contagious strain, raising the disease's morbidity and mortality risk. In this research, we used molecular docking and molecular dynamics simulation approaches to examine the effectiveness of Curcumin, a naturally occurring bioactive compound, in preventing spike protein from binding to ACE2 protein in both native and E484K mutant viruses. For computational modeling of the viral spike protein, we utilized the I-TASSER server. The PyMol molecular visualization tool was used to develop the spike protein E484K mutation. A SwissDock server was utilized to conduct the docking investigations, while JMOL software was used to visualize the complex. The curcumin-spike protein combination had a roughly similar free energy change in both its native and mutant forms. Interestingly, a reliable C-score value was obtained, which makes Curcumin the best candidate to suppress spike-ACE-2 interaction regardless of the viral mutation.

Keywords: SARS-CoV-2, Curcumin, Spike protein, ACE2 protein, E484K mutation, Molecular docking, Molecular dynamics simulation.

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