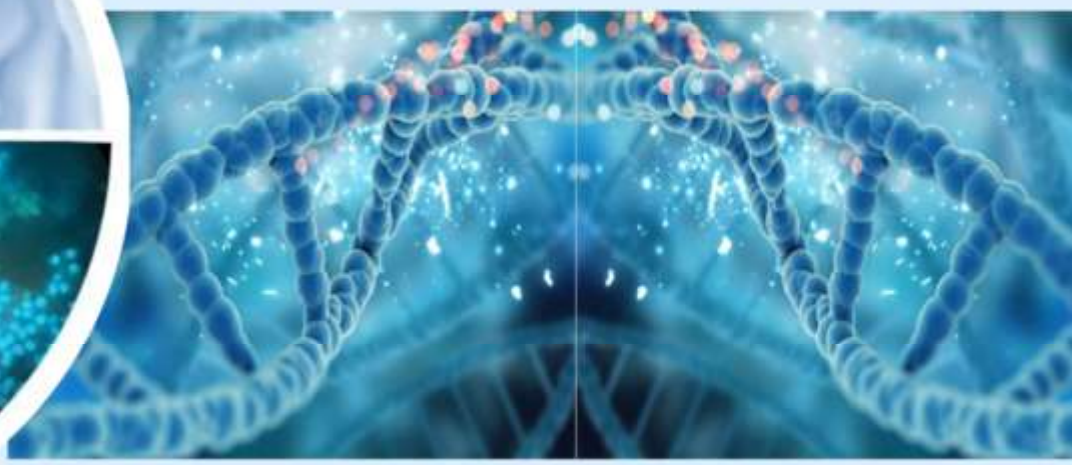
VSRD INTERNATIONAL JOURNAL OF
BIO-TECHNOLOGY AND PHARMACEUTICAL SCIENCES
ISSN: 2278-9197 (Special Issue Vol. XIV, January 2025)

8th International Conference on "ADVANCES IN BIOSCIENCES AND BIOTECHNOLOGY 2025"

ICABB-2025



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Department of Biotechnology

JAYPEE INSTITUTE OF INFORMATION TECHNOLOGY

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● Volume XIV ● Issue (Special Issue) ● January 2025

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ISSN: 2278-9197

DBT and ANRF Sponsored

8th INTERNATIONAL CONFERENCE ON ADVANCES IN BIOSCIENCES AND BIOTECHNOLOGY 2025 (ICABB-2025)

January 29, 2025 - January 29, 2025

CHIEF EDITOR

Prof. Pammi Gauba

EDITORS

Dr. Shalini Mani

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Printed & Bound in India

VSRD INTERNATIONAL JOURNALS

A Research Division of Visual Soft (India) Pvt. Ltd.

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MANOJ GAUR
Chancellor

January 01, 2025

MESSAGE

It is a matter of great pleasure for me to know that the **Department of Biotechnology, Jaypee Institute of Information Technology, Noida**, is organizing the **'International Conference on Advances in Biosciences and Biotechnology (ICABB-2025)'** from 29th January till 31st January 2025, with its theme as **"Innovations in Biomedicine, Biotechnology & Computational Biology"**.

I am certain that this International Conference will provide a wide opportunity to all the participants to share their research outcomes and also grasp new ideas and valuable suggestions for their researches. Discussions and deliberations during the conference will encourage students, researchers and scientists, motivating them to develop interest in the entire chain of events from lab to market.

I convey my best wishes to the organizers and participants of the conference and also wish them a grand success in organizing this event.

With best wishes,

(Mr. Manoj Gaur)

Jaypee Institute of Information Technology

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Prof. S.C. Saxena
Pro-Chancellor

January 01, 2025

MESSAGE

It brings me great joy to announce the upcoming **"International Conference on Advances in Bioscience and Biotechnology (ICABB-2025)"** organized by the **Department of Biotechnology at Jaypee Institute of Information Technology, Noida**. This is the 8th edition unfolding from January 29 to January 31, 2025, focusing on the theme **"Innovations in Biomedicine, Biotechnology & Computational Biology."**

Conferences play a vital role in the scientific community, acting as key platforms for researchers, scientists, and professionals to come together, exchange ideas, and build valuable connections. To foster cross-disciplinary collaboration, I believe that ICABB-2025 will be an outstanding forum, opening up new opportunities for research in computational biology and drug discovery, as well as in the broader biotechnology field. Your participation and input will be crucial to the success of this conference, and I am confident that the knowledge shared and partnerships formed will significantly benefit all attendees.

I would like to extend my sincere appreciation to the organizers for their dedicated efforts in orchestrating this event. Their commitment and hard work are instrumental in ensuring that ICABB-2025 will be a resounding success.

With best wishes,

(Prof. S.C. Saxena)

Jaypee Institute of Information Technology

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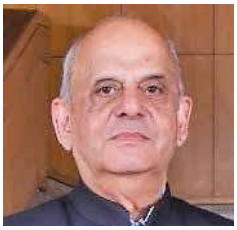
Prof. B.R. Mehta
Vice-Chancellor

January 01, 2025



MESSAGE

The Department of Biotechnology has been organizing international conferences 2015, each edition providing a vibrant platform for the exchange of ideas, and fostering collaborations. The present **"International Conference on Advances in Bioscience and Biotechnology"** (ICABB-2025) edition is 8th in the series, from 29-31 January, 2025, and has a specific focus on the theme **"Innovations in Biomedicine, Biotechnology & Computational Biology."**

As a part of the transformative **'Decade of Innovation'** (2021-2030), envisioned by Hon'ble Chancellor Sh. Manoj Gaur ji, JIIT has been at the forefront of nurturing an innovation centric ecosystem, marked by the establishment of dedicated incubator facilities and a strong focus on digital technology led education. Establishment of RIDE and funding of 21 start-ups is a huge step in this direction. The Department of Biotechnology, Along with RIDE, are in the process of setting up Bio-Incubator funded by DBT.

Precision in biomedicine, driven by advanced computational techniques, is an exceptionally dynamic and fast-evolving field, playing a crucial role in shaping our economy. The theme of this conference resonates perfectly with India's progress and aspirations and setting up of high-performance computational facility (Ramanujan Universe) at JIIT. I extend a warm welcome to all the esteemed delegates at ICABB-2025. We are looking forward to a series of insightful sessions and impactful presentations.

My best wishes to the organizers for grand success.

(Prof. B.R. Mehta)

Jaypee Institute of Information Technology

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MESSAGE FROM THE ORGANIZERS

It is with great anticipation and excitement that we extend our warmest welcome to each of you for the 8th "International Conference on Advances in Bioscience and Biotechnology (ICABB- 2025)" hosted by the Department of Biotechnology at Jaypee Institute of Information Technology, Noida from 29th to 31st January, 2025. The theme for this year's event is **"Innovations in Biomedicine, Biotechnology & Computational Biology"**, that would be an amalgamation of multi- disciplinary fields of Biotechnology, providing opportunities for exchange of ideas and scientific knowledge to everyone. It will also be a place for exchanging varied experiences among researchers, academicians, scientists and students from Biological, Medical and Computational fields.

Recent advancements in biomedicine, biotechnology, and computational biology are revolutionizing the way we approach healthcare and scientific research. These multidisciplinary developments address global healthcare concerns while facilitating advances in drug discovery, targeted therapeutics, and disease diagnostics. While biotechnology employs engineering ideas to harness biological processes for purposes like vaccine production and customized medicine, biomedicine concentrates on comprehending complicated biological systems to develop therapies and interventions. Collectively, these developments are changing the scientific landscape, encouraging interdisciplinary cooperation, and opening the door to a more sustainable and healthy future.

We are deeply grateful to all the speakers and delegates who graciously accepted our invitation and have shown such enthusiastic interest in this event. We also extend our heartfelt thanks to our Advisory Committee members, whose guidance has been invaluable throughout this journey. The dedicated efforts of our organizing team are truly appreciated, including our faculty and students, whose meticulous planning and hard work have made this event possible.

We are profoundly thankful for the support from our sponsors, the Department of Biotechnology (DBT), Government of India and the Department of Science and Technology (DST), Government of India, as well as our industry and publishing partners.

We thank Shri Manoj Gaur ji, Hon'ble Chancellor, Prof. S.C. Saxena, Hon'ble Pro-Chancellor, and Prof. B.R. Mehta, Vice-Chancellor for their continued guidance and motivation which have helped to crystallize this event and make it happen.

Finally, on behalf of the organising committee we wish you a comfortable stay and a fulfilling research experience during the conference. Thank you all once again, and we look forward to a productive event.

Prof. Pammi Gauba
Chairperson

Dr. Shalini Mani
Convenor

Dr. Nidhi Batra
Convenor

SPEAKERS

Prof. Keshav K. Singh

Genetics, Pathology and Environmental Health and the Director of the Cancer Genetics Program, University of Alabama at Birmingham (UAB), USA

Prof. Keshav. K. Singh is a globally recognized expert in mitochondrial biology, with a focus on its role in health, disease, genetic diversity, and health disparities. As the Joy and Bill Harbert Endowed Chair and Director of Cancer Genetics at the University of Alabama at Birmingham (UAB), he also serves as a Professor in Genetics, Dermatology, Pathology, and Environmental Health. Prof. Singh's pioneering work extends to mitochondrial genetics, numtogenesis, cancer genetics, and health disparities, making him a key figure in these areas. Notably, he is the founding Editor-in-Chief of the journal Mitochondrion

Prof. Singh's academic journey spans continents, beginning with his undergraduate studies in India, a Ph.D. in Australia, and postdoctoral research at Harvard. He later held esteemed positions at Johns Hopkins School of Medicine and Roswell Park Cancer Institute before joining UAB.

His work has been widely celebrated and featured in prominent outlets such as Nature, Newsweek, National Geographic, and Forbes. He founded the Mitochondria Research and Medicine Society in the US and India and is instrumental in promoting understanding and awareness of mitochondrial diseases around the globe. With over 100 research publications, three books, and numerous awards, including recognition as a Global Indian by Newsweek, his contributions have left an indelible mark on the scientific community.

Dr. Chandra Verma

*Bioinformatics Institute (BII) A*STAR, Singapore*

Dr. Chandra Verma is a Senior Principal Investigator at the prestigious A*STAR Bioinformatics Institute (BII), where he leads a distinguished research team specializing in computational protein dynamics within the *Biomolecular Modelling and Design Division*. His work advances our understanding of intricate biological processes by leveraging cutting-edge atomistic computer models and simulations to design and optimize novel molecules, peptides, and proteins with the potential for use as innovative reagents and therapeutic agents.

Dr. Verma's research is at the forefront of computational biology, where he combines the power of high-performance computing with in-depth biomolecular analysis to uncover critical insights into protein behavior and interactions. His team's groundbreaking work aims to bridge the gap between fundamental science and practical applications in drug development, offering new avenues for the creation of more effective and targeted medical therapies. Dr. Verma earned his Ph.D. in Bioinformatics from the University of York, where his research laid the foundation for his future career in molecular modeling and bioengineering. Prior to his doctoral studies, he completed his undergraduate degree at the Indian Institute of Technology Kanpur (IIT-Kanpur), one of India's foremost institutions for technological and scientific education.

Dr. Kamal Dua

Graduate School of Health, Discipline of Pharmacy,
University of Technology, Sydney, New South Wales, Australia

Dr. Kamal Dua is an award-winning researcher and educator in pharmaceutics and drug delivery, with extensive experience across three continents. Holding dual doctoral degrees in *Pharmaceutical Sciences* and *Immunology & Microbiology*, he has also completed four professional diplomas in clinical research, drug development, and intellectual property. As an Associate Professor at the Graduate School of Health, University of Technology Sydney (UTS), Dr. Dua teaches in the Pharmacy program and coordinates a suite of Good Manufacturing Practice (GMP) courses. He integrates innovative, student-centered teaching approaches, blending traditional and modern methodologies. Dr. Dua holds multiple adjunct roles internationally, including *Adjunct Assistant Professor* at the University of Alberta, *Core Member* at the Australian Research Centre in Complementary and Integrative Medicine (ARCCIM), and *Research Associate* at the Australia-China Relations Institute. His industry collaborations include consulting on GMP for *ULTI Pharmaceuticals* in New Zealand. His research focuses on managing chronic inflammatory diseases, particularly airway diseases, using novel nano-carriers for targeted drug delivery. Dr. Dua's work has led to over 190 peer-reviewed publications, more than 16,000 citations, and over 100 conference presentations.

In 2024, he was recognized as one of *Australia's Top 250 Researchers*, ranking #1 in Toxicology. His numerous awards include the *Excellence Award in Pharmacy* (2018) and the *Young Scientist Award* (2011).

Prof. Brian Oliver

University Technology, Sydney, New South Wales, Australia

Prof. Brian Oliver is a distinguished scientist whose groundbreaking work delves into the molecular and genetic dysfunctions underlying chronic diseases. With a career that bridges prestigious institutions and diverse research domains, his contributions continue to shape our understanding of environmental and respiratory health.

Brian's academic journey commenced at Imperial College London, where he laid the foundation for his scientific expertise. He further honed his skills in molecular biology at the University of Leeds and expanded his horizons into respiratory virology while training in the renowned laboratory of Professor Sebastian Johnston at Imperial College London. Subsequently, he embarked on his PhD at the University of Sydney, under the mentorship of Professor Judith Black, solidifying his position as a leader in his field.

Currently, Professor Oliver leads a dynamic research team based at the University of Technology Sydney (UTS) and the Woolcock Institute of Medical Research, where he serves as a Research Leader. His comprehensive research portfolio encompasses environmental health, respiratory virology, and respiratory pharmacology, addressing some of the most pressing challenges in modern healthcare.

In the realm of environmental health, Professor Oliver's team is at the forefront of investigating the profound impacts of air pollution exposure on human health, offering vital insights into the environmental triggers of chronic respiratory conditions. His pioneering work in respiratory virology seeks to unravel the complex interplay between lung responses and viral infections. By examining why common respiratory viruses, such as the cold virus, can escalate into severe, life-threatening illnesses, his research provides a pathway to improved preventive and therapeutic strategies. In the area of respiratory pharmacology, Brian has explored the cellular responses to nicotine exposure, including the effects of cigarette smoke and e-cigarettes.

Dr. Ankur Sood

School of Chemical Engineering, Yeungnam University, South Korea

Dr. Ankur Sood is a distinguished researcher in Nanotechnology, specializing in drug delivery and imaging applications. He completed his Ph.D. on *"Iron Oxide-Gold Core-Shell Nanoparticles for Drug Delivery and Imaging Applications"*, focusing on the use of gold-coated iron oxide nanoparticles for targeted drug delivery and their high-contrast properties for MR and ultrasound imaging.

Dr. Sood's expertise lies in applying material science and nanotechnology within biomedical sciences. He has extensive experience in in-vitro and in-vivo nanoparticle therapeutics, including enhancing radiosensitivity in cancer therapies. He began his career as a Council of Scientific & Industrial Research (CSIR)-Senior Research Fellow (SRF) at GGSIP University (2012-2016), later receiving a Short-Term Research Fellowship (STRF) from 2016-2018. Prior to his Ph.D., Dr. Sood worked at INMAS-DRDO, developing radioprotectant drugs.

Dr. Sood also worked as a Research Associate at the Institute of Nanoscience and Technology (2018-2020) and Senior Project Scientist at IIT Mandi (2020-2021). He completed a Postdoctoral Fellowship at Yeungnam University, South Korea (2021-2022) and currently serves as an International Research Professor at Yeungnam University, focusing on biomaterials and advanced drug delivery systems.

Prof. Vetriselvan Subramaniyan

Department of Medical Sciences, Sunway University, Malaysia

Prof. Vetriselvan Subramaniyan is a preeminent pharmacologist with a remarkable career spanning over fifteen years, dedicated to teaching, research, and academic leadership across renowned institutions in Malaysia, Ethiopia, and India. His exceptional contributions to academia include serving in pivotal roles such as Acting Dean and Deputy Dean, where he demonstrated visionary leadership and academic excellence.

An ardent advocate of global health, Professor Vetriselvan has actively participated in initiatives under the auspices of the United Nations Development Programme (UNDP), contributing to transformative health policies and practices worldwide. His prolific research portfolio, encompassing over 240 peer-reviewed publications and eight internationally recognized patents, underscores his profound impact on pharmacological sciences. He has also been the recipient of numerous prestigious grants, reflecting his ability to attract substantial funding for groundbreaking research. Professor Vetriselvan is also a fellow of multiple esteemed scientific societies and a sought-after keynote speaker at international conferences. He has served as an examiner for Ph.D. dissertations and holds visiting professorships in India and China, further solidifying his reputation as a global academic luminary. In addition, he plays a strategic role as an overseas executive member of the Indian Pharmacological Society, contributing to the advancement of pharmacology both within India and on the global stage.

Dr. Debasisa Mohanty

National Institute of Immunology, New Delhi

Dr. Debasisa Mohanty is a renowned Indian computational biologist and bioinformatician, currently serving as the Director of the National Institute of Immunology (NII), India. Acclaimed for his groundbreaking research in protein structure prediction, genome analysis, and biomolecular simulations, Dr. Mohanty is a Fellow of India's three premier science academies: the Indian Academy of Sciences, Indian National Science Academy, and National Academy of Sciences, India. His contributions to biosciences earned him the National Bioscience Award for Career Development in 2009.

An alumnus of IIT Kanpur, where he earned his MSc in Physics, and the Indian Institute of Science, where he completed a PhD in computational biophysics, Dr. Mohanty refined his expertise with postdoctoral work at the Hebrew University of Jerusalem and Scripps Research Institute. At NII, he leads initiatives like the RiPPMiner Bioinformatics Resource and mentors emerging researchers. With over 100 publications and multiple awards, including the Samanta Chandrashekhar Award and Rajib Goyal Young Scientist Prize, Dr. Mohanty has significantly advanced computational biology and bioinformatics, earning a lasting legacy in the scientific community.

Prof. Ganesh Bagler

Department of Computational Biology,
Indraprastha Institute of Information Technology, New Delhi, India

Prof. Ganesh Bagler is a visionary computational researcher whose interdisciplinary expertise spans physics, computer science, and computational biology. He is globally recognized for his pioneering contributions to the emerging field of Computational Gastronomy, a novel data-driven science at the intersection of food and artificial intelligence. By curating foundational data repositories, designing innovative algorithms, and developing transformative applications, Prof. Bagler has laid the groundwork for this revolutionary discipline, which explores the intricate relationships between food, flavors, nutrition, and public health.

As the driving force behind groundbreaking research, Prof. Bagler's work has redefined how we understand and interact with food systems. His lab has produced trailblazing insights that extend beyond gastronomy, delving into the structure, function, evolution, and design of complex systems, including proteins, the brain, health, languages, and creativity. His audacious vision of "Making Food Computable" underscores his ambition to reshape the global food landscape by leveraging the power of computational science to address pressing challenges in nutrition, health, and sustainability. Prof. Bagler is also an engaging science communicator and TEDx speaker, inspiring audiences with his unique blend of curiosity and innovation.

Dr. Ramesh V Sonti

Director ICGEB, New Delhi

Dr. Ramesh Sonti is a renowned scientist in the field of plant genetics, celebrated for his groundbreaking contributions to agricultural biotechnology and molecular biology. With a stellar academic foundation, he earned his B.Sc. in Botany, Zoology, and Chemistry from Andhra University in 1980, followed by an M.Sc. with distinction and a Gold Medal and an M.Phil. in Plant Sciences from the University of Hyderabad. He later completed his Ph.D. in Bacterial Genetics at the prestigious University of Utah, USA. His academic journey was further enriched through postdoctoral research on plant genetics at the Massachusetts Institute of Technology (MIT), Cambridge, USA.

In 1993, Dr. Sonti joined the Centre for Cellular and Molecular Biology (CCMB), Hyderabad, where he made transformative contributions to plant science research. In November 2017, he assumed the role of Director at the National Institute of Plant Genome Research (NIPGR), New Delhi, where he continues to lead cutting-edge initiatives in plant genomics and biotechnology.

Dr. Sonti's illustrious career is adorned with numerous accolades, including the Shanthi Swarup Bhatnagar Prize in Biological Sciences and the National Bioscience Award from the Department of Biotechnology, Government of India. He has been honored with the prestigious J.C. Bose Fellowship by the Department of Science and Technology and is an elected fellow of several esteemed academies, including the Indian National Science Academy (New Delhi).

Prof. Saurabh Raghuvanshi

Department of Plant Molecular Biology, University of Delhi South Campus, Delhi, India

Prof. Saurabh Raghuvanshi is a distinguished researcher whose work focuses on unraveling the intricate regulatory networks that govern higher organisms. His research aims to decipher these networks as multi-dimensional systems comprising diverse genomic elements—such as proteins, regulatory RNAs, and cis-acting elements—that interact dynamically in response to developmental and environmental cues. At the forefront of this exploration is his lab's groundbreaking work on microRNAs (miRNAs), a critical dimension of these regulatory systems known to influence a wide range of developmental and metabolic processes in plants and animals.

A key objective of Prof. Raghuvanshi's research is the identification of novel miRNAs and their interacting partners in plants. His team employs deep sequencing technologies combined with advanced bioinformatics to analyze the entire small RNA population from various tissues and developmental stages of rice. By characterizing global changes in miRNA populations under different developmental and environmental conditions, this work provides transformative insights into plant regulatory mechanisms and adaptive responses.

In parallel, Prof. Raghuvanshi's lab is spearheading an ambitious initiative to create a protein-centric interaction database for rice. This database goes beyond simple data aggregation; it seeks to interconnect genomic elements through manual literature-based curation, providing a logical framework based on published findings. Designed as a self-sustaining, collaborative hub, this database aims to empower researchers worldwide by offering a rich, interconnected repository of information. It also fosters global collaboration, enabling research groups to actively contribute and share discoveries.

Dr. Shantanu Chowdhury

CSIR Institute of Genomics and Integrative Biology, New Delhi

Dr. Shantanu Chowdhury is a distinguished scientist renowned for his contributions to functional genomics and gene regulation. He completed his master's degree in chemistry from Jadavpur University, Kolkata, followed by a Ph.D. from the Indian Institute of Chemical Technology, Hyderabad, in 1998. His academic journey continued with postdoctoral research at the University of Nebraska and the Max Planck Institute for Terrestrial Microbiology, where he honed his expertise in biochemistry and molecular biology.

Since joining the Institute of Genomics and Integrative Biology (IGIB) in 2002, Dr. Chowdhury has served as a professor of functional genomics, leading pioneering research in gene regulation mechanisms and DNA secondary structures, such as G-quadruplexes. His groundbreaking work has illuminated the role of NME2, a metastasis suppressor, in telomerase function and gene transcription processes. Under his leadership, his team has developed novel insights into the biological action of DNA structures, contributing to our understanding of genetic and epigenetic regulation.

Dr. Chowdhury's extensive research portfolio is reflected in numerous high-impact publications indexed in PubMed. Beyond his academic pursuits, he serves as a member of the scientific advisory board for Bionivid, a Bengaluru-based bioinformatics company, and holds editorial positions on the boards of Human Genomics and the Journal of Biological Chemistry.

Dr. Dhiraj Kumar

International Centre for Genetic Engineering and Biotechnology ICGEB, New Delhi

Dr. Dhiraj Kumar is a distinguished scientist leading the Cellular Immunology Group at the International Centre for Genetic Engineering and Biotechnology (ICGEB), New Delhi. A Senior Fellow at the institute, he is renowned for his groundbreaking research in the cellular and molecular mechanisms underpinning infectious diseases, particularly Mycobacterium tuberculosis and HIV infections. His work focuses on phagocyte cell biology, innate immune responses, and the integration of high-throughput and computational biology in studying complex biological systems.

Dr. Kumar earned his MSc from the Indian Council of Agricultural Research in 2002 and completed his PhD at ICGEB in 2007. His research has advanced our understanding of host-pathogen interactions, shedding light on tuberculosis, a critical global health challenge. His exceptional contributions to medical science earned him the prestigious Shanti Swarup Bhatnagar Prize for Science and Technology in 2019. Recognized as a leader in his field, Dr. Kumar was elected a Fellow of the Indian Academy of Sciences in 2024, reflecting his dedication to advancing science.

Prof. Sachin Kumar Singh

Pharmaceutical Analysis, Lovely Professional University, Jalandhar - Punjab, India

Prof. Sachin Kumar Singh is an accomplished pharmaceutical analyst and academician, blending extensive research expertise with a passion for teaching. Currently serving as an Associate Professor at the School of Pharmaceutical Sciences, Lovely Professional University, Prof. Singh has carved out a distinguished career characterized by innovation, dedication, and impactful translational research.

Prof. Singh holds a Master of Pharmacy in Pharmaceutical Analysis from J.S.S. College of Pharmacy, Ooty, Tamil Nadu, and earned his Ph.D. in Pharmaceutical Sciences from Karpagam University, Coimbatore. His professional journey is marked by a unique interplay of research and teaching, enabling him to develop cutting-edge solutions while mentoring the next generation of pharmaceutical scientists. A cornerstone of his research achievements is the development and validation of a dissolution method for Protodioscin, a potent antidiabetic compound found in FENFURO Capsules, which are now successfully marketed in India. This translational research highlights his commitment to bridging the gap between the lab and patient care. His work in developing Self-Nanoemulsifying Drug Delivery Systems (SNEDDS) for polypeptide-K, funded by a DST/SERB Fast Track Young Scientists Scheme grant of □23 lakhs in 2013, further underscores his innovative approach to addressing diabetes treatment.

Prof. Sachin's research portfolio extends back to his master's degree, during which he collaborated with Neo Pharma, Abu Dhabi, on Comparative Bioavailability Studies of Simvastatin Tablets using LC/MS in healthy human volunteers. His dedication to pharmaceutical research has earned him prestigious accolades, including the Bharat Shiksha Ratan Award (2014) and the Global Teacher Role Model Award (2015). These honors recognize not only his research contributions but also his role as an inspiring educator. With a strong focus on mentorship, Prof. Singh has successfully guided 15 master's students to graduation and currently supervises 5 Ph.D. scholars. His deep interest in translational research drives his ambition to ensure that his findings make a tangible impact, reaching the patient's bedside to improve healthcare outcomes.

Dr. Hemant Agrawal

Flow Cytometry solutions (FlowSols) India

Dr. Hemant Agrawal is a distinguished expert in flow cytometry and a passionate advocate for advancing education and training in this specialized field. With a prolific career encompassing numerous peer-reviewed scientific publications, Dr. Aggarwal has been a sought-after speaker at prestigious national and international conferences. His contributions extend beyond research, as he plays a pivotal role in shaping the future of cytometry education through his leadership in the Trust for Education and Training in Cytometry (TETC), India. This organization is renowned for conducting the highly regarded Indo-US Cytometry Workshops and other cytometry-focused meetings across India and neighboring regions.

A seasoned practitioner, Dr. Aggarwal possesses extensive expertise in designing and executing flow cytometry experiments. His skill set includes immunophenotyping, intracellular staining, cell proliferation, cell cycle analysis, apoptosis studies, and cytometric bead array applications. To bridge the gap between complex scientific methodologies and practical implementation, Dr. Aggarwal founded Flow cytometry Solutions (P) Ltd. (FlowSols), a consultancy that offers hands-on training and expert guidance in flow cytometry to researchers, clinicians, and students across India and neighboring countries. Dr. Aggarwal's dedication to education is exemplified by his organization of over 85 onsite workshops and 40 online courses, where thousands of participants have been trained in designing, acquiring, and analyzing flow cytometry data. In 2023, his organization launched the Annual Online Certificate Course in Flow Cytometry, a groundbreaking initiative and the first of its kind globally. This course has garnered widespread recognition for its comprehensive curriculum and accessibility to learners worldwide.

Dr. Shrilaxmi Desiraju

CEO, Co-founder of AA Probics

Dr. Shrilaxmi Desiraju is a trailblazing technopreneur and an accomplished leader in the nutraceutical and pharmaceutical industries, with over 22 years of expertise spanning research commercialization, strategic partnerships, and business development. Armed with a Ph.D. in Natural Product and Medicinal Chemistry and an MBA specializing in Technology Commercialization, she has seamlessly merged her deep scientific knowledge with entrepreneurial acumen, carving a distinguished niche for herself as the Co-founder of Triphase Pharmaceuticals, a cutting-edge probiotic R&D company.

Dr. Desiraju's unique academic foundation enables her to approach innovation from a dual perspective—scientific rigor and commercial viability. Her proficiency extends to out-licensing deals, R&D services, and both B2B and B2C marketing, demonstrating her versatile capabilities in navigating complex market dynamics. With a proven track record in the pharma and nutraceutical sectors, she has also excelled in academia, contributing to a holistic understanding of innovation and enterprise.

As a first-generation entrepreneur, Dr. Desiraju has successfully navigated the high-stakes landscape of business funding. She has secured diverse forms of financial support, including debt financing from banks and Series A funding from investors, exemplifying her adeptness at managing the financial intricacies of a high-risk industry. Her expertise also encompasses the comprehensive processes of intellectual property (IP) management, as well as regulatory and financial compliance, ensuring robust foundations for sustainable growth.

Mr. Raghu Rangaswamy

Molecular Solutions, Bangalore, India

Mr. Raghu Rangaswamy is the visionary CEO of Molecular Solutions Software Pvt. Ltd., a trailblazing company that stands at the forefront of revolutionizing the drug discovery process with cutting-edge software solutions. With a wealth of expertise in computational chemistry, Raghu brings a unique blend of technical acumen and strategic foresight to the company's operations. His leadership focuses on making advanced research tools more accessible to both academic institutions and pharmaceutical companies, with an unwavering commitment to innovation and cost-effectiveness.

Under Raghu's guidance, Molecular Solutions has forged valuable partnerships with some of the most renowned software providers in the industry, including Dotmatics, ChemAIRS, Simulations Plus, and Nanome. Together, they offer a diverse range of solutions that encompass Retrosynthesis, ADMET prediction, molecular modeling, DMPK, ELN, and AI/ML applications, catering specifically to the drug discovery and life sciences sectors.

Raghu's dedication to empowering the scientific community is evident in the company's continuous efforts to streamline research processes and accelerate the pace of discovery. Through his leadership, Molecular Solutions is setting new benchmarks in the industry, delivering tools that not only enhance the efficiency of research but also drive groundbreaking advancements in drug development.

Dr. Rahul Solanki

Agilent Technologies India

Dr. Rahul Solanki is a distinguished molecular and cellular biologist, having earned his Ph.D. from the prestigious Institute of Microbial Technology, Chandigarh. With over 12 years of dedicated experience in the field of genomics, his expertise spans cutting-edge areas such as Next-Generation Sequencing (NGS), Single-Cell Genomics, and Microarray technologies.

Dr. Rahul has collaborated closely with prominent leaders in the domains of NGS and Microarray, contributing significantly to several high-impact projects. His achievements include facilitating deep sequencing studies of *Mycobacterium tuberculosis*, spearheading shotgun and 16S metagenomics analyses, and advancing methodologies for NGS using liquid biopsies. His work reflects a profound commitment to advancing genomic research and innovation, making him a vital contributor to the scientific community.

Dr. Amit Bhattacharya

Incise Infotech Private Limited, Nandi Infotech Building, Whitefield, Bengaluru, Karnataka

Dr. Amit Bhattacharya is a distinguished expert with a PhD in Cancer Cell Biology from the Centre for Cellular and Molecular Biology, Hyderabad. With over two decades of extensive experience in technology and product marketing within the realms of cellular and tissue analysis, he has contributed significantly to the advancement of cutting-edge methodologies and tools. His expertise spans high-resolution fluorescence microscopy, high-parameter flow cytometry, mass cytometry, and imaging cytometry, making him a leading specialist in 3D and high-resolution fluorescence microscopy applications.

Dr. Bhattacharya has held pivotal roles in renowned multinational corporations, including Bio-Rad Laboratories, Carl Zeiss, Leica Microsystems, and Danaher Corporation. His recent endeavors focus on automated and high-throughput microscopy, tissue analysis, digital pathology, and multi-omic single-cell analysis, particularly in precision medicine and pharmaceutical research.

Currently, Dr. Bhattacharya is affiliated with Incise Infotech, where he is spearheading efforts to establish business ventures in live-cell confocal microscopy, digital pathology, and tissue analysis. He collaborates with innovative companies such as Crest Optics, Huron, and TissueGnostics, furthering advancements in these cutting-edge domains.

Dr. Deeksha Bhartiya

Founder, Genomiki Solutions, U.P, India

Dr. Deeksha Bhartiya is an accomplished researcher with over a decade of expertise in genomics, utilizing advanced computational and programming skills to study complex diseases such as malaria, tuberculosis, and various cancers. She holds a Ph.D. in Bioinformatics from the esteemed CSIR-Institute of Genomics and Integrative Biology and has accumulated over nine years of impactful postdoctoral experience. She specializes in analyzing and interpreting Next-Generation Sequencing (NGS) datasets, including whole-genome sequencing, RNA-seq, and CLIP-seq.

Her research in genome informatics has made significant strides in understanding non-coding RNAs, evaluating the functional impact of genetic variations, and developing computational algorithms to analyze regulatory features of microRNAs, long non-coding RNAs, and small nucleolar RNAs. Dr. Bhartiya has also created comprehensive computational resources for genomic studies on human, model organisms like zebrafish, and pathogens such as *Mycobacterium tuberculosis*.

Currently, her work focuses on studying the whole-genome sequencing datasets of clinical isolates of *Salmonella enterica* serovar Typhi to identify small RNAs. She has also explored gene dysregulation in oral cancer and investigated the impact of smokeless tobacco compounds on disease pathways.

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सत्यमेव जयते

India's biosciences journey began with the establishment of the Department of Biotechnology (DBT) in 1986, focusing on human resource development, infrastructure, R&D, and regulatory frameworks. Over the years, DBT has fostered prestigious institutes, strategic collaborations, and industry partnerships, advancing healthcare, agriculture, and environmental security. It also promotes biotechnology through financial support for conferences, travel, exhibitions, and popular lectures under the CTEP program.

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The Anusandhan National Research Foundation (ANRF), established under the ANRF 2023 Act, aims to promote R&D and a culture of innovation across India's Educational and Research Institutions. Acting as the apex body for scientific research as per NEP recommendations, ANRF subsumes the Science and Engineering Research Board (SERB) and promotes collaborations between Industry, Academia, Government, and State entities.

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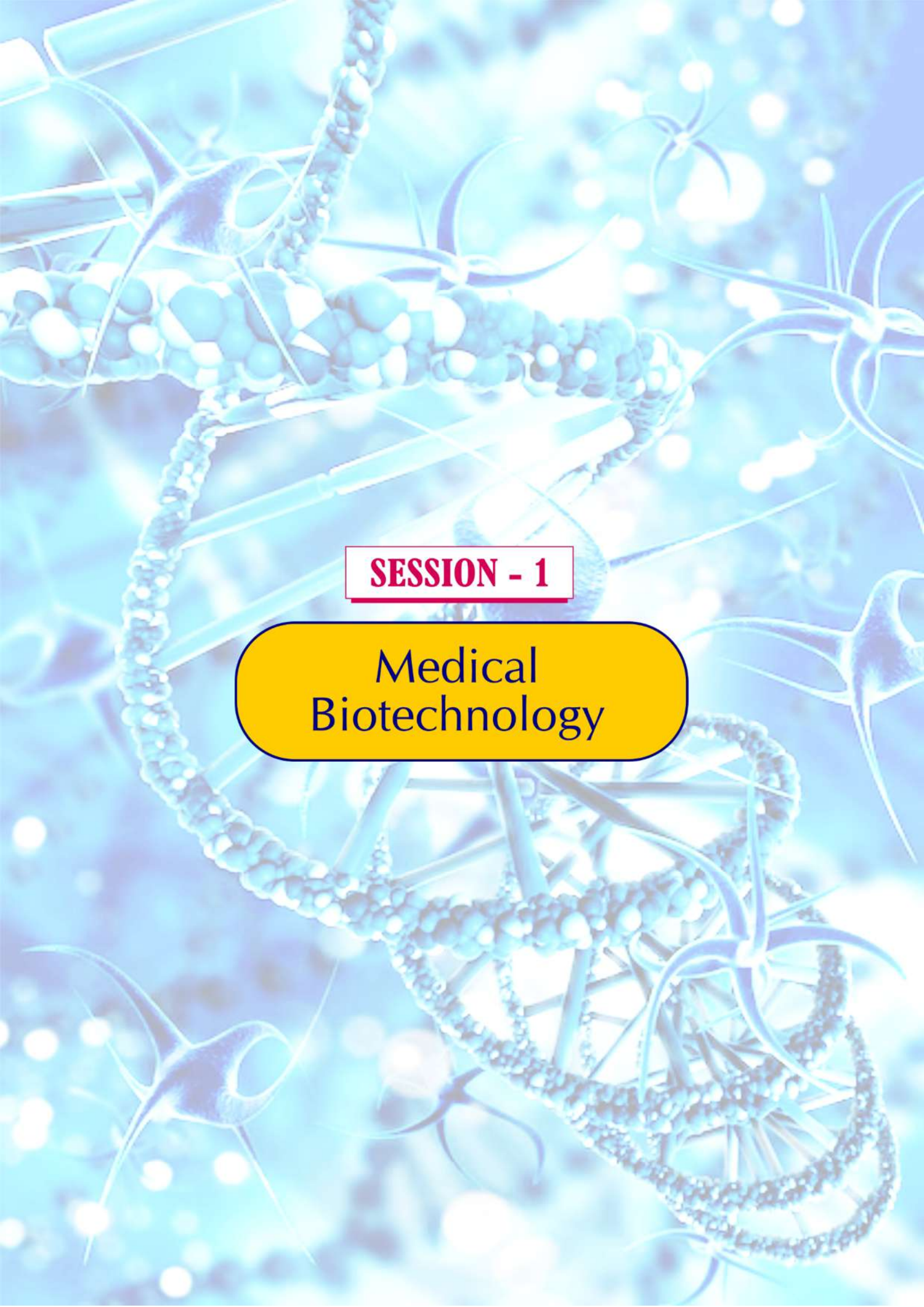

SESSION - 1

Medical Biotechnology

MBPP01

Extraction of Collagen from Animal Tissue

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ABSTRACT

Collagen, particularly atelocollagen, is in high demand for applications in cosmetics, medicine, wound healing, tissue regeneration, and anti-aging formulations. The structural arrangement of polypeptide chains and variations at the terminal ends differentiate types of collagens into fibrillar and non-fibrillar forms. Collagen types exhibit diverse conformations, resulting in different helix lengths and distributions of non-helical segments. These structural characteristics classify collagen into distinct categories, with fibrillar collagen being one of the primary groups. The chemical extraction methods, which are often cumbersome and involve multiple steps, are environmentally harmful, expensive, and time-consuming. These conventional processes include salting-out, alkaline, acid, enzymatic treatments, and ion-exchange chromatography. Researchers have developed an innovative method using supercritical carbon dioxide (SCCO2) technology to purify collagen from pig skin, addressing the rapidly growing demand for high-purity collagen. Fish-derived collagen, particularly from Mozambique tilapia scales, has emerged as a cost-effective and highly bioavailable ingredient for promoting hair and skin health. The extraction process aims to eliminate non-collagenous substances and obtain purified collagen as the final product. The recovery process typically involves the pretreatment of source tissue, followed by collagen extraction and further purification. This abstract discusses the growing need for collagen, especially atelocollagen, across a range of fields like cosmetics, medicine, wound care, tissue repair, and anti-aging products. It explains that collagen types differ in their structure, with some forming fibrils while others do not, largely due to variations in how their polypeptide chains are arranged.

Keywords: Collagen Extraction; Collagen Structure; Tissue Regeneration; Chemical Extraction; Supercritical Carbon Dioxide ($SCCO_2$).

MBPP02

Impact of Dietary Supplements on Aging

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ABSTRACT

Various biological factors, including genetic damage, telomere shortening, mitochondrial dysfunction, and the decline of cellular processes such as autophagy and proteostasis influence aging. All of these elements work together to cause the body's cellular senescence and diminished capacity for regeneration. As a result, dietary supplements are widely promoted as ways to improve general health and lessen the consequences of ageing. These supplements frequently contain vitamins, minerals, antioxidants, alkaloids, polyphenols, saponins, ginsenosides, and polyphenols, each of which is said to target aging-related processes through a different method. For instance, alkaloids like caffeine and berberine are known to lower oxidative stress and enhance cellular energy balance, whereas polyphenols have been researched for their anti-inflammatory and neuroprotective qualities.

Heart health, bone strength, immunological function, and energy levels are just a few of the health characteristics that these supplements are said to promote. Their efficacy varies widely, though, and is mostly dependent on a patient's unique medical circumstances, dose, and any drug interactions. Serious adverse consequences, like vitamin or mineral poisoning, can result from taking too many supplements. For example, too many fat-soluble vitamins, such as A, D, E, and K, can build up to toxic amounts in the body and pose serious health hazards. The profit-driven nature of the supplement industry presents more issues. Manufacturers and other economic players heavily promote these items, frequently putting profits ahead of consumer safety. The controversy surrounding the herbal supplement Ephedra, which was outlawed after causing serious health problems, serves as a reminder of the risks associated with unregulated or insufficiently vetted supplements.

Keywords: Anti-inflammatory; Autophagy; Cellular Energy Balance; Dietary Supplements; Supplements.

MBPP03

Molecular Characterization and Genomic Analysis of Extremophilic Priestia Megaterium CL-1, Isolated from Chilka Lake

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ABSTRACT

Bacteria have intrinsic ability to tolerate and survive in several stress conditions including salt stress. In the present study, we evaluated the stress tolerance ability of salt-tolerant bacterium known as Priestia megaterium CL-1 isolated from Chilka salt lake, Orissa by genome analysis. P.megaterium is a gram-positive, spore-forming halophilic bacterium that is ubiquitous in various environments. The ability to survive under a wide temperature environment (3 to 45 ℃), salt conditions and utilization of different carbon sources, makes it suitable for industrial applications. A number of P. megaterium strains have been developed and characterized for several features including sporulation, auxotrophy, recombination, division, germination, and antibiotic resistance, etc. The cell surface hydrophobicity and co-aggregation assay against different bacterial strains illustrated its putative pathogenic nature. The complete genome size of CL-1 was 4.1 Mb, 1.66% GC-content, and total gene numbers of 6,068 were predicted. The genome analysis of CL-1 unravelled the presence of an open reading frame (ORF) encoding the functions related to environmental stress tolerance, adhesion processes, multidrug efflux systems, and heavy metal resistance. Genome annotation identified the various genes for chemotaxis, flagellar motility, and biofilm production, illustrating its strong colonization ability. The current findings provide the in-depth investigation of P. megaterium CL-1 acterium that possessed various genome features that enable the bacterium to survive under diverse conditions. The strain possesses the strong ability for probiotic application purposes.

Keywords: Chilika Lake; Intrinsic Ability; Gram-positive Bacteria; Salt-tolerant Bacterium; Probiotics.

MBPP04

Functional Role of Taurine in Aging and Cardiovascular Health

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ABSTRACT

Taurine, a sulphur-containing amino acid that occurs naturally, has attracted significant attention because of its wide range of health advantages. Commonly found in a variety of foods and regularly included in energy drinks and dietary supplements, taurine plays a pivotal role in human physiology. This review explores the compound's functional roles across multiple domains, with a primary focus on aging and cardiovascular health. Its effects on metabolic processes, neurological function, and athletic performance are also evaluated.

Emerging evidence from both human and animal studies underscores taurine's potential to enhance cardiovascular well-being by regulating blood pressure, improving heart function, and promoting vascular health. Its ability to neutralize oxidative stress and support cellular function positions taurine as a candidate for anti-aging interventions. Furthermore, taurine's involvement in energy metabolism and its neuroprotective properties provide a foundation for addressing age-related health issues.

The review also looks at some of the current recommendations for taurine diet and possible safety issues associated with supplementation. Although being widely accepted as safe, specific guidance based on each person's unique medical condition is still crucial. This analysis highlights taurine's adaptation in maintaining health and minimizing aging-related risks by applying results from scholarly literature.

Keywords: Aging; Anti-Aging; Cardiovascular health; Supplementation; Taurine.

MBPP05

Host-Pathogen Dynamics: Mycobacterium tuberculosis Cording and the Strategic Interplay of Immunity

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ABSTRACT

Tuberculosis (TB), caused by Mycobacterium tuberculosis (M. tb), is a major global health challenge, complicated by the pathogen's immune evasion strategies and multidrug resistance. This review examines the roles of M. tb's virulence factors, particularly the cord factor trehalose di-mycolate (TDM) and the Ag85 protein family. TDM promotes cord formation and granuloma development, aiding M. tb's persistence within host tissues. Advanced imaging techniques, including confocal microscopy and correlative light and electron microscopy (CLEM), have clarified the structural roles of these cords in immune modulation.

Key virulence factors such as TDM and Ag85 enable M. tb to evade immune defences, contributing to treatment challenges. Targeting Ag85 proteins with inhibitors like I3-AG85, is a promising strategy for disrupting M. tb's cell wall integrity, potentially increasing susceptibility to host responses and improving therapeutic efficacy.

Significant challenges persist, especially in overcoming drug resistance and ensuring specificity in therapeutic targeting. This review consolidates current insights and underscores the need for innovative approaches to enhance TB treatment and prevention strategies.

Keywords: Mycobacterium Tuberculosis, Trehalose Dimycolate, Ag85 Proteins, Immune Evasion, Multidrug Resistance.

MBPP06

In Silico Assessment of Phytoactives Against Staphylococcus aureus and Pseudomonas aeruginosa: A Strategic Approach to Address Antimicrobial Resistance

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ABSTRACT

In the complex ecosystem of microorganisms, antimicrobial resistance (AMR) develops as pathogens undergo adaptive changes, resulting in a significant reduction in the efficacy of the most potent antimicrobial agents against these increasingly resilient organisms.The escalating threat of antibiotic resistance necessitates innovative strategies to combat pathogenic bacteria like Staphylococcus aureus and Pseudomonas aeruginosa. In order to look for other alternatives to fight against AMR, the present study was conducted by identifying the molecular marker responsible for AMR which were further docked with natural compounds belonging to the popular categories of flavonoids, carboxylic acids and alkaloids. Docking of these compounds with virulence factors hemolysin, TTSS and clumping factors, known for their severe infection potential due to various virulence strategies, including adherence, immune evasion, and biofilm formation, revealed that cevadine, lupeol, mangiferin, ellagic acid and friedelin were having the lowest negative energies in comparison to the standard antibiotic: Fusidic acid. This study advocates further exploration of phytotherapeutics in clinical settings, highlighting the necessity for innovative approaches to combat pathogenic bacteria effectively. The study emphasizes the significant anti-virulence properties of specific phyto-compounds, particularly flavonoids, phenolic acids, and benzenoids, in mitigating these virulence mechanisms.

Keywords: Staphylococcus Aureus; Pseudomonas Aeruginosa; Antimicrobial Resistance; Fusidic Acid; Biofilm Formation.

MBPP07

Exosome-Mediated Targeted Drug Delivery and Biomarker Discovery in Lung Cancer Therapy

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ABSTRACT

Lung cancer is a leading cause of cancer-related deaths globally, with a mortality rate of approximately 18.4%. Recent research is focusing on exosome-based targeted therapies as a potential treatment option. These therapies utilize exosomes derived from lung cancer cells, which can enhance drug delivery and improve treatment efficacy by targeting tumour sites more precisely. Exosomes are nano-sized endosomal vesicles secreted by cells via outward budding. They contain various bioactive molecules like DNA, RNA, lipids, metabolites, cytosolic and cell surface protein, from the cells. Exosomes are also capable of transferring biological molecules, such as proteins, from host cells to recipient cells. Their phospholipid bilayer and low immunogenicity facilitate their ability to cross biological barriers with greater ease. Exosomes from various bodily fluids serve as promising biomarkers for cancer diagnosis and prognosis. Their ability to encapsulate diverse biomolecules, cross biological barriers, and be engineered for targeted delivery makes them valuable for both diagnostics and precise drug delivery to cancer cells, offering new possibilities in cancer research and treatment. Stem cell-derived exosomes from Mesenchymal stem cells (MSCs) have the therapeutic properties of their parent cell and can help in wound healing, tissue regeneration, immunomodulation, neuroprotection, and anti-apoptotic effects. They have significant advantages over stem cells, including non-immunogenicity, safety, easy access, and freedom from ethical concerns. Their therapeutic effects operate via tissue-specific responses and molecular signalling pathways. Notably, exosomes can both stimulate and suppress the immune system. The inclusion of antigens and MHC complexes in exosomes positions them as promising candidates for anticancer vaccines. Exosomal delivery of drugs, such as chemotherapeutic agents, strengthens this field as a novel platform to alleviate the side effects of toxic drugs. The current study is focused in analyzing the therapeutic potential of exosomes for lung cancer therapeutics.

Keywords: Exosomes; Lung Cancer; Mesenchymal Stem Cells; Immune Response; Therapies.

MBPP09

Harnessing the Power of Hairy Roots: Efficient Production of Bioactive Compounds

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ABSTRACT

Hairy root cultures, or HRCs, are one new and renewable source of the production of bioactive chemicals. Their advantages in usage over the traditional ways that include the cultivation of a whole plant and chemical synthesis are high-speed growth and genetic stability and can produce potential varieties of secondary metabolites. There are many advantages of HRCs, one of which involves being able to produce bioactive compounds that are either difficult to extract or could not be obtained from sources with natural origins. For instance, HRCs are effectively used in synthesizing a variety of alkaloids and their derivatives, terpenoids, and phenolics bearing extensive medicinal properties. These chemicals can be used in various new pharmaceuticals, nutraceuticals, and cosmeceuticals being developed. Several researchers who work on different parameters like culture conditions, elicitation, methodologies, and genetic engineering techniques, investigate the optimization of bioactive compound production in HRCs. Alterations in these variables increase the productivity along with the quality of the product molecule. For example, certain elicitors such as plant hormones or abiotic stress factors increase the synthesis of secondary metabolites. Genetic engineering can be used to include or overexpress specific genes responsible for particular molecules. HRCs are also more environmentally friendly compared to the traditional approach to the production of bioactive compounds. This project explores the advancement of hairy root culture, its applications, problems, and future prospects. It also discusses novel methods of increasing pharmaceutical production using hairy root-based root culture.

Keywords: Hairy Root Culture; Traditional Medicine; Bioactive Compounds; Genetic Engineering; Elicitors.

MBPP10

Assessment of Age from Alkaline Phosphatase Enzyme from Serum and Saliva Samples

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ABSTRACT

Alkaline Phosphatase (ALP) is a membrane-bound hydrolase enzyme. ALP works in basic conditions. The enzyme has been studied for several years, but only little information is present about the in vivo function of this enzyme. ALP distribution in nature is very vast. It is present in prokaryotes, eukaryotes, and all kinds of plants. The main function of ALP is to convert phosphate monoesterase into alcohol and free phosphate. Alkaline Phosphatase is used as an indicator of the health status of an individual. ALP can be classified into two main types. The first one is tissue-specific (placental, intestinal, and germ cell ALP), and the other one is tissue non-specific (liver, bone, and kidney). The ALP level of a healthy individual changes with age. Many researchers show that there is a significant relationship between the level of ALP in serum and the individual's age.Both types of samples (fresh and dried) are used in this study. Samples were collected and prepared using appropriate methods. Samples were analyzed for measuring ALP levels using the kinetic method on a bioanalyzer. Data was collected and interpreted using appropriate statistical methods.There is a relationship between age and ALP levels in blood serum and saliva. Both fresh and dried samples gave significant results. However, in saliva, only fresh samples were found to be useful for age assessment. This finding emphasizes the potential utility of dried samples in research, clinical diagnostics, and other areas where sample accessibility and stability are crucial.

Keywords: Alkaline Phosphatase; Age Assessment; Blood Serum; Saliva Samples; Bioanalyzer.

MBPP11

Gene Therapy for Obesity: Targeting MC4R Deficiency

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ABSTRACT

Melanocortin 4 receptor (MC4R) gene mutations are one of the major genetic components of obesity, which is a complex condition. Particularly in cases with an early onset, these abnormalities cause severe obesity by interfering with normal energy balance and appetite regulation. Previously the methods were exercising, diet plan , and drugs like Orlistat: (Alli, Xenical), Phentermine-topiramate: (Qsymia),Bupropion-naltrexone: (Contrave),Liraglutide: (Saxend Setmelanotide,(Imcivree) but they were not very effective. New developments in gene therapy, particularly the delivery of brain-derived neurotrophic factor (BDNF) via adeno-associated virus (AAV) vectors, present encouraging approaches to treating MC4R deficiency. According to preclinical research, BDNF gene therapy can improve metabolic health and lessen hyperphagia by restoring MC4R signalling. Patients with MC4R mutations may benefit from weight management, according to preliminary clinical research. In order to improve treatment outcomes, this review emphasises the significance of genetic profiling for patient classification. All things considered, gene therapy is a revolutionary way to treat obesity associated with MC4R deficits; nevertheless, more study is required to improve delivery strategies and address immunological reactions.

Keywords: Gene Therapy; MC4R Deficiency; Obesity; Brain-Derived Neurotrophic Factor (BDNF); Hyperphagia.

MBPP12

mRNA Vaccines: A New Era of Cancer Immunotherapy

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ABSTRACT

mRNA vaccines have transformed the field of infectious disease prevention, most significantly through unprecedented development and application during the COVID-19 pandemic. Such a technological achievement opens avenues into a new anticancer immunotherapy approach by encoding tumor-associated antigens to instruct cells that produce the antigens in question, thereby inducing strong immune responses against cancer cells. Some of the key advantages of mRNA cancer vaccines include their versatility, good safety profile, and the ability to induce innate as well as adaptive immunity. Unlike traditional cancer vaccines, mRNA vaccines can be designed and manufactured relatively quickly with the potential to approach personalized treatment within an individual patient based on the characteristics of their specific tumor. In addition, mRNA vaccines can also be combined with other immunotherapies, including checkpoint inhibitors, to enhance anti-tumor responses. The actual challenges for these vaccines lie in optimizing the delivery method, increasing the immunogenicity of these vaccines, and reducing potential immune tolerance. There are a number of active clinical studies about the use of mRNA cancer vaccines in different tumor types, and as research advances, there is a great deal of promise for the future; as a result, mRNA cancer vaccines seem to have bright futures. The current review delves into bringing a revolutionary change in the treatment strategies for cancer through mRNA cancer vaccine.

Keywords: COVID-19; Anticancer Immunotherapy; mRNA vaccines; Immunogenicity; Immunotherapies.

MBPP13

Exploring the Potential of Natural Compounds in the Treatment of Schizophrenia

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ABSTRACT

Schizophrenia is a psychosis disorder that leads to chronic mental health issues and behavioral disorders which include hallucinations, delusions, disorganized thoughts, and social withdrawal. The disorder is generally caused by defects in dopamine, glutamate, and serotonin pathways, and the other factors include genetic, environmental, prenatal infections, oxidative stress, immune system activation, and inflammation. The treatment of Schizophrenia is usually carried out with typical and atypical antipsychotics, that have significant side effects, therefore an alternative way that can significantly treat Schizophrenia is with natural compounds with reduced side effects and increased efficacy and effectiveness. The utilization of natural compounds also reduces neurotoxicity and oxidative stress, neuroinflammation, and various neurological anomalies in the brain tissues. The review focuses on the utilization of natural compounds for their neuroprotective actions, for the treatment of schizophrenia with reduced side effects, the natural compounds that have active ingredients such as flavonoids, alkaloids, terpenoids, terpenes, polypropanoids, lactones, and glycosides have increased effectiveness in treating the disorder.

Keywords: Schizophrenia; Dopamine; Antipsychotics; Neuroprotective; Neurotoxicity.

MBPP14

Screening and Genotyping of HPV in Cervical Cancer Patients: A Case-Control Study in North India

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ABSTRACT

India contributes to 1/3rd of worldwide cervical cancer deaths caused by HPV. High-risk human papillomavirus (hr-HPV)16 and 18 infections are responsible for more than 70% of cases. Early detection of hr-HPV infection can help in prevention and disease management. This case-control study evaluated the prevalence and genotyping of HPV and its association with socio-demographic characteristics and clinical stages of cervical intraepithelial neoplasia (CIN) among 200 North Indian women (65 CaCx cases and 135 controls). Genomic DNA was extracted from cervical specimens and analyzed using polymerase chain reaction (PCR) for HPV detection and genotyping. HPV prevalence was higher in cases (42%) compared to controls (8.8%), with HPV-16 identified as the most common genotype. Early marriage and higher parity were significant risk factors. HPV positivity correlated with advanced CIN stages, emphasizing the importance of genotyping in early detection and prevention. These findings underscore the need for targeted screening and vaccination strategies in high-risk populations.

Keywords: Human Papillomavirus (HPV); Cervical Cancer (CaCx); Cervical Intraepithelial Neoplasia (CIN); High-Risk HPV 16; Genotyping.

MBPP15

The Use of CRISPR Technology in Creating Models for Neurodegenerative Diseases

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ABSTRACT

CRISPR/Cas9 gene-editing technology offers transformative potential in understanding and treating amyotrophic lateral sclerosis (ALS), a neurodegenerative disease characterized by the progressive loss of motor neurons. With its complex genetic basis, including mutations in genes such as SOD1, FUS, and C9orf72, ALS remains incurable, and therapeutic options are limited. CRISPR/Cas9 enables precise correction of disease-causing mutations in patient-derived induced pluripotent stem cells (iPSCs), which can be differentiated into motor neurons to model ALS in vitro. This approach allows for the creation of isogenic cell lines, eliminating genetic variability and enabling a focused study of mutation-specific effects on cellular pathways such as oxidative stress, RNA misprocessing, excitotoxicity, and endoplasmic reticulum dysfunction. Gene correction using CRISPR/Cas9 has demonstrated the ability to reverse toxic phenotypes, restore cellular functions, and identify critical molecular mechanisms, paving the way for novel therapeutic strategies. By facilitating detailed investigations of ALS pathogenesis and offering a platform for targeted drug development, CRISPR/Cas9 holds great promise in advancing personalized treatments and addressing the unmet medical needs of ALS patients.

Keywords: Gene editing; CRISPR/Cas9; Neurodegenerative disease; Amyotrophic lateral sclerosis; Induced pluripotent stem cells; Endoplasmic reticulum dysfunction.

MBPP16

Pharmaceutical Fallout: The Escalating Environmental Impact of Drug Residues

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ABSTRACT

Pharmaceutical pollutants have now emerged as a burning issue all over the world with disastrous impacts on ecosystems and human health. Pharmaceutical products involve antibiotics, analgesics, and other personal care products. These residues result from improper disposal, run-off from agricultural sources, and excretion from the human body, building up in water, soil, and even air. This substantially alters aquatic ecosystems and what breeds antibiotic resistance and challenges biodiversity. For example, the pervasiveness of high levels of paracetamol, triclosan, and antibiotics gives it a prevalent nature within regions without adequate infrastructures to handle waste correctly. Existing remediation measures have failed to adequately control the persistence and complexity with which these pollutants are viewed. This paper presents synthetic approaches for novel and sustainable remediation measures. Targeted pathways are developed by using genetic circuits and synthetic enzymes with engineered microbes toward the degradation of pharmaceutical pollutants, turning them into harmless byproducts. Synthetic biofilms and biosensors capture pollutants through sophisticated real-time methods, whereas metabolic engineering forms an exact alteration in the microbial pathways, capable of enhancing biodegradation. Strict regulation and public awareness initiatives, with an interdisciplinary approach, are highly advocated in research to minimize pharmaceutical pollution. Leverage of synthetic biology has made it possible for this study to develop scalable, effective solutions toward environmental problems within the context of pharmaceutical residues that guarantee long-term sustainability and resilience. Therefore, Synthetic biology solutions, together with environmental remediation, are critical in defending ecosystems and public health from the growing threat of pharmaceutical contamination.

Keywords: Pharmaceutical Pollutants; antibiotic resistance; Synthetic Biology; Bioremediation; Biosensors.

MBPP17

Role of Traditional Medicines in the Treatment of Major Depressive Disorder

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ABSTRACT

Depression is one of the most common neuropsychiatric disorders, and the fourth leading cause of long-term disability throughout the world. Despite the availability of different classes of antidepressant drugs, most of them are not completely effective and above all are associated with many serious adverse effects. Traditional herbal medicine has been used for the treatment of various disorders including depression for a long history with multi-targets, multi-levels and multi-ways, attracting great attention from scholars. Recently, 11 natural products obtained from plants such as Hypericum perforatum, Catha edulis, Tinospora cordifolia, Curcuma longa, Ferula foetida, Rhodia larosea, Glycyrrhiza glabra, Crocus sativus, Ocimumba silicum and Embelica officinalis have been commercialized as antidepressants which have become increasingly popular in the world health drug markets due to lower cost with zero side-effects. This review aims to briefly discuss the traditional use of herbal medicines and especially recapitulate the natural products with antidepressant activity and their pharmacological functions and mechanism of action, which may contribute to a better understanding of potential therapeutic effects of natural products and the development of promising drugs with high efficacy and low toxicity for the treatment of stress-induced depression.

Keywords: Depression; Traditional Herbal; Antidepressant Drugs; Multi-Targets; Stress-Induced Depression.

MBPP18

Hypothesis: Mitophagy Modulators can Control Skin Aging by Renewing Mitochondrial Homeostasis

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ABSTRACT

Skin ageing is a multifactorial process, which is intrinsically as well as extrinsically regulated. A key regulator of skin function and structural homeostasis is mitochondrial functioning. Impairment of mitochondrial quality control through intrinsic or extrinsic stressors (redox imbalance, inflammation, UV radiation, pollution) lead to aberrant mitochondrial dynamics, low biogenesis, and defective mitophagy. Mitochondria targeted interventions are emerging as promising therapy in combating aging and other age associated diseases. Quality control of mitochondria via selective degradation of damaged mitochondria – mitophagy, is an emerging target. Damaged mitochondria exacerbate the cellular redox balance, compromise cellular bioenergetics due to failure of OXPHOS system, accumulation of mtDNA mutations, denatured proteins and lipids, loss in cellular viability and division mechanisms, are eliminated via a well-recognized autophagic process. Mitophagy dysregulation is recognized in age-related clinical scenarios such as Alzheimer's, Parkinson, sarcopenia and cardiovascular distress. Although its role in skin ageing and ensuing diseases are yet unexplored.

Mitophagy modulators are classified as activators, inducers and inhibitors. Activators upregulate the expression of mitophagy related genes, inducers are known to trigger the mitophgy pathways, and inhibitors block excessive mitophagy and mitochondrial loss. Some highly cited mitophagy modulators are nicotinamide riboside, urolithin A, kaempfrol, rhapontigenin, UMI-77 and tomatidine. Another innovative strategy to target mitochondrial quality control is mitochondrial transplant, where damaged mitochondria are transplanted with the healthy mitochondrial preparation. It is finding application in neurodegenerative, cardiovascular diseases, and dermal aging. In the present review we hypothesize the quality control of mitochondria in skin cells using chemical/natural mitophagy modulators for potential development of cosmeceutical or dermatological interventions.

Keywords: Skin Ageing; Mitophagy; OXPHOS System; Cosmeceutical; Dermatological Interventions.

MBPP19

Cloning and Recombinant Expression of the Novel Protein from the Food Vacuole of Malaria Parasite, Plasmodium Falciparum

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ABSTRACT

Malaria remains one of the leading causes of mortality worldwide. It is a serious disease caused by parasites of the Plasmodium genus, transmitted to humans through the bite of an infected female Anopheles mosquito. A significant number of genes within the Plasmodium genome remain uncharacterized. Understanding the roles of these uncharacterized genes is crucial for gaining deeper insights into the parasite's biology and identifying potential drug targets. During the asexual erythrocytic stage, Plasmodium relies on hemoglobin as its primary amino acid source. Hemoglobin degradation and hemozoin formation occur in the food vacuole, a lysosome-like organelle, but the exact mechanisms are not yet fully understood. Furthermore, many of the proteins involved in these processes are still unknown. Using available genomic and proteomic data, we have identified a gene expressed in the food vacuole of Plasmodium falciparum. We cloned our gene of interest into the desired vector at specific restriction sites. Further, we transformed this recombinant vector into the bacterial strain E. coli BL21 DE3. The transformation was confirmed using restriction digestion, plasmid PCR, and sequencing. The cells were induced with varying IPTG concentrations, temperatures, and time durations. The harvested cells were analyzed using SDS-PAGE, followed by western blotting, confirming this protein's expression. Optimal expression was achieved with a 0.4 mM IPTG concentration at 37 °C for 4 hrs. This recombinant protein on purification will help to better understand the functional role of this novel protein, which might help researchers build potential malaria therapeutics.

Keywords: Malaria; Plasmodium; Food Vacuole; Protein; Cloning and Expression.

MBPP20

An Insight into the Mechanistic Aspects of Traditional Medicine in Neurological Disorders

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ABSTRACT

The prevalence of Central Nervous System (CNS) ailments and conditions is predicted to grow rapidly in the future years, owing largely to the increasing global population. Neurological Disorders are frequently overlooked, either due to diverse brain function,complex disease mechanisms, progressive loss in an individual's skills with no obvious root cause thus making the treatment challenging. Pharmacological therapies, Cognitive-Behavioral Therapy (CBT), somatic approaches, and electroconvulsive therapy are common options for managing conditions of brain disorders. However, the drugs used to manage these disorders pose some major problems like drug interactions, adverse effects at high dose, low tolerance, and limited therapeutic efficacy. Moreover, natural medicines have gained greater study attention due to their low toxicity profile, neuroprotective properties and the potential to reduce inflammation and oxidative stress, most of which plays a prominent role in the progression of neurological diseases such as Alzheimer's, Parkinson's, Schizophrenia and Epilepsy. Experimental investigations have revealed that phytochemicals such as alkaloids, terpenes, flavonoids, phenolic acids, and lipids have great therapeutic promise in in vitro and in vivo models of neurological disorders.

Compounds such as curcumin from turmeric, quercetin from fruits and vegetables, and ellagic acid from berries have shown advantages of neuroplasticity, decline in cognition, and resilience to stressful circumstances. This review article compiles and highlights the latest studies that have been carried out to evaluate the effectiveness of these natural compounds and highlight them as safer and more effective alternatives to the marketed drugs.

Keywords: Central Nervous System (CNS); Pharmacological Therapies; Cognitive-Behavioral Therapy (CBT); Neurological Diseases; Electroconvulsive Therapy.

MBPP21

Analysis of Gut Microbiota in Coronary Heart Disease and Obesity: Opportunities and Challenges

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ABSTRACT

Today, obesity and coronary heart disease (CHD) are two of the biggest global health issues, driven by a combination of lifestyle, environmental, and genetic factors. Recent research finds that gut flora, specifically the diverse and intricate population of bacteria in our digestive tract known as the microbiome, plays a key role in influencing obesity and coronary heart disease by significantly affecting immunological responses, host metabolism, and disease development. Increased fat deposition, low-grade inflammation, and metabolic dysfunction have been linked to dysbiosis, an imbalance in the makeup of gut microbes that contributes to obesity. Along with that, key metabolites like lipopolysaccharides and short-chain fatty acids disrupt energy balance and fat metabolism, thereby worsening obesity and related conditions. Furthermore, recent studies suggest a connection between gut microbiota and CHD, where microbial metabolites may impact inflammation and immunological responses, ultimately impacting cardiovascular health. The primary objective of modern therapeutic strategies to lower obesity and coronary heart disease (CHD) is to alter the gut microbiome, with many approaches, including dietary changes, next generation probiotics etc, aimed at promoting metabolic health. However, more investigation is required to better understand the role of the gut microbiota in the development of disease and to create customized microbiome-based treatments. This review summarizes recent research on the relationship between gut microbiota, obesity, and CHD, emphasizing the need for an interdisciplinary approach to uncover the underlying mechanisms and improve therapeutic strategies for better clinical outcomes.

Keywords: Obesity; Coronary Heart Disease; Gut Microbiota; Probiotics; Prebiotic.

MBPP22

Repurposing of Drugs for Cancer Treatment

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ABSTRACT

Cancer, a multifactorial and complex disease, continues to pose a significant challenge to global health. Despite advancements in surgical, radiotherapeutic, and immunological approaches, drug therapy remains essential but is often limited by issues such as drug resistance and severe toxic side effects. Drug repurposing, the practice of identifying new therapeutic applications for existing, clinically approved drugs, has emerged as a promising strategy to address these challenges. This approach is cost-effective, expedites drug development due to established safety profiles, and offers innovative avenues for enhancing cancer treatment. The paper ahead will provide a comprehensive examination of drug repurposing in cancer therapy, highlighting various methodologies, including experimental and computational strategies. It explores the antitumor properties of repurposed drugs, their ability to target cancer hallmarks, and the potential for integration with nanotechnology to improve drug delivery. This paper explores the current drug repurposing strategies, their integration with nanotechnology, the challenges faced, and future prospects in advancing cancer treatment.

Keywords: Cancer; Radiotherapeutics; Drug Delivery; Nanotechnology; Immunological Approaches.

MBPP23

Profiling of the Indole-Based Derivatives for Anti-Cancer Efficacy: An In-silico and In-vitro Approach

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ABSTRACT

Cancer can arise from various causes, but a common factor is uncontrolled cell growth, often due to changes in signaling pathways. One key group of receptors involved in this process is the ErbB family, particularly EGFR (Epidermal Growth Factor Receptor). EGFR is known to contribute to cancer development in several types, including breast, lung, and ovarian cancers. While many drugs have been created to block EGFR, they often fail due to toxicity and side effects. Therefore, developing new, safer drugs is essential.

This study focused on 23 annomontine-based compounds with an indole structure. These compounds were tested against EGFR using molecular docking with the Glide tool in Schrodinger software. The best-performing compounds were further analyzed for their ADMET properties, which assess their safety and effectiveness as potential drugs. The results showed that these compounds had good binding affinity to EGFR, with promising docking scores. Compared to well-known cancer drugs like Osimertinib and Toceranib, these compounds demonstrated potential as new drug candidates. This research highlights the promise of indole-based annomontine derivatives as EGFR inhibitors, offering hope for more specific and less toxic cancer treatments.

Keywords: Cancer; Indole; Anti-cancer; ADMET; Cytotoxicity; Molecular Docking; Simulation.

MBPP24

Emerging Biomarkers for Traumatic Brain Injury

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ABSTRACT

Traumatic Brain Injury (TBI) affects approximately 55 million individuals globally. The disease has a higher prevalence compared to other neurological conditions in the world like stroke, Alzheimer's, and Parkinson's disease. In India, road traffic accidents account for 60% of TBI cases, followed by falls (20-25%) and violence (10%). It is one of the most catastrophic injuries, particularly in young adults and children; however, both diagnosis and prognosis remain challenging. Biomarkers are a potential solution for such scenarios because they help elucidate cellular damage even when the imaging results are normal. The injury to the brain may disrupt the blood-brain barrier, which leads to the release of several biomarkers into the bloodstream or the cerebrospinal fluid. They may include neuron-specific enolase (NSE), ubiquitin C-terminal hydrolase-L1 (UCH-L1), neurofilament protein, tau, S100β, glial fibrillary acidic protein (GFAP), and myelin basic protein (MBP). The last few years have also shown a growing interest in microRNAs (miRNAs) and extracellular vesicles (EVs) as key indicators for TBI. The current application of brain-derived blood biomarkers in the clinic is largely limited to GFAP and UCH-L1, whereas many other potential candidates remain unvalidated. There is a need for broad biomarker panels that include markers of neuronal injury, neuroinflammation, and oxidative stress. Longitudinal studies might further improve these tools by observing biomarker levels over time and illuminating how factors like age, sex, and genetic predisposition influence their expression. Eliminating such research gaps would advance the clinical context of TBI towards enhancing diagnostic accuracy, predictive assessments, and therapeutic management.

Keywords: Biomarkers, Blood-Brain Barrier, Neuroinflammation, Oxidative Stress, Traumatic Brain Injury (TBI).

MBPP25

Innovative Techniques for Cancer Stem Cell Identification and Extraction: Current Research and Therapeutic Applications

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ABSTRACT

Cancer stem cells (CSCs) are a special subpopulation of tumor cells that are distinguished by their ability to self-renew, differentiate, and initiate tumors. These cells are the key drivers of cancer progression, metastasis, therapy resistance, and recurrence, making them the prime targets for improving therapeutic outcomes. CSCs rely on key signaling pathways such as Wnt, Hedgehog, and Notch to maintain their stemness and survival. Processes such as epithelial-mesenchymal transition (EMT) and autophagy further enable them to evade immune responses and resist apoptosis, contributing to therapy resistance and disease relapse. Biomarkers that include CD44, ALDH, and CD24 have enabled the identification of CSCs and their segregation, which has helped uncover their biology and develop new targeted therapeutic approaches. A number of therapies targeting CSC-specific mechanisms, including pathway inhibitors and immunotherapies, have been promising. Preclinical studies have shown encouraging data for combination therapies targeting not only CSCs but the bulk tumor population. However, there are still challenges that persist due to the heterogeneity of CSCs and their interactions with the tumor microenvironment. This complexity necessitates further research to overcome resistance mechanisms and improve therapeutic efficacy. This review underlines the importance of CSCs in cancer progression and sheds light on innovative therapies to achieve sustained cancer control.

Keywords: Cancer Stem Cells (CSCs); Biomarkers; Isolation Techniques; Self-Renewal Pathways; Targeted Therapeutics.

MBPP26

Code to Cure, mRNA Leap in Cancer Treatment, Personalized mRNA Vaccines in Cancer Treatment

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ABSTRACT

Personalized mRNA vaccines are a ground breaking approach in treatment of cancer. These vaccines are made specially for each patient by studying their cancer cells, that is why they are called Personalized vaccines. These vaccines have mRNA, a molecule that gives instruction to make specific proteins, that are only found in patient's tumor, this helps the immune system to learn the strategy to recognize & attack the cancer cells.

In the beginning, patient's tumor is analyzed to find unique changes called neo antigens, these neo antigens are used to design the vaccine that can target the cancer, when the vaccine is given, it trains the immune system, especially T -cells, to destroy the cancer cells.

Advantage of this method include, can be made quickly, safe, and fewer side effects than traditional treatment, because the mRNA doesn't enter the cells nucleus, meaning it can't alter DNA, it's also broken down by the body naturally after it has done its job.

But still there are some challenges, such as Delivering the mRNA effectively into the body without being destroyed by the body, reducing unwanted reactions while still triggering a Strong immune response and also producing these vaccines on a large scale affordably is difficult.

This abstract explains how personalized mRNA vaccines work and why they are a promising future Treatment for cancer. By solving current Challenges these vaccines could offer a more effective and targeted way to treat cancer, helping many patients.

Keywords: Neo Antigens; Immune Response; Tumor; T -cells; Cancer.

MBPP27

Deciphering the Role of CD317 Mediated Proteostasis in Multiple Myeloma

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ABSTRACT

Multiple myeloma (MM) is a type of blood cancer that affects plasma cells, which are a type of white blood cell (WBC) found in the bone marrow. Plasma cells are a key part of the immune system, responsible for producing antibodies to fight diseases. In multiple myeloma, these cells become abnormal, grow uncontrollably, and crowd out healthy blood cells, leading to various health issues such as calcium elevation (hypercalcemia), renal failure, anemia, and bone damage (bone resorption). CD317, also known as HM1.24 or bone marrow stromal antigen 2 (BSA2), is a type of glycosylated type II transmembrane protein that is over-expressed in MM cells. It plays a significant role in maintaining proteostasis and cell survival, particularly when treated with proteasome inhibitors (PIs). CD317 interacts with calnexin (CNX) to regulate calcium uptake and protein folding in the endoplasmic reticulum (ER), creating a stable environment for proper protein formation and cellular function. Additionally, reduced levels of CD317 promote the degradation of CNX through a process called autophagic degradation involving another protein called RACK1. This degradation reduces CNX levels, which in turn disrupts calcium balance and impairs proteostasis. These mechanisms profoundly impact not only the survival capabilities of MM cells but also contribute to therapeutic resistance. Targeting CD317 with monoclonal antibodies has emerged as a promising strategy to enhance the immune response against MM cells and tackle drug resistance. Immunotherapy approaches that focus on CD317 could lead to new and effective therapies that improve outcomes for patients with multiple myeloma.

Keywords: Multiple myeloma; Plasma Cells; CD317; Proteostasis; Immunotherapy; Drug Resistance.

MBPP28

The Role of CRISPR Gene Therapy in Duchenne Muscular Dystrophy

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ABSTRACT

Duchenne muscular dystrophy (DMD) is an X-linked recessive disorder caused by a mutation in the DMD gene. It has a prevalence of 1 in 3500 males and is characterized by progressive muscle degeneration, cardiomyopathy, and elevated creatine kinase levels. The DMD gene is the largest in the human body and codes for dystrophin protein, which acts as a tether between the cytoskeleton and extracellular matrix, and provides membrane stability as a part of the dystrophin-glycoprotein complex. The current therapeutic strategies, like corticosteroids and physical therapy help in merely managing symptoms and delaying disease progression but do not stop the degeneration of muscles. Recent advances in gene therapy and CRISPR technology offer a promising approach to restore dystrophin protein partially and converting severe DMD into milder Becker's Muscular Dystrophy. This innovative treatment is based on correcting the mutations or inducing exon-skipping mechanisms to produce variants of functional dystrophin. Despite these advancements, challenges such as off-target effects and immune responses to the therapy remain. It is essential to develop refined and safe strategies to create effective treatments for DMD. While direct human trials for CRISPR applications in DMD have not yet begun, the promising results from animal studies indicate that researchers are gearing up to move forward with clinical testing soon.

Keywords: Duchenne Muscular Dystrophy; CRISPR; Gene Therapy; Dystrophin; Muscle Degeneration; Becker's Muscular Dystrophy.

MBPP29

Renewing the Heart: Advances in Cardiac Repair

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ABSTRACT

Heart failure, a leading cause of death in developed countries, is primarily due to a deficiency of cardiomyocytes, the muscle-forming cells of the heart. Millions of patients might find a new path towards survival by developing regeneration for heart tissues, but it does have a very limited capability of regeneration in the human heart. Although mammals and amphibians generally lead to scarring when the heart is injured, the zebrafish can regenerate up to 20% of its ventricular tissue within two months by rapidly proliferating heart cells at the edges of new muscle. This is why zebrafish are an excellent model for studying heart regeneration. The differentiation of stem and progenitor cells also differs. Some studies mainly focus on the differentiation capability of bone marrow-derived stem cells, which are capable of differentiating from cardiomyocytes and other cell types as well. Heart-derived stem cells can give rise to various heart cell types, including cardiomyocytes. Mesenchymal stem cells differentiate into cardiac lineage. Endothelial progenitor cells are involved with the process of angiogenesis, and vascularization in cardiac tissue repair. The latest works in regenerative medicine include research on the applications of iPSCs that can reconstitute heart tissue. Research into miRNAs and molecular pathways driving cardiomyocyte proliferation are well on their way to providing benefits for cardiac regeneration. Thus, scientists are now crafting new tools to bypass the natural limitations of the heart concerning regeneration. So, these innovations may introduce different perspectives regarding treatments for regenerative purposes.

Keywords: Cardiomyocytes; Stem Cells; Zebrafish; Induced Pluripotent Stem Cells (iPSCs); Angiogenesis.

MBPP30

Repurposing Potential of Antiviral Plant Derivatives Against STDs: Current Updates

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ABSTRACT

Sexually transmitted diseases (STDs), often referred to as sexually transmitted infections (STIs), are infections primarily transmitted through sexual contact, including oral, anal, and vaginal intercourse. The World Health Organization (WHO) estimates that over 1 million curable STIs are acquired daily worldwide, emphasizing the pressing need for innovative treatment strategies. The increasing prevalence of these infections has driven the exploration of the use of antiviral plant derivatives, which are derived from natural compounds with inherent bioactive properties. These compounds exhibit a variety of mechanisms, including modulation of immune responses, inhibition of viral replication, and prevention of viral penetration into host cells. Their anti-inflammatory properties further enhance their suitability for managing sexually transmitted diseases by alleviating symptoms and promoting recovery. Repurposing antiviral plant derivatives offers a multifaceted approach to treatment by inhibiting viral replication and modulating immune responses, thus, increasing the efficiency and reducing the side effects. Cassia alata shows strong antibacterial activity against Neisseria gonorrhoeae, while Aloe ferox demonstrates dual-action potential against both gonorrhea and syphilis. Moreover, Commiphora angolensis contributes unique bioactive compounds targeting gonorrheal pathogens. The antiviral and anti-inflammatory properties of these plants alleviate symptoms and promote recovery, making them excellent compounds for future therapeutic development. This review highlights the repurposing potential of antiviral plant derivatives for STD management, focusing on their mechanisms—such as disrupting viral envelopes, inhibiting viral gene expression, and interfering with host cell attachment. Additionally, these derivatives could complement existing antiviral therapies, addressing resistance and side effects. By integrating pharmacological, botanical, and molecular biological research, the development of novel plant-based STD treatments holds immense promise for future healthcare solutions.

Keywords: STDs, Medicinal Plants, Bioactive Compounds, Therapeutic Potential, Natural Derivatives.

MBPP31

Enhancing Herbal Efficiency Through Phytosomal Formulations

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ABSTRACT

Recently, novel drug delivery systems have been highly prevalent in the medical field due to their availability and overall therapy within a short time. Herbal medicine has become progressively more common in recent years due to its accessibility, affordability, and lack of side effects. One of the most advanced herbal drug delivery methods is the phytolipid system. The alternative term for it is Phytosome. The state-of-the-art drug delivery technique called Phytosome technology solves these problems by improving the permeability of polyphenolic phytoconstituents into the skin and their absorption in the gastrointestinal tract. The herb's active ingredients are contained in the phytosomes, which are microscopic cell-like structures attached to phospholipids, mainly phosphatidylcholine.

The phospholipid molecular structure consists of two fat-soluble tails and a water-soluble head. This dual solubility makes it an excellent emulsifier, enabling it to create a lipid-compatible molecular complex. Cell-like complexes are typically formed when the active herbal compounds of phytosomes bond to the phospholipids. This creates a lipid-compatible molecular complex that is soluble in fat and water, increasing the bioavailability of the herbal actives. This innovative technology has been proven to make significant gains in treatment effectiveness. After all, it targets drug delivery to specific areas. Likely, Ongoing research and collaboration in this area will likely continue to fuel the creation of novel phytosome-based formulations for the treatment of human illnesses, thus establishing phytosome technology as a promising strategy in contemporary herbal medicine. This review discusses key successes, manufacturing aspects, and clinical applications of Phytosome technology, along with a comparative analysis of traditional herbal extracts and their enhanced counterparts.

Keywords: Phytosome; Phosholipids; Phosphatidylcholine; Herbal Medications.

MBPP32

Advancing Oncology Through Nature by The Role of Plant Derived Medicines

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ABSTRACT

Cancer remains one of the leading causes of death worldwide, accounting for approximately 9.7 million fatalities annually, making it the second most common cause of death after cardiovascular diseases. Despite extensive research and the development of various treatment methods such as chemotherapy and radiation therapy, a definitive cure for cancer remains far fetched. Moreover, these conventional treatments often cause significant side effects, prompting the need for alternative approaches with fewer adverse effects. In this context, plant based medicines have emerged as a promising area of research, offering potential benefits in mitigating side effects and complementing cancer therapy. Numerous plants' anti-inflammatory and antioxidant properties contribute to their anticancer potential, highlighting their therapeutic significance. Given the vast diversity of the plant kingdom, extensive research is ongoing, with much still to be explored. This manuscript delves into the role of plant-based medicines in cancer treatment, focusing on their therapeutic benefits, and the potential they hold for future advancements in oncology.

Keywords: Cancer; Plant-Based Medicine; Anti-cancer; Anti-Inflammatory; Antioxidant; Therapeutics; Phytomedicine.

MBPP33

Pro-Oxidant Mediated Cytotoxicity Induction in Cancer Cells: A Novel Therapeutic Approach

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ABSTRACT

Cancer remains a significant global health challenge, conventional treatments such as surgery, chemotherapy, and radiation therapy, while effective to some extent, are often accompanied by considerable limitations, including systemic toxicity, development of resistance, and procedural invasiveness. These challenges underscore the urgent need for innovative therapeutic approaches that selectively target cancer cells while sparing normal tissue.

One promising avenue involves the use of prooxidants, agents that exacerbate oxidative stress within cancer cells to cytotoxic levels. Cancer cells are inherently under oxidative stress due to their high metabolic activity and altered redox homeostasis, rendering them more vulnerable to further disruptions in reactive oxygen species (ROS) equilibrium. By elevating ROS levels beyond the tolerable threshold, prooxidants can selectively induce oxidative damage in cancer cells, ultimately triggering apoptosis or programmed cell death, while sparing normal cells.

Recent advancements have identified a range of natural and synthetic prooxidants with significant anticancer potential. This review comprehensively explores these agents, highlighting their mechanisms of action, which include targeting mitochondrial function, modulating antioxidant defense pathways, and disrupting redox signaling. Additionally, the limitations and challenges associated with prooxidant-based therapies, such as specificity, delivery mechanisms, and potential off-target effects, are critically examined. By addressing these barriers, prooxidants could emerge as a promising therapeutic strategy in the oncological landscape, paving the way for more effective and less invasive cancer treatments.

Keyword: Proxidants; Oxidative Stress; Reactive Oxygen Species; Mitochondrial Function; Antioxidant Defense Pathway.

MBPP34

Metabolic Rewiring in Cancer: The Role of HK 2 as a Key Therapeutic Target

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ABSTRACT

Hexokinase 2 (HK2) plays a pivotal role in cancer cell metabolism by driving the glycolytic shift characteristic of the Warburg effect. This review provides a detailed examination of HK2's structure, function, and its contribution to tumor progression. Overexpression of HK2 in various cancers promotes enhanced glucose uptake and metabolism, facilitating tumor growth while conferring resistance to apoptosis. The review also explores the enzyme's isoforms, catalytic mechanisms, and key binding sites, emphasizing its centrality in glycolysis and tumor metabolism.

We investigate the Warburg effect's role in maintaining cancer cell survival, highlighting HK2's facilitation of the metabolic transition from oxidative phosphorylation to glycolysis. Targeting HK2 has emerged as a promising therapeutic strategy, with pharmacological agents such as 2-deoxy-D-glucose (2-DG) and novel synthetic compounds demonstrating efficacy in disrupting its enzymatic activity. Furthermore, natural product compounds (NPCs) are being explored as alternative inhibitors of HK2, offering a potentially broader therapeutic repertoire.

The review also discusses the potential of identifying biomarkers associated with HK2 expression, which could enhance the specificity and effectiveness of targeted therapies. This review underscores the therapeutic potential of targeting HK2 to disrupt the metabolic pathways critical to cancer cell survival and proliferation, offering new prospects for personalized cancer treatment.

Keywords: Hexokinase 2 (HK2); Warburg Effect; Natural Product Compounds (NPCs); 2-deoxy-D-glucose (2-DG); Personalized Cancer Treatment.

MBPP35

Exploring the Potential of Biopolymers in Tissue Engineering

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ABSTRACT

In recent years, biopolymers have gained attention as novel and viable options in the field of tissue engineering, presenting a greener and more compatible way of designing scaffolds and materials in regenerative medicine. These natural polymers are made from renewable materials such as e.g. collagen and silk fibroin, or polysaccharides like chitosan or alginate whose distinct physicochemical properties make them suitable candidates for enhancing the growth or differentiation of cells. Biopolymers resemble the extracellular matrix (ECM) by not only having structural features but also providing biological cues which are important in facilitating the process of tissue engineering and regeneration. Nonetheless, in addition to biodegradable rosins structural monomer grades offer also low immunogenicity as well as active encouraging – promoting cellular adhesion, growth and blood vessels formation – bioactive characteristics within themselves. Furthermore, biopolymer enhancement methods have permitted the creation of advanced scaffolds for bone, cartilage, and skin aimed applications that do not only have enhanced mechanical properties but also designed porosity and functionalities as required. For instance, nanocomposites of biopolymers and bioactive nanoparticles have proven promising for scaffold properties, including antimicrobial activity and mineralization, these being critical for applications in bone tissue engineering. There are many biopolymer-based hydrogels that have gained attention as a possible synthesis pathway for creating soft tissue substitutes, given their excellent water-retaining and tunable properties.

Keywords: Biopolymer, Tissue Engineering, Extracellular Matrix, 3D Bioprinting, Regenerative.

MBPP36

Epigenetics in Cardiovascular Medicine: Bridging the Gap Between Risk and Remedy

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ABSTRACT

Epigenetics is a pivotal field in understanding the complex mechanisms underlying cardiovascular diseases (CVDs). It examines heritable variations in gene expression that do not involve changes to the DNA sequence. Key mechanisms, including DNA methylation, histone modification, and noncoding RNAs like microRNAs, regulate gene expression by altering chromatin structure and DNA accessibility, leading to dysregulated processes involved in CVD development and progression. Genome-wide linkage and association studies highlight the multigenic complexity of CVDs, but epigenetics plays a critical role in regulation and treatment strategies. Environmental factors such as nutrition, pollution, stress, and prenatal influences significantly impact cardiovascular health through epigenetic modifications, particularly histone acetylation and DNA methylation. These changes increase susceptibility to CVDs, accelerating disease progression. Early-life environmental epigenetic changes are especially concerning, as they can predispose individuals to cardiovascular and chronic diseases later in life. Understanding the interplay between environmental exposures, epigenetic mechanisms, and cardiovascular health is essential for developing preventative measures and therapeutic approaches. Targeting epigenetic enzymes offers a promising avenue for treatment. Exploring these relationships will enhance preclinical and clinical advancements, addressing both the pathogenesis and potential treatment of CVDs.

By unraveling the impact of epigenetic mechanisms and their interactions with environmental factors, epigenetics emerges as a frontier in diagnosing and treating cardiovascular illnesses. This knowledge paves the way for innovative strategies to mitigate risk and improve outcomes in human medicine.

Keywords: Epigenetics, Cardiovascular Diseases (CVDs), DNA Methylation, Environmental Exposures, Histone Modification, Noncoding RNA.

MBPP37

Advancements in Nanotechnology for Chronic Wound Treatment: Formulations, Mechanisms and Future Directions

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ABSTRACT

Chronic wounds are a real concern for the modern healthcare system because they have low healing capacity, prolonged inflammation, and a high probability of infection. Few traditional methods of chronic wound care have successfully addressed the challenges presented by the biological mechanisms involved in wound healing. Nanotechnology has become groundbreaking in wound care and is promising for managing chronic wounds. Nanotechnology has been successfully integrated into wound dressings, leading to significant improvements. These advancements include increased durability and the ability to precisely control the release of medications, enabling customized treatments for specific wounds. Nanotechnology effectively anchors bioactive molecules at the wound site ensures controlled and prolonged drug release, and significantly enhances the therapeutic efficacy of the incorporated agents. Their ability to localize treatment while minimizing systemic side effects has positioned them as a transformative tool in skin repair and regeneration. This review underscores the transformative potential of nano-drug delivery systems in redefining the landscape of skin regeneration and chronic wound management.

Keywords: Chronic Wound Healing, Nanoparticles, Skin Regeneration, Nano-Drug.

MBPP38

Advancing Ligand-Based Drug Discovery: A Paradigm Shift in Pharmacological Interaction and Natural Product Analytics for Microbial Diseases

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ABSTRACT

Microbial diseases, particularly those caused by multidrug-resistant (MDR) pathogens such as the ESCAPE group, are a leading cause of global mortality, driving the urgent need for innovative drug discovery and development strategies. This study introduces a transformative approach to ligand-based drug discovery by integrating advanced Quantitative Structure-Activity Relationship (QSAR) models. Focusing on natural products as a rich source of bioactive compounds, the research investigates their pharmacological interactions and therapeutic potential in targeting microbial diseases, with an emphasis on identifying potential biomarkers and therapeutically significant ligand molecules. The advanced QSAR models employed in this study leverage state-of-the-art computational techniques, including machine learning algorithms and molecular descriptor optimization, to achieve accurate and reliable predictions of biological activity. Key findings highlight the capability of natural products to target critical pathways involved in microbial disease progression, with several identified ligands demonstrating strong binding affinities and favourable pharmacokinetic properties. Furthermore, the robustness of QSAR models in elucidating structure-activity relationships and identifying novel lead compounds is emphasized. This work not only advances the field of ligand-based drug discovery but also provides valuable insights into the application of QSAR models as a powerful tool for pharmacological research. These findings pave the way for new opportunities in the development of targeted therapeutics, offering promising solutions for improved microbial disease management and treatment strategies.

Keywords: Microbe, Pharmacophore, Machine Learning, Molecular Descriptors, QSAR.

MBPP39

Stem Cell Based Applications on Modern Day Reproductive Challenges: in Vitro Gametogenesis

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ABSTRACT

IVG stands for in-vitro gametogenesis, it is the stem cell-based technology that involves developing gametes i.e. reproductive cells like eggs or sperm outside of the body in laboratory. It's is the promising new technology that could help people with fertility issue to have their own children. Like for infertile people, cancer survivor, old women, same sex couple. IVG can works through 2 type of stem cell-based therapy that are ESC (Embryonic stem cell) and iPSC (Induced Pluripotent stem cell).

ESCs are derived from the inner cell mass of a blastocyst (an early-stage embryo, typically 4-5 days post-fertilization). These are pluripotent stem cells, meaning they can divide into more stem cells or can become any type of cell in the body. iPSCs are derived by reprogramming adult somatic cells (such as skin or blood cells or hair) back into a pluripotent state. This is achieved through the activation of specific genes. Recent advancements in iPSC technology enable the direct transformation of skin cells into kidney organoids, closely resembling natural kidney tissue.

*In IVG, ESCs are directed to become primordial germ cells (PGCs)***,** *from which are the early precursors to sperm and eggs. In IVG, iPSCs are reprogrammed or de-differentiate from the cell in the body into the pluripotent stem cell that is differentiate into PGCLCs (primordial germ cell-like cells). These PGCs then mature into functional gametes. After that we fertilize the gamete with gamete of opposite sex to create an embryo. Controlled by pluripotency factors like OCT4, SOX2, and NANOG, hESCs. Advanced methods include 2D culture, 3D organoid system, co-culture with gonadal cells, gene editing vis CRISPR, and animal model transplantation.*

IVG holds promise to infertility treatments, same sex couple, cancer patients, genetic disease modelling and reproductive biology advancements despite of ongoing challenge. But it comes with number of challenges and limitations that includes complexity of cell differentiation, tumorigenicity, low efficiency, genetic and epigenetic instability. Ethically IVG raises concern about reproductive autonomy, eugenics, same sex reproductive gametes (for same sex couple or from single individual) and creation of gametes from non-traditional source raise questions for parentage and identity, potential of misuse.

Keywords: Stem Cell; Pluripotent State; Primordial Germ Cell; Epigenetics; Eugenics.

MBPP40

Flavoring Dynamics in Tobacco Products

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ABSTRACT

Tobacco, derived from the leaves of the Nicotiana plant, is a widely used psychoactive substance that posess significant health risks, including addiction and a variety of diseases. Flavored tobacco products, such as cigarettes, cigars, e-cigarettes, and smokeless tobacco, are supplemented with a variety of flavors, including fruit (e.g., berry, citrus), mint (e.g., menthol), chocolate, vanilla, and spice etc, to enhance palatability and reduce the harshness associated with traditional cigarettes. These flavours are strategically added to make tobacco products more appealing, especially to new and younger consumers, by masking the natural bitterness and sharpness of tobacco smoke. Addition of flavours serves several purposes: they can enhance the sensory experience, increase the appeal of the product and promote milder tobacco consumption. However, while flavors make tobacco products more enjoyable, they also contribute to increased smoking initiation and the likelihood of developing nicotine dependence, posing serious public health concerns. Flavored tobacco products are associated with high rates of experimentation and regular use among young people, and may lead to long-term addiction. This paper explores the dual nature of flavored tobacco, discussing both its potential to enhance user experience and its role in encouraging tobacco consumption among vulnerable populations. It also reviews the regulatory environment surrounding flavored tobacco, noting that many countries have implemented bans or restrictions to mitigate these risks. Authors highlight the urgent need for improved surveillance tools to monitor flavored tobacco use and advocate for further research into the behavioral and toxicological effects of flavors. This research is essential for developing effective regulatory strategies that can protect public health while addressing the problems associated with flavored tobacco products.

Keywords: Tobacco, Flavored goods, Addiction, Public health, Regulation, Dependence on Nicotine.

MBPP41

Deer Antler Stem Cells: Potential Therapeutic Avenue for Regenerative Medicine

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ABSTRACT

Antlers, osseous cranial appendages found in male deer, exhibit a remarkable ability for complete annual renewal through a stem cell-based epimorphic process. This makes them a fascinating model for studying how mammals can regenerate tissues and organs. This regrowth happens through a process driven by special stem cells called antler stem cells (ASC's), which are found in special areas like the pedicle periosteum, antlerogenic periosteum, and reserve mesenchyme. These stem cells share characteristics with both mesenchymal and embryonic stem cells, allowing them to turn into different types of tissues, such as bone, cartilage, and nerves.

The review explores how antlers grow and identifies key signalling pathways, like Wnt and PTHrP, which control antlers growth. Unlike uncontrolled tumor growth, antler growth is highly regulated by specific genes, including TP73 and ADAMTS18, which acts as tumor suppressors. The growth of antlers is influenced by factors like testosterone and other growth signals, including IGF-1 and vitamin A derivatives.

ASC's present immense human therapeutic applications and by unravelling the genetic and cellular basis of antler renewal, we can understand mammalian tissue/organ regeneration, opening pathways for translational medicine. Possible applications include - organ regeneration therapies, bone remodelling, cancer etc. However, challenges remain, such as immune rejection and ethical limitations which need to be addressed before clinical applications in humans.

Keywords: Antler Stem Cells (ASC's), STEM Cell-Based Epimorphic Process, WNT Signalling Pathway, PTHrP Signalling Pathway, TP73 Gene.

MBPP42

Therapeutic Benefits and Biomarker Insights of Yoga: A Comprehensive Review

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ABSTRACT

This review highlights the therapeutic potential of yoga as a complementary and alternative medicine in managing lifestyle disorders, neurodegenerative diseases, cardiovascular conditions, and aging-related complications. Yoga integrates physical postures (asanas), breathing techniques (pranayama), and meditation to promote mental and physical health. The findings indicate that yoga significantly enhances redox balance by increasing antioxidant levels such as glutathione and superoxide dismutase while reducing oxidative stress markers like malondialdehyde. These effects contribute to improved cellular health and reduced disease risk.

In cardiovascular health, yoga lowers heart rate, blood pressure, and inflammatory markers such as interleukin-6 and high-sensitivity C-reactive protein, enhancing autonomic regulation and heart function. Anti-aging benefits include increased telomerase activity, improved telomere length, and reduced DNA damage, indicating delayed cellular aging. Yoga also demonstrates efficacy in alleviating stress, anxiety, and depression, improving neurocognitive function, and reducing markers of neurodegeneration.

This study aims to evaluate the therapeutic potential of yoga as a complementary and alternative medicine by analyzing its impact on biological markers associated with oxidative stress, cardiovascular health, neurodegenerative disorders, and aging-related processes. The study seeks to consolidate evidence on the role of yoga in improving mental and physical health, identifying measurable biomarkers that demonstrate its efficacy, and highlighting areas for further research to establish its clinical applications.

Keywords: Yoga, Neurodegenerative Diseases, Cardiovascular Diseases, Oxidative Stress, Anti-Aging, Lifestyle Disorders.

MBPP43

Therapeutic peptides for Neurodegenerative Disorders

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ABSTRACT

Neurodegenerative disorders, including Alzheimer's disease (AD), Parkinson's disease (PD), Huntington's disease (HD), and amyotrophic lateral sclerosis (ALS), are characterized by the progressive degeneration of neurons, leading to behavioural, motor, psychiatric, and cognitive impairments. These diseases, which account for approximately 25% of global deaths and disabilities, often result from abnormal protein or peptide aggregations that disrupt neuronal signaling and induce cell death. Key pathological mechanisms include mitochondrial dysfunction, oxidative stress, transcriptional dysregulation, and apoptosis.

Therapeutic peptides have attracted significant attention for their potential to address the complex pathogenesis of neurodegenerative disorders. These peptides exhibit diverse therapeutic properties, including antioxidant, antimicrobial, and antithrombotic effects. Compared to small molecules, peptides offer advantages such as high specificity, potent biological activity, cost-effectiveness, and superior membrane penetration. However, challenges like stability, toxicity, and immunogenicity remain hurdles for peptide-based drug development.

Peptides such as neurotrophins (e.g., NGF, BDNF, and GDNF), vasoactive intestinal peptide, glucagon-like peptide, glutathione, cholecystokinin, and neurotensin have shown potential in mitigating disease progression. By targeting key processes like protein aggregation, oxidative stress, and mitochondrial dysfunction, peptides hold promise as innovative therapeutic agents.

Keywords: Alzheimer's Disease (AD), Parkinson's Disease (PD), Huntington's Disease (HD), Amyotrophic Lateral Sclerosis (ALS), NGF (Nerve Growth Factor).

MBPP44

Edible Vaccines Transforming Global Health Systems

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ABSTRACT

Edible vaccines represent a groundbreaking innovation in biotechnology, offering a transformative approach to immunization by integrating accessibility, affordability, and safety. By employing advanced genetic engineering techniques such as Agrobacterium mediated gene transfer, biolistics, and electroporation, antigenic genes are introduced into plants, enabling them to produce vaccine proteins that stimulate both mucosal and systemic immunity when consumed. These vaccines hold the potential to combat infectious diseases such as hepatitis B, cholera, malaria, and HIV, addressing critical gaps in global health infrastructure, especially in low-resource settings.

The strategic selection of plants like bananas, maize, and soybeans leverages their protein content, shelf stability, and suitability for mass cultivation. Edible vaccines eliminate the need for cold storage, needles, and specialized personnel, thereby simplifying vaccine delivery while enhancing compliance, particularly among children. Despite challenges such as antigen stability, dosage standardization, and immune tolerance, recent advancements in bioencapsulation and lyophilization have shown promising results in addressing these obstacles.

This novel approach not only reduces reliance on antibiotics but also offers a scalable, eco friendly solution to global immunization challenges. Future directions focus on enhancing antigen yield, improving stability, and expanding applications to include diseases like anthrax and smallpox. Edible vaccines hold the promise to revolutionize public health, making life saving immunization accessible to the most underserved populations and fostering a healthier, more equitable world. With their unparalleled potential to bridge global health disparities, edible vaccines symbolize a paradigm shift in modern medicine.

Keywords: Edible Vaccines, Plant-Based Vaccines, Oral Immunization, Bioencapsulation, Sustainable Vaccination.

MBPP45

Peptide-Based Nanovaccines in the Treatment of Cervical Cancer: Opportunities and Challenges

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ABSTRACT

Cervical cancer remains a significant global health challenge, especially in low- and middle-income countries. Traditional treatment approaches, including surgery, chemotherapy, and radiotherapy, have made progress in reducing mortality but often come with severe side effects. Vaccination can be one of the solutions for this. Vaccine is a biological preparation that helps the body develop immunity to a specific disease. Cancer vaccines are of different types: Subunit, mRNA, Viral vector. In recent years, peptide-based nanovaccines have emerged as a promising immunotherapeutic strategy in the treatment of cervical cancer. The present review explores advances in peptide-based nanovaccines, focusing on their design, delivery mechanisms, and therapeutic potential. These nanovaccines leverage synthetic peptides that mimic tumor-associated antigens to elicit strong and specific immune responses. By incorporating nanotechnology, peptide-based vaccines benefit from enhanced stability, targeted delivery, and improved uptake by immune cells. Furthermore, advancements in adjuvant formulations and nanocarrier systems, such as liposomes, polymeric nanoparticles, and dendrimers, have significantly improved the efficacy and specificity of these vaccines. Preclinical and early-stage clinical trials demonstrate promising outcomes, showing tumor regression and prolonged survival in patients. This abstract summarizes key developments in this field, discusses challenges such as immunogenicity and delivery efficiency, and highlights future directions for the clinical translation of peptide-based nanovaccines in cervical cancer therapy.

Keywords: Antigen, Nanovaccine, Immunogenicity, Liposomes, hpv, Cervical Cancer.

MBPP46

Ovarian Cancer Unveiled: Advancements in Biomarker Discovery and Targeted Therapy Strategies

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ABSTRACT

The worst gynaecologic disease, ovarian cancer is still hard to identify early and treat. Efforts to understand the molecular biology and origins of the disease, particularly the fallopian tube as a precursor site, have also led to advancements in screening and therapies. Current screening approaches like the CA125-based two-stage regimen linked to TVS have shown promise in the early detection of ovarian cancer, but these methodologies have poor sensitivity and high false positive rates. New biomarkers, such as autoantibodies against TP53, HE4, miRNA panels, circulating tumor DNA (ctDNA), and DNA methylation, are under investigation to improve early detection. New imaging modalities, including magnetic relaxometry and autofluorescence, seek to address challenges in the visibility of small lesions and fallopian tubes.

On a therapeutic front, precision medicine targeting morphomolecular subtypes of ovarian cancer is gaining momentum. Clinical trials have revealed promising results for agents targeted against DNA damage response pathways, immune checkpoint inhibitors and angiogenesis. To overcome the drug resistance of phosphatidylinositol 3-kinase and PARP inhibitors, various combinatory therapies including cell cycle inhibitors with PARP inhibitors have been in the research phase. Antibody-drug conjugates directed against folate receptor-α also represent promising options for targeted and efficient treatment.

Facilitating earlier detection and targeted treatment modalities through advanced screening approaches and targeted therapies, the integration of these strategies has the potential to change outcomes in ovarian cancer. Future work to further reduce mortality and improve patient quality of life will rely on refined biomarkers, optimized therapeutic combinations, and robust clinical trials.

Keywords: CA125, Combinatory Therapies, Morphomolecular Subtypes, PARP Inhibitors, Transvaginal Ultrasound (TVS).

MBPP47

Advancing Chronic Wound Care: Innovations in Antiseptics and Biomaterial Strategies

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ABSTRACT

In the medical field, the proper healing of wounds, especially infected chronic wounds, is one of the most formidable challenges. This review summarizes the latest developments of antiseptics and novel biomaterials for wound healing. Povidone iodine (PVP-I) is a broad-spectrum antimicrobial with potent activity against a wide range of microbes associated with healthcare-associated infections (HAIs), including biofilm-associated bacteria, and has a low potential for the development of resistant strains (more than 20 years prevalence). PVP-I could accelerate wound healing attributed to its anti-inflammatory effects, and stimulation of neovascularization and re-epithelialization processes has been documented.

In addition to classic antiseptics, antibiotic and immune-modulating microneedle (MN) patches emerge as an intriguing alternative specifically to treat infected wounds. The MN platform combines chemodynamic therapy, photothermal therapy, and macrophage polarization, which will significantly promote biofilm elimination and the transformation of the immune microenvironment to accelerate wound healing. The use of polydopamine-loaded nanoparticles in conjunction with mesoporous silica produces a synergistic antibacterial and anti-inflammatory effect, demonstrating enhanced efficacy in the context of chronic wounds.

Antibacterial strategies, whether traditional or modern, highlight the necessity for addressing bacterial biofilms and antibiotic resistance, both of which are significant hindrances to effective wound management. Combining well-known antiseptics with advanced biomaterials is a multidimensional solution that provides the opportunity for more effective treatment plans. These systems can advance as the therapeutic response becomes more predictable and can efficiently account for diverse wound scenarios, which could be the way forward.

Keywords: Immune Modulating Microneedle (MN), Neovascularization, PVP-I (Povidone iodine), Re-Epithelialization.

MBPP48

Variations in Oral Microbiota Associated with Oral Cancer

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ABSTRACT

Oral cancer, particularly oral squamous cell carcinoma (OSCC), is a major health concern globally, and emerging evidence highlights the critical role of the oral microbiome in its development and progression. With an emphasis on microbial dysbiosis and its possible carcinogenic processes, this review summarises the results of current investigations into the relationship between oral microbiota and oral cancer.

By causing chronic inflammation, altering apoptosis, and producing carcinogenic compounds, certain bacterial taxa—such as Porphyromonas gingivalis, Streptococcus sp., Peptostreptococcus sp., and Fusobacterium nucleatum—have been linked to the development and spread of oral cancer. Furthermore, compared to healthy oral tissues, OSCC lesions have shown significant changes in microbial diversity and composition, with periodontitis

associated bacteria showing a notable enrichment in cancer samples. These results highlight the value of the oral microbiota as a tool for oral cancer diagnosis and prognosis. In addition to highlighting prospective directions for future research and therapeutic applications, this review attempts to enhance our understanding of oral microbiome variations during oral cancer by examining microbial processes, community shifts, and diagnostic potentials.

Keywords: Oral Squamous Cell Carcinoma (OSCC), Oral Microbiome, Microbial Dysbiosis Carcinogenic Processes, Periodontitis-Associated Bacteria, Diagnostic.

MBPP49

Role of Probiotics in Enhancing Cognitive Function and Mental Well-Being

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ABSTRACT

In humans, cognitive functions in humans are regulated by the central nervous system, primarily controlled by the brain. Neuronal damage can lead to neurodegenerative conditions such as Parkinson's disease, Alzheimer's disease, autism, and epilepsy. Emerging evidence highlights the impact of diet, particularly probiotics, on brain health and stress regulation. Probiotics are beneficial microbes consumed in adequate quantities that positively influence gut microbiota, which in turn affects cognitive function, stress management, and mental health through the microbiota-gut-brain (MGB) axis. Although in vitro, in vivo, and pre-clinical studies suggest that probiotics can improve cognitive performance and decision-making, clinical findings on their effects on anxiety and depression have been inconsistent. In this study, the probiotic strain Lactobacillus plantarum P-8 was administered to adults for 12 weeks, demonstrating a reduction in stress and anxiety levels. Gut microbiota analysis revealed greater microbial stability in the probiotic group (n = 43) compared to the placebo group (n = 36). Diversity, measured using the Shannon diversity index, significantly decreased in the placebo group but remained stable in the probiotic group. Beneficial bacteria such as Bifidobacterium adolescentis, Bifidobacterium longum, and Fecalibacterium prausnitzii increased in the probiotic group, while less favorable bacteria like Roseburia faecis decreased. Additionally, the probiotic group exhibited higher levels of bacteria associated with neurotransmitters and beneficial metabolites, including short-chain fatty acids and gamma-aminobutyric acid (GABA), both critical for mental health. These findings underscore the potential of targeted probiotics in maintaining gut microbial balance and enhancing cognitive and emotional well-being through the gut-brain connection, warranting further investigation in clinical settings.

Keywords: Probiotics, Cognitive Function, Stress Management, Neurotransmitters.

MBPP50

Advancements in Rapid Diagnostic Methods for Tuberculosis Detection in Resource-Limited Settings

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ABSTRACT

The increasing prevalence of tuberculosis (TB), especially in resource-limited areas, emphasizes the urgent need for quicker, more sensitive, and efficient diagnostic methods. One of the focuses for these new advanced diagnostic methods is on the development of an immunochromatographic (IC) strip test using monoclonal antibodies. One of the targets chosen for such strips is Ag85B protein, a major antigen in mycobacterial infections. Two versions of the IC strips based on this antigen have been designed: one for detecting both MTBC and NTM, and another specifically for MTBC. They are shown high sensitivity of 93.9% for MTBC and 63.2% for NTM, making the test a promising rapid alternative to traditional methods. Although direct sputum samples presented challenges due to their viscosity and lower Ag85B levels, the test successfully identified mycobacteria in cultured samples. Another popular advanced method utilized is Fluorescence In Situ Hybridization (FISH) assay, utilizing DNA probes to differentiate MTBC from NTM in sputum samples. This method provides results in under 2 hours and demonstrates high sensitivity (89.7%) and specificity (95.5%). A third approach involved the CrfA-based 96-well assay, designed to detect MTBC by identifying the CrfA enzyme. With a rapid turnaround time of 6-8 hours, this test showed 100% specificity and 90% sensitivity. Compared to traditional assays like MPT64, the CrfA test provides quicker results, further improving TB detection. These studies highlight the potential of novel diagnostic tools to enhance the speed, accuracy, and efficiency of TB detection, particularly in resource-poor settings, ultimately improving patient management and control efforts. This review examines several innovative approaches for detecting Mycobacterium tuberculosis complex (MTBC) and non-tuberculous mycobacteria (NTM), comparing them to the limitations of conventional culture and staining techniques.

Keywords: MTBC, NTM, Ag85B Protein, FISH, CrfA-Based Assay.

MBPP51

Identifying Novel Therapeutic Targets and Intervention Strategies: Insights from RSV Pathophysiology

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ABSTRACT

Respiratory Syncytial Virus (RSV) is a major cause of acute respiratory infections worldwide, posing significant health risks to infants, older adults, and immunocompromised populations. Annually, 33 million cases of RSV LRTI (Lower Respiratory Tract Infections) occur in children younger than 5 years resulting in 3.6 million hospitalizations and 118,200 deaths. The global burden of RSV underscores the need for effective therapeutic and preventive strategies. This study explores the molecular pathogenesis of RSV focusing on identifying novel therapeutic targets and intervention strategies. RSV genome encodes 11 proteins (2 non structural protein and 9 structural proteins), which play crucial roles in the virus's ability to infect host cells, replicate and evade the immune response. Key therapeutic advancements include targeting RSV-specific proteins such as NS1 and NS2, which suppress the host's interferon response, using small-molecule inhibitors and RNA-based therapeutics. The pre fusion (PreF) protein, known for its high immunogenicity, has demonstrated high efficacy in vaccine formulations. Emerging research also highlights the potential of blocking the G protein's CX3C motif and SH protein's ion channel activity to enhance host immunity and curb viral evasion. Additional promising strategies include siRNA-based therapeutics, epigenetic modulators, monoclonal antibodies, maternal immunization, infant immunization and Toll-like receptor (TLR) agonists as adjuvants. This review emphasizes the revolutionary influence of advancements in RSV management by unraveling its molecular pathogenesis, addressing critical gaps in therapeutic and prevention. By leveraging these novel approaches, the global RSV burden can be effectively mitigated, offering new hope for vulnerable populations.

Keywords: RSV; Pathophysiology; Vaccines; Respiratory Infections; Antiviral Strategies; Viral Proteins.

MBPP55

Decoding Ribose-5-Phosphate Isomerase Deficiency: Advances in Diagnosis and Understanding a Rare Metabolic Disorder

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ABSTRACT

Ribose-5-phosphate isomerase (RPI) deficiency is a rare metabolic disorder caused by mutations in the RPIA gene, which produces the enzyme ribose-5-phosphate isomerase. This enzyme plays a crucial role in the pentose phosphate pathway, a key metabolic process involved in nucleotide production and maintaining cellular redox balance.

RPI deficiency can present with a wide range of symptoms, including developmental delays, neurological challenges, and metabolic irregularities, making it difficult to diagnose. An effective diagnosis often requires combining biochemical, genetic, and imaging techniques. Biochemical testing typically identifies elevated levels of certain sugar alcohols, such as ribitol and arabitol, in body fluids. These abnormalities are detected using sophisticated methods like gas chromatography-mass spectrometry (GC-MS) or liquid chromatography-mass spectrometry (LC MS). Genetic testing, such as next-generation sequencing (NGS) or whole-exome sequencing (WES), is critical for identifying specific mutations in the RPIA gene, and confirming the condition.

Newer tools like metabolomics provide a broader understanding of the metabolic changes linked to the disorder, while functional tests measuring residual RPI enzyme activity offer additional evidence. Imaging techniques, particularly magnetic resonance spectroscopy (MRS), help reveal brain abnormalities often associated with the condition, further supporting the diagnosis.

Early and accurate identification of RPI deficiency is vital for proper treatment and genetic counselling. A multidisciplinary approach that includes clinical evaluation, metabolic testing, and molecular analysis is key to improving diagnostic accuracy and unravelling the complexities of the disease. Ongoing research is essential to refine diagnostic methods and develop effective therapies for this rare yet impactful condition.

Keywords: Ribose 5-phosphate Isomerase, RPI Allele, Gene Sequencing, Leukoencephalopathy, Magnetic Resonance Spectroscopy.

MBPP56

Antibody Drug Conjugate: An Insight in to the Manufacturing Issues

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ABSTRACT

Antibody-Drug Conjugates (ADCs) are immunoconjugates that comprise of a monoclonal antibody(mAb) covalently attached to a cytotoxic drug (payload) via a chemical linker. Chemotherapeutic drugs affect the functioning of neoplastic cells upon reaching the site of action and not only do they inhibit cell proliferation and multiplication of tumor cells but also result in toxic effects on the normal cells. ADCs combine the specificity of monoclonal antibodies and the toxicity of chemotherapeutic drugs and selectively deliver the payload to the cancerous cells thus reducing systemic toxicity. ADCs like Mylotarg (treatment of relapsed AML), Adcetris (Hodgkin lymphoma), Kadcyla (HER2-positive mBC) etc. recognize specific antigens on the surface of cancerous cells and bind to them post which they are internalized to deliver the payload which biochemically interacts with the cellular machinery leading to tubulin binding and/or DNA cleavage. ADCs are manufactured by assimilating its composites via bioconjugation techniques which comes with its set of struggles due to their complex structure, strict quality requirements and multidisciplinary production process. ADCs are prone to contamination disrupting efficacy and safety of the drug, scalability becomes an issue and so does maintaining the drug-antibody ratio during scale-up. Moreover, probability of exposure to toxicity during large scale manufacturing manifolds. ADCs are a novel solution for cancer. Many ADCs are currently in preclinical development or in ADC clinical trials waiting for their FDA approval. In this article, we provide a brief overview of the manufacturing standards for ADCs and the challenges encountered during the process.

Keywords: Antibody Drug Conjugates; Monoclonal Antibody; Payload; Manfacturing Standards.

MBPP57

Recent Drug Targets of Mycobacterium Tuberculosis

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ABSTRACT

Tuberculosis is a fatal infectious disease that affects millions of people annually, make it one of the leading cause of illness and death globally. However, rising drug resistance, prolonged and harmful treatment regimens and a lack of new are the main obstacles to tuberculosis control. Herein, we report about the latest anti-TB targets Gyr A/B, DprE1, MmpL3, ATP - Synthase. These drug targets can be screened virtually with large chemical/natural compound libraries using Structure - based approaches (computer aided drug design (CADD) and high throughput screening (HTS)) to identify new anti-TB drug candidates. This approach can assist in identifying novel lead molecules for potential treatment of for the TB, to overcome the present therapeutic obstacles associated with tuberculosis.

Keywords: Mycobacterium Tuberculosis; Drug Targets; Drug Resistance; Infectious Disease; anti-TB drugs.

MBPP58

Natural Phytochemicals as Neuroprotective Agents: Exploring Their Therapeutic Potential

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ABSTRACT

Neurodegenerative diseases, including Alzheimer's, Parkinson's, and Huntington's disease, pose significant challenges to global healthcare systems. The growing interest in natural plant-derived compounds for neuroprotection highlights their therapeutic potential. Plants, as a rich source of bioactive compounds such as flavonoids, alkaloids, terpenoids, and polyphenols, offer multifaceted benefits, including antioxidant, anti-inflammatory, and anti-apoptotic properties. These mechanisms help mitigate oxidative stress, reduce neuroinflammation, and protect neuronal integrity, which are central to the pathophysiology of neurodegeneration.

Prominent examples include Ginkgo biloba, known for enhancing cognitive function and memory, and Bacopa monnieri, which supports synaptic activity and neural regeneration. Curcumin from turmeric exhibits significant antioxidant effects, while Withania somnifera (Ashwagandha) and Panax ginseng are recognized for their neurorestorative properties. Recent research also explores the synergistic potential of plant-based compounds with conventional therapies, paving the way for integrative treatment approaches.

This review underscores the importance of further studies to elucidate the molecular mechanisms, optimize dosage forms, and evaluate long-term safety profiles. Natural plants hold promise not only in mitigating neurodegeneration but also in promoting overall brain health and emotional well-being, offering a sustainable and accessible avenue for global mental health challenges.

Keywords: Neurodegenerative Diseases, Natural Phytochemicals, Bioactive Compounds, Neuroprotection.

MBPP59

Role of Essential Oils in Cancer Symptom Relief: Mechanisms, Efficacy and Future Directions

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ABSTRACT

Cancer, a leading cause of death, results from abnormal cell growth. Cancer patients often experience complications resulting from chemotherapy and radiotherapy. These treatments harm healthy cells along with cancer cells, causing side effects such as pain, nausea, and anxiety. Essential oils present a promising complementary approach for managing such symptoms in palliative cancer care.

The therapeutic effects of essential oils in cancer palliation are mediated through psychological and physiological pathways. Essential oils influence brain function by altering neurotransmitter production and perception. Inhalation of these oils has demonstrated anxiolytic and antidepressant properties, lowered cortisol levels, and promoted relaxation.

Active compounds present in essential oils can cross the blood-brain barrier, triggering the release of neurotransmitters such as endorphins, serotonin, and dopamine - commonly referred to as "feel-good" chemicals. The modulation of neurotransmitter activity can affect the autonomic nervous system, promoting relaxation, reducing pain perception, and alleviating stress, depending on the type of essential oil used. The sedative properties of essential oils are believed to occur through the modulation of GABAergic neurotransmission, enhancing inhibitory signalling in the brain. This mechanism contributes to calming the central nervous system, thereby improving mood, reducing pain and anxiety, and enhancing sleep quality.

Current evidence, though inconclusive, supports the efficacy of essential oils in symptom relief through the physiological activation of neurological and sensory receptors. However, further research is needed to elucidate the underlying neurological mechanisms and establish standardized treatment protocols for clinical application.

Keywords: Aromatherapy; Essential Oils; Palliative Care; Symptom Management; Complementary Cancer Therapies.

MBPP60

Addressing Antimicrobial Resistance: The One Health Approach

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ABSTRACT

The abusive use of antimicrobials in the healthcare sector, animal sector, and farming sector speeds up the genesis and spread of resistant pathogens. Antimicrobial resistance is a worldwide challenge which threatens human, animal, and environmental health. The ONE HEALTH approach is a collaborative and integrated work system that is extremely beneficial in addressing AMR effectively by suggesting the interdependence of human, animal, and environmental health. This integrated system emphasizes coordinated efforts across sectors to address the root cause of resistance and promote sustainable use of antimicrobials. Key strategies against AMR include the promotion of antimicrobial stewardship which includes treatment of contaminated water to prevent the release of antibiotics and resistant microbes into natural ecosystems, limiting environmental contamination from pharmaceuticals, rational prescribing of drugs, and implementation of alternative healthcare therapy such as gene therapy or vaccinations. Secondly, robust surveillance systems help in tracking the antimicrobial use and resistance trends in humans, animals, and the environment. This approach also includes awareness campaigns to reduce the demands for unnecessary antimicrobials and encourages international collaborations among WHO, FAO, OIE, and UNEP to implement AMR action plans. They also promote the studies of the transmission dynamics of resistant microbes between humans, animals, and the environment. The ONE HEALTH Approach is a complex, resource-demanding, and coordinated approach which serves as its drawbacks for combating AMR. Strategic planning, investments, and global cooperation are essential to work with the ONE HEALTH approach.

Keywords: Antimicrobial, One Health, Vaccination, Antimicrobial Stewardship, Robust Surveillance, Antibiotics, Gene Therapy.

MBPP61

Targeting the Neuromuscular Junction Degeneration in Sarcopenia

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ABSTRACT

The gradual decline in muscle mass, strength and function known as sarcopenia, significantly contributes to weakness and impairment in older population. This condition is a key factor in the development of frailty and disability among aging individuals. This disease is mostly caused by neuromuscular system degeneration which disrupts communication between motor neurons and muscle fibers. This dysfunction leads to the loss of motor neurons, neuromuscular junction (NMJ) instability, and subsequent muscle fiber atrophy particularly in Type II fibers which are critical for strength and power.

Emerging evidence has highlighted the multifactorial nature of neuromuscular degeneration in sarcopenia. Oxidative damage, mitochondrial dysfunction, chronic low-grade inflammation (also known as "inflammaging"), and dysregulated protein turnover are critical dysregulated processes. Together, these mechanisms weaken the integrity of the NMJ and accelerate muscle deterioration.

Despite progress in the understanding of sarcopenia some critical research gaps remain – accurate and early diagnostic evaluations or imaging modalities are yet evolving. The only established clinical regime for managing sarcopenia appears to be resistance training alongside a sufficient protein intake. Effective treatment approaches targeting muscle and NMJ synapse are unexplored. An interesting area of exploration can also be stem cell therapies or inflammaging interventions as NMJ stabilizers that may slow the progression of sarcopenia and restore function.

Additionally, there is a void of creating individualized treatment approaches that integrate exercise, nutrition and advanced therapies. By connecting laboratory discoveries with practical clinical applications, future innovations can offer effective methods to prevent and address sarcopenia, especially targeted to NMJ, ultimately enhancing the independence and quality of life for older adults.

Keywords: Sarcopenia; Neuromuscular Junction (NMJ); Type II Muscle Fibers; Inflammaging; Mitochondrial Dysfunction.

MBPP62

Targeting PLpro of Re-emerging β-Coronaviruses

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ABSTRACT

Evolving β-Coronaviruses (β-CoVs) have posed a significant global health threat in recent years. The Coronavirus disease 2019 (COVID-19) pandemic caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has caused substantial morbidity and mortality worldwide. Despite the availability of vaccines and antivirals targeting β-CoVs, the emergence of new variants with enhanced resistance, adaptability and transmissibility due to rapid mutation rates poses a significant risk of future outbreaks and pandemics. This necessitates constant antiviral discovery of novel antivirals against essential targets. One such target is Papain like protease (PLpro), a conserved cysteine protease in β-CoVs. This protease is responsible for proteolytic processing of viral polyproteins into functional nonstructural proteins and host immune evasion. Onset of mutation-mediated drug resistance against RNA Dependent RNA polymerase and main protease inhibitors has made PLpro a promising target for developing broad-range antiviral. Discovery of multiple small molecules such as GRL0617(Fu, Ziyang et al. Nature Communications Vol. 12,1 488. 20 Jan. 2021), Jun12682(Yang, Mianling et al. Acta Pharmaceutica Sinica. B Vol. 14,9 2024), PF-07957472(Garnsey, Michelle R., et al. Science Advances, Vol. 10, no. 35, Aug. 2024) and other novel non-covalent PLpro inhibitors have exhibited promising antiviral activity in preclinical models against SARS CoV-2. This review highlights the future potential of PLpro inhibitors in tackling β-coronavirus outbreaks and new variants of re-emerging β coronaviruses like SARS-CoV, MERS-CoV and SARS-CoV-2. Additionally, the review also discusses the challenges faced by these potential drug candidates in translation from the lab to clinical trials and explore ways to improve their effectiveness and safety.

Keywords: β-coronaviruses; PLpro; PLpro inhibitors; SARS-CoV; MERS-CoV; SARS-CoV-2.

MBPP63

Unlocking Novel Drug Targets and Therapeutic Advancements Against RNA Viruses: Insights from HMPV and SARS-CoV-2

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ABSTRACT

Re-emerging RNA viruses pose a significant global health threat due to their high mutation rates, potential for zoonotic transmission, and capacity to cause widespread outbreaks such as Human Metapneumovirus (HMPV), SARS-CoV-2, Influenza etc. The rapid evolution and re-emergence of these viruses necessitate the development of novel drug targets and therapeutic strategies to combat existing and future outbreaks. This study focuses on structural as well as non-structural targets of these RNA viruses such as viral entry proteins, RNA-dependent RNA polymerases (RdRp), and other viral proteins involved in interaction with host factors and immune invasion for therapeutic interventions. For HMPV, fusion (F) protein is a key target for drug discovery which contains an RGD (Arg-Gly-Asp) motif, that binds RGD-binding integrins to mediate pH-independent membrane fusion. Masking this motif, using natural inhibitors like ginkgolic acid, can block HMPV infection. SARS-CoV-2 treatments mostly target Spike protein and RdRp inhibitors. Natural product inhibitors of RdRp such as epigallocatechin gallate (EGCG) and theaflavins mimic nucleotide substrates, and disrupt viral RNA synthesis by causing premature termination or blocking further nucleotide addition. Specifically, SARS-Cov-2 RdRp forms a trimeric complex with nsp7 and nsp8 for its activity, and therefore, targeting these essential accessory proteins offers another strategy to inhibit viral replication and prevent infection. This study highlights some novel strategies for developing effective therapeutics against HMPV and COVID-19, laying the groundwork for enhanced pandemic preparedness and response.

Keywords: RNA Viruses; Novel Drug Target/Novel Drug; F protein; RdRp; Natural Inhibitors.

MBPP64

Investigating HLA Class II Genetic Variants as influencers of Type 2 Diabetes Risk and Related Complications Across Diverse Populations

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ABSTRACT

The human leukocyte antigen (HLA) system, particularly the class II genes, is significantly implicated in the genetic susceptibility to type 2 diabetes (T2D). Recent investigations have clarified the associations between specific HLA alleles and T2D risk, revealing intricate genetic interactions. For instance, the HLA-DRB102 allele has been recognized as a notable protective factor, enhancing self-tolerance and potentially reducing autoimmune responses that may impair insulin secretion. In contrast, alleles such as HLA-DR4 and haplotypes including DRB107:01~DQA102:01~DQB103:03 are linked to heightened susceptibility to T2D. Ethnic diversity adds complexity to these associations, with varying allele frequencies across populations indicating that the genetic architecture of T2D may differ significantly among ethnic groups. Furthermore, specific HLA alleles correlate with diabetes-related complications, such as diabetic nephropathy. For example, HLA-DQA10301 and HLA-DQA10501 alleles have been identified as susceptibility markers for T2D in certain populations, while HLA-DQB10501 has demonstrated a protective effect against diabetic nephropathy. These findings highlight the critical role of the HLA class II locus not only in understanding T2D pathophysiology but also in developing targeted prevention and therapeutic strategies. The shared genetic components between type 1 and type 2 diabetes underscore the necessity for further research into the immunological pathways influenced by HLA variations. This exploration could enhance our understanding of T2D mechanisms and improve management strategies for affected individuals. The current study intricates the associations between human leukocyte antigen (HLA) class II alleles and the genetic susceptibility to type 2 diabetes (T2D), emphasizing both protective and risk factors across diverse populations. The findings underscore the role of ethnic diversity in shaping these genetic associations, revealing that allele frequencies can vary significantly among different populations.

Keywords: Type 2 Diabetes, Human Leukocyte Antigen, Haplotypes, Ethnic Diversity.

MBPP66

Differential Hypoxic Adaptive Response of Rat Thymus and Liver Exposed to Hypobaric Hypoxia

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ABSTRACT

Organisms have developed oxygen-sensing system and tissues respond appropriately to the varied concentration of oxygen. The objective of the study is to determine molecular mechanism of hypoxic adaptive response of rat thymus and liver exposed to hypobaric hypoxia for 1, 3, and 7 d interval at 25,000 fts and after exposure, liver and thymus was collected to analyze redox status (GSH, MDA and antioxidant status) and molecular adaptive markers (HIF1α, VEGF and erythropoietin). The total antioxidant status in liver was significantly decreased on day 3 and 7 of exposure while in thymus it was compromised on day 7 of exposure. Moreover, HIF1α and its dependent factors were differentially expressed in liver and thymus. Liver HIF1α increases after day 1 and day 7 exposure but in thymus increases after day 7 of exposure. Liver VEGF was enhanced on day 1 and day 7 of exposure however VEGF was highly expressed on day 3 exposure in thymus. There was involvement of erythropoietin in adaptive response in liver but was not significant in thymus. Overall, hypobaric hypoxia exposure initiate activation of different components of HIF1α machinery in liver and thymus at various exposure time points reflecting differential sensitivity to hypobaric hypoxia.

Keywords: Hypobaric Hypoxia, Adaptive response, Oxygen Sensing, HIF1α, VEGF.

MBPP67

Pharmacological Properties of Ganoderma lucidum against Hypoxia

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ABSTRACT

Ganoderma lucidum (GL) commonly known as lingzhi or reishi is a traditional Chinese medicinal mushroom is gaining recognition for it's unique bioactive constituents and their varied therapeutic potential.

Hypoxia, a condition of compromised oxygen bioavailability in body or tissues, triggers a cascade of cellular and molecular responses to maintain adequate oxygen homeostasis. These adaptive responses are complex and constitute a series of physiological adjustments alongside certain pathological responses such as overt inflammation, redox imbalance, compromised vascular barrier integrity, cellular turnover in tissues etc.

Recent investigations report that GL has many pharmacological benefits, particularly in hypoxic condition, due to it's multiple bio-active components such as polysaccharides, triterpinoides and other antioxidants. This review elaborates the pharmacological properties of GL in hypoxia, focusing on it's role in modulating HIF (Hypoxia Inducible Factor – master transcriptional modulator of hypoxia adaptation), reducing oxidative stress, and improving cellular energy metabolism. Additionally, GL improves oxygen utilization and protect cells and tissues against hypoxic damage by regulating angiogensis, erythropoiesis and inflammatory responses.

Understanding the pharmacological potential of GL under hypoxic environment provides valuable insights into it's applications in managing diseases such as ischemia, pulmonary disorders, cancer and other high altitude related diseases.

Keywords: Ganoderma Lucidum, Hypobaric Hypoxia, Inflammation, Hypoxia Inducible Factor, Molecular Adaptation, Medicinal Mushroom.

MBPP68

Future of Metabolic Drug Repurposing in Cancer Therapy

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ABSTRACT

Cancer remains a leading global cause of morbidity and mortality, characterized by dysregulated cell proliferation, invasion, and metastasis. Conventional therapeutic modalities, including surgery, chemotherapy, and radiation, often face significant limitations, such as suboptimal efficacy, high treatment costs, and adverse side effects. Drug repurposing—identifying new therapeutic indications for existing, approved drugs—has emerged as a promising strategy to mitigate these challenges. This approach capitalizes on the established safety profiles, known pharmacokinetics, and existing manufacturing processes of repurposed drugs, offering a cost-effective and time-efficient alternative to traditional drug discovery. Among the various classes of drugs investigated for repurposing in cancer therapy, metabolic drugs have gained significant attention due to their role in modulating the tumor microenvironment and cellular metabolism. Drugs originally developed for metabolic disorders, such as type 2 diabetes, obesity, cardiovascular disease, hypertension, and some others are being explored for their potential anti-cancer effects. For example, there are nearly 60 FDA-approved drugs are available for the treatment of type 2 diabetes mellitus, with metformin being extensively studied for its anti-carcinogenic potential. Similarly, among the 7 FDA-approved obesity medications, many are currently being explored for their potential anti-cancer effects. Other metabolic modulators, including statins, thiazolidinediones, and glucagon-like peptide-1 analogs, are being investigated for their ability to interfere with cancer cell proliferation and survival. However, Certain drugs may exhibit synergistic effects and hold promise for combination therapy, offering a potential strategy for more effective treatment. This review highlights the translational potential of drug repurposing, emphasizing the use of existing metabolic drugs to enhance therapeutic outcomes in cancer patients.

Keywords: Cancer, Drug repurposing, Metabolic Disorders, Diabetes, Drug Discovery, Metformin.

MBPP69

Breathing Immunity: The Revolutionary Rise of Nasal Vaccines

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ABSTRACT

Nasal vaccines, as the name suggests, are administered through the nasal passage, instead of traditional vaccines. They have a greater advantage over the traditional approach as they are safe, painless and easy to administer. The nasal vaccines have an ability to give an immediate immune response. The nasal cavity is lined with mucosa membrane and acts as the first line of defence against respiratory diseases like influenza and COVID-19. Nasal vaccines stimulate the nasal mucosa to produce an immune response rather than entering into blood directly. They primarily stimulate the mucosal immunity in the nasal cavity as well as the nearby lymphoid tissues, with limited entry into the bloodstream. Specialized cells, such as dendritic and epithelial cells, capture antigens, which cross the mucosal barrier through processes like endocytosis. These antigens are transported to nasal-associated lymphoid tissue (NALT) from where they trigger local and systemic immune responses. Activated immune cells and antibodies are circulated via the bloodstream, while plasma cells produce IgG antibodies for systemic protection. Some vaccine components may even enter directly into the bloodstream via the nasal cavity's rich vascular network. By targeting mucosal surfaces, nasal vaccines provide robust protection against respiratory infections. They prevent transmission of diseases from person to person that spread via needles, contamination and solve the disposal issues related to needle-based vaccines. They are generally suitable for all age groups.

EXAMPLES: Smallpox, Influenza, COVID-19: (inCOVACC, Razi Cov Pars, Sputnik, and Convidicia).

Keywords: Nasal Vaccines; Mucosal Immunity; Endocytosis; Nasal-Associated Lymphoid Tissue (NALT); IgG Antibodies.

MBPP70

Mesenchymal Stem Cell Therapy: A Regenerative Approach to Vitiligo Treatment

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ABSTRACT

Vitiligo is an acquired autoimmune disorder characterized by the progressive destruction of melanocytes, resulting in skin depigmentation and significant psychosocial distress. Current therapeutic options are limited in achieving long-term repigmentation and fail to address the multifaceted etiology involving oxidative stress, immune dysregulation, and melanocyte apoptosis. Emerging evidence highlights mesenchymal stem cells (MSCs) as a promising intervention due to their dual roles in immunomodulation and tissue regeneration. This review delves into the mechanisms by which MSCs contribute to vitiligo treatment, focusing on their ability to suppress the hyperactivity of CD8+ T cells and modulate cytokine production in the perilesional environment. Furthermore, MSCs mitigate oxidative damage by enhancing antioxidant pathways, thereby preserving melanocyte viability. Studies demonstrate that MSC-derived paracrine factors promote melanocyte proliferation and repair through pathways like PI3K/AKT while downregulating detrimental PTEN signaling. Experimental models and clinical trials show significant improvements in repigmentation and lesion stability when MSCs are integrated into autologous melanocyte transplantation protocols. Despite these promising outcomes, challenges remain in standardizing MSC sources, optimizing delivery methods, and understanding their long-term effects on skin homeostasis. By addressing these gaps, MSC-based therapies have the potential to revolutionize vitiligo management, of ering durable solutions that target the disease's immune and cellular dimensions. This review underscores the significance of MSCs in advancing regenerative medicine for autoimmune skin disorders and highlights the translational potential of integrating MSCs with existing therapeutic frameworks.

Keywords: Vitiligo, Mesenchymal Stem Cells (MSCs), Melanocyte Regeneration, Immune Modulation, Regenerative Medicine, Melanocyte Transplantation, PTEN/PI3K/AKT Pathway, Cytokine Regulation

MBPP71

Role of Senolytic Agents in Skin Care

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ABSTRACT

Aging is the natural process that all lifeforms undergo, it can be defined as time-related deterioration of physiological functions. Fibroblasts in the dermal layer of skin play an important role in building collagen and wound healing, as humans age, factors such as UV radiation, pollution and inflammation can cause damage to these fibroblasts which then either go through apoptosis (programmed cell death), divide and propagate the damage or become senescent cells (SCs). Cellular senescence is the phenomenon in which cells exit the cell cycle and enter the "G0" phase during which they remain alive but do not participate in cell division, resulting in permanent growth arrest. These senescent cells develop Senescence- Associated Secretory Phenotype (SASP) which contributes to chronic inflammation which leads to further skin aging.

Senomorphics are molecules that suppress SASP and senolytics are agents which eliminate senescent cells, together they form a new class of drugs known as senotherapeutics. Senescent cells do not respond to apoptosis and have anti-apoptotic pathways which help them to survive. Senolytics work by disrupting these anti-apoptotic pathways and inducing apoptosis in senescent cells. In this way senolytic agents can remove SCs and rejuvenate the skin making it look more youthful. Examples of compounds that have the senolytic potential to kill SCs include quercetin, fisetin, curcumin analogs. More research is required along with appropriate animal models and clinical trial paradigms to develop successful senolytic agents for treating skin aging.

Keywords: Aging, Fibroblasts, Cellular Senescence, SASP, SCs, Apoptosis, Senolytics.

MBPP72

Expression Patterns of TRIM33 and SMAD4 in Esophageal Squamous Cell Carcinoma: Correlation with Clinical and Pathological Features

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ABSTRACT

*SMAD4 and TRIM33 are tumor-suppressor genes involved in the regulation of the TGF-β pathway, with potential roles in the tumorigenesis of esophageal squamous cell carcinoma (ESCC). In this study, mRNA expression levels of SMAD4 and TRIM33 were determined in 39 ESCC fresh tumors and normal tissues using qRT-PCR. Expression was normalized to GAPDH, and fold changes were calculated using the $2^{-\Delta\Delta Ct}$ method, followed by analysis with the Kruskal Wallis test. The association between the expression and clinicopathological characteristic were analyzed. The mean age of cohort was 54.8±12.6 years, comprising 20 males and 19 females. Tumor were located middle-third (n=18) and lower-third thoracic (n=18) esophagus in 46% each. Stage distribution showed 13, 15, 11 patients in stage II, III and IV respectively. Results revealed downregulation of TRIM33 (74.35%) and SMAD4 (58.97%) were observed with a fold change of 7.47 ± 4.65 and 6.12 ± 4.92, respectively. A positive correlation was found between fold change of TRIM33 and SMAD4 (r=0.633, p=**0.0001**, 95% CI: 0.397-0.791). Moreover, downregulation of SMAD4 and TRIM33 was observed progressively from stage 2 to 4, with SMAD4 downregulated in (53%, 53%, and 72%) and TRIM33 in (76%, 66%, and 81%) of cases, respectively. These findings suggest that the downregulation of TRIM33 and SMAD4 contributes to ESCC progression, with incidence of downregulation increasing with advanced stage. Meanwhile we observed a trend with tumor progression, stage, location, and differentiation, though statistically not significant.*

Keywords: TGF-β pathway; TRIM33; SMAD4; ESCC.

MBPP73

Powdered Sachets for Instant Relief

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ABSTRACT

Packed sachets for instant relief represent a novel development between traditional medicine and consumer health offering solutions for stomach aches, headaches, and blood pressure. Re-analyzed in this review is their possibility of being cheap, portable, and fast-acting medical substitutes based on natural ingredients such as peppermint, ginger and magnesium which are proven to be effective in clinics. The pedology of these sachets fills huge gaps in the fast-growing demand for convenience, on-the-go health solutions especially considering the growing trend of consumer interest in organically derived and eco-friendly ingredients. Here we evaluate the pharmacological properties and mechanisms of action of key ingredients and overcome the limitations in rapid and massive absorption enhancing formulation technologies. In addition, the adoption of biodegradable packaging materials in this study was explored in conjunction with progresses in product standardization, scalability, and compliance with regulations. This paper also seeks to integrate knowledge from other sectors such as scientific journals, clinical trials of theories, as well as market trends to see the prospects of packed sachets as modern-day transformation in the medicine world. This review aims at further development and research, the findings should naturally contribute to the integration of such products into mainstream health care while, indeed, paying due homage to sustainable and consumer-led priorities.

Keywords: Consumer Health, Natural Ingredients, On-the-go Health Solutions, Biodegradable Packaging, Convenience.

MBPP74

Bridging Ancient Wisdom: Integrating Vedic Knowledge with Modern Stem Cell Therapy

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ABSTRACT

Stem cell therapy is that lately discovered wonderful way of regenerative medicine which is intended to treat degenerative diseases, tissue repair, and organ regeneration and thus, it is among those prominently having potential breakthroughs. Meanwhile, the old Vedic system of treatment, especially Ayurveda, gives a deep insight into the body's natural healing and rejuvenating processes that are also in line with the modern advances in the field of biomedical sciences. This overview reports the meeting of these two paradigms, being based on the recent studies that explore the Ayurvedic treatments and their effect on stem cell function. Studies indicate that Ashwagandha and Guduchi, the Ayurvedic herbs, strengthen the process of stem cell proliferation and resistance to oxidative stress, which finally becomes the cause of the elevation of therapeutic results. Also, neuroprotective, anti-inflammatory, and regenerative effects, seen with the medication like Brahmi, Turmeric, and Shilajite, have shown the further increment of stem cell survival and the growth of the effector stem cells. Additionally, Ayurveda-based treatments, such as yoga, pranayama, and meditation, have been documented to mitigate oxidative stress as well as systemic inflammation, and so to, help the body in the natural way of healing and the cells becoming more effective under stem cell treatment. Moreover, the rise of molecular biology and bioinformatics gave a clear understanding of the cellular pathways affected through Ayurvedic compounds and the consequent tissue regeneration. The merger of modern stem cell techniques with these traditional Vedic therapies can drive the possibility of curing AIDS, that is, creating new biological ways of the healing process of the person on a personal level. This review calls for rigid preclinical and clinical trials that will confirm the feasibility of this holistic approach which has tremendous potential for the advancing of tissue regeneration and medical science.

Keywords: Stem Cell Therapy, Regenerative Medicine, Tissue Repair, Organ Regeneration, Ayurvedic Compounds.

MBPP75

Venous Thromboembolism (VTE) at High Altitudes

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ABSTRACT

High-altitude environments can have an immense physiological effect on the human body, which may lead to the development of various disorders due to reduced oxygen availability. This condition is known as hypoxia. Venous thromboembolism is one of these disorders. About 10 million individuals worldwide suffer from this deadly cardiovascular disease annually; the actual figure is likely higher because most cases of venous thromboembolism go undetected or are misdiagnosed. VTE is the third most prevalent vascular disease after myocardial infarction, and stroke. A blood clot forming in one of the deep veins, typically found in the leg, is the first sign of venous thromboembolism. A pulmonary embolism is a dangerous consequence that occurs when this clot breaks free and travels to the lungs; these two conditions are collectively referred to as venous thromboembolism. We detect DVT using ultrasound and PE with pulmonary angiography. Despite its poor specificity, the D-dimer test remains the most often used diagnostic marker for thrombosis in clinical settings today. Although a variety of anticoagulants are prevalent in today's pharmaceutical market, they offer a concern. Their use in high-altitude environments is challenging since they may interfere with the body's normal physiological parameters in such unfavorable settings. It is critical to understand the symptoms and risk factors of VTE. The likelihood of consequences from this illness can be considerably decreased with early detection and treatment. Further research needs to be done to develop specialized treatment strategies ensuring effective prevention and timely intervention for individuals at risk.

Keywords: VTE; DVT; PE; D-dimer Test; Hypoxia; Specificity; Ultrasound; Pulmonary Angiography.

MBPP76

Neurogenetics and Crime: Can Medical Biotechnology Diagnose Potential Killers

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ABSTRACT

Psychopaths aren't born—they're made.

The harsh treatment of society with scarring and callousness affects the mind, and a victim becomes a predator with time. This cold transformation. In itself, this invokes a darkened landscape not just of experiences but of the brain that holds them. With the help of modern medical biotechnology, the relation of mental disorders like schizophrenia, abnormality of the brain, and violent criminal determination is becoming less vague than it used to be.

Schizophrenia is an illness characterized by a fractured mind and altered thought processes that change the mind. Studies in neurology have revealed abnormality in some part of the brain, like the prefrontal cortex, which controls decision-making impulse. Violent criminals such as serial killers often develop such deficiencies and are unrepentant. By way of neuroimaging and genetic profiling, forensic science now has the capability to map these dark minds and reveal the physiological markers of violence.

Diseases usually spread due to infection through contacts from sick to healthy. However, on rare occasions, it also spreads through the environment. As research advances, integrating criminology with psychology offers easier routes to criminal profiling that are more accurate. Likewise, targeted psychiatric treatment is another advantage. Nonetheless, this doesn't mean we wait till the person becomes a monstrous serial killer. In this dark reality, the marriage of neuroscience and biotechnology may hold a promise of salvation—for society and for those lost in the corridors of their own broken minds.

Keywords: Schizophrenia; Neuroimaging; Genetic Profiling; Forensic Science; Criminology.

MBPP77

The Role of Artificial Oxygenation Systems in Preventing High-Altitude Pulmonary Edema (HAPE)

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ABSTRACT

High-altitude pulmonary edema, or HAPE is a serious condition that occurs in areas with low oxygen levels at high altitudes (2740 m and above). It is caused by fluid accumulation in the lungs due to increased pressure in the lungs and poor oxygen exchange, which can lead to breathing problems or even death if not treated right away. The biggest risk factor for HAPE is ascending too quickly. Artificial oxygenation systems, like portable oxygen tanks, hyperbaric chambers, and other advanced devices, play a key role in helping prevent and treat HAPE for those at risk. These systems work by providing extra oxygen to keep blood oxygen levels healthy and balanced, easing lung pressure, and stopping fluid from building up. Portable oxygen concentrators can provide brief relief, but contain too little oxygen for sustained improvement. Hyperbaric chambers, which simulate lower altitudes by increasing atmospheric pressure, enhancing oxygen uptake, and providing immediate relief. While these systems are lifesaving, they come with challenges such as high costs, reliance on resources, and limited portability in remote locations. However, recent innovations, such as lighter devices and smart, sensor-based monitoring, make artificial oxygenation more accessible and practical for people on high-altitude expeditions. In addition to oxygen support, proper acclimatization and medications such as nifedipine and dexamethasone can further reduce the risk of HAPE. Other treatments for HAPE includes rest, descent to a lower altitude, and pulmonary vasodilator medications. The use of artificial oxygenation systems is crucial in managing HAPE and provides crucial assistance in extreme environments. With continuous developments, these systems are becoming cheaper and more accessible, making high-altitude travel safer for everyone.

Keywords: HAPE; Oxygen Tanks; Hyperbaric Chambers; Artificial Oxygenation; Nifedipine; Dexamethasone.

MBPP78

Therapeutic Implications of Exosomal Cargo in the Therapy of Mental Disorders

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ABSTRACT

According to WHO, mental disorder is defined as a clinically substantial impairment in an individual's cognition, emotional regulation, or behavior. In key areas of functioning, it is typically linked to distress or disability. There are numerous forms of mental ailments spread worldwide like depression, bipolar disorder, schizophrenia, and post-traumatic stress disorder, etc. Blood-brain barrier (BBB) obstruction, drug tolerance, inadequate therapeutic targeting, and the absence of reliable biomarkers are some of the difficulties in diagnosing and treating these disorders. Exosomes are small extracellular vesicles that play a crucial role in intercellular communication and have emerged as promising vehicles for therapeutic delivery, particularly in the context of mental disorders. Their unique properties allow them to cross the blood-brain barrier (BBB), making them suitable for delivering therapeutic agents directly to the brain. They also act as disease biomarkers, therapeutic agents, and drug delivery vehicles, thus occupying vital roles in a variety of processes, both physiological and pathological. Certain subsets of cytosolic proteins, lipids, membrane proteins, nucleic acids, and other signaling molecules have been identified inside exosomes known as Exosomal Cargo. Once inside recipient cells, these cargo molecules determine their functional roles and targeting specificity. This review revolves around the therapeutic benefits of exosomal cargo in the treatment of mental disorders, along with the advantages of exosomal therapy over alternative therapeutic approaches due to its ability to maintain medication stability due to low toxicity and low immunogenicity, and improving therapeutic efficiency.

Keywords: Mental Disorders, Blood-Brain Barrier (BBB), Biomarkers, Drug Delivery, Exosomes, Exosomal Cargo.

MBPP79

Repurposing Potential of Antiviral Plant Derivatives Against STDs: Current Updates

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ABSTRACT

Sexually transmitted diseases (STDs), often referred to as sexually transmitted infections (STIs), are infections primarily transmitted through sexual contact, including oral, anal, and vaginal intercourse. The World Health Organization (WHO) estimates that over 1 million curable STIs are acquired daily worldwide, emphasizing the pressing need for innovative treatment strategies. The increasing prevalence of these infections has driven the exploration of the use of antiviral plant derivatives, which are derived from natural compounds with inherent bioactive properties. These compounds exhibit a variety of mechanisms, including modulation of immune responses, inhibition of viral replication, and prevention of viral penetration into host cells. Their anti-inflammatory properties further enhance their suitability for managing sexually transmitted diseases by alleviating symptoms and promoting recovery. Repurposing antiviral plant derivatives offers a multifaceted approach to treatment by inhibiting viral replication and modulating immune responses, thus, increasing the efficiency and reducing the side effects. Cassia alata shows strong antibacterial activity against Neisseria gonorrhoeae, while Aloe ferox demonstrates dual-action potential against both gonorrhea and syphilis. Moreover, Commiphora angolensis contributes unique bioactive compounds targeting gonorrheal pathogens. The antiviral and anti-inflammatory properties of these plants alleviate symptoms and promote recovery, making them excellent compounds for future therapeutic development. This review highlights the repurposing potential of antiviral plant derivatives for STD management, focusing on their mechanisms—such as disrupting viral envelopes, inhibiting viral gene expression, and interfering with host cell attachment. Additionally, these derivatives could complement existing antiviral therapies, addressing resistance and side effects. By integrating pharmacological, botanical, and molecular biological research, the development of novel plant-based STD treatments holds immense promise for future healthcare solutions.

Keywords: STDs, Medicinal Plants, Bioactive Compounds, Therapeutic Potential, Natural Derivatives.

MBPP80

Understanding Iron Management in Acinetobacter baumannii: Structural Insights into Key Proteins

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ABSTRACT

The multidrug-resistant (MDR) pathogen Acinetobacter baumannii has emerged as a global healthcare challenge due to its ability to survive under host-imposed iron-limiting conditions. This study focuses on two key iron storage proteins, ferritin (Ftn) and bacterioferritin (Bfr), which play complementary roles in maintaining intracellular iron homeostasis. While Ftn primarily stores iron in a mineralized, non-toxic form, Bfr facilitates dynamic iron mobilization, supported by its heme-binding properties and interaction with bacterioferritin-associated ferredoxin (Bfd). These proteins collectively enable A. baumannii to counter oxidative stress, support metabolic processes, and enhance virulence under iron-restricted conditions.

This review examines the iron acquisition mechanisms in Acinetobacter baumannii, with a focus on bacterioferritin (Bfr) and its heme-binding properties, which facilitate dynamic iron transfer through interactions with bacterioferritin-associated ferredoxin (Bfd). Recent computational and experimental studies have identified compounds that inhibit the Bfr-Bfd interaction, disrupting bacterial iron metabolism and showing potential as therapeutic strategies against multidrug-resistant strains.

The integration of insights from structural biology, computational modelling, and experiment provides a perspective on A. baumannii's iron metabolism and how such a metabolism functions in survival during changing conditions. The complexity that A. baumannii evinces in handling iron for the bacterium necessitates its place as an encouraging target for the development of antimicrobial drugs in the future.

Keywords: Acinetobacter Baumannii, Bacterioferritin, Iron Metabolism, Multidrug Resistance, Structural Biology, Drug Discovery, Bfr-Bfd Interaction.

MBPP81

Protective Role of Picrorhiza kurroa and Apocynin against Particulate Matter from Environmental Pollutants and Tobacco Smoke Induced Cytotoxicity in Yeast Model System

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ABSTRACT

Respiratory ailments like bronchitis and asthma often result from overexposure to smoke from various sources, including tobacco and other environmental pollutants. Picrorhiza kurroa (PK) and its primary bioactive compound, apocynin (Apo), have shown protective effects against oxidative stress (OS) and inflammation caused in many situations. In the present study, yeast cells were exposed to various smoke sources, including Tobacco Smoke Extract (TSE) [0.5% to 5%], carbon particles, petrol soot, diesel soot, candle soot, and kerosene soot in the range of 0.01 to 10 µg/ml. To assess the preventive effects of Picrorhiza kurroa Extract (PKE) and Apo against environmental pollutants and tobacco smoke induced OS, the cells were pretreated with various concentrations of PKE [1, 2.5, and 5 µg/ml] and apocynin [0.5 and 1 µg/ml] for 1 hour at 37°C, prior to smoke exposure, which significantly prevented the cytotoxic effects of smoke exposure, with cell viability increasing from 14% to 60% ($p < 0.05$) in TSE-treated cells and 12% to 80% ($p < 0.01$) in carbon particles treated cells, respectively, compared to the untreated control. Apo showed positive results on total protein content, redox system, anti-inflammatory and antioxidant properties as indicated by increased superoxide dismutase (SOD) and catalase activities ($p < 0.01$), and reduced levels of NO synthase, NADPH oxidase and DNA fragmentation. These findings suggest that PK and Apo could be developed into therapeutics for environmental pollution and tobacco smoke related diseases but further research is needed to investigate their efficacy in animal model systems.

Keywords: Picrorhiza Kurroa; Apocynin; Saccharomyces Cerevisiae; Oxidative Stress; Tobacco Smoke.

MBPP82

Impact of Antiepileptic Drug Monotherapy on Endogenous Hormonal Profiles in People with Epilepsy: A Meta-Analytical Perspective

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ABSTRACT

Antiepileptic drug (AED) therapy influences endocrine pathways, but its impact on endogenous sex hormone profiles in people with epilepsy (PWE) remains incompletely understood. This meta-analysis evaluates the effects of enzyme-inducing AEDs (EIAEDs), weak-EIAEDs, and non-EIAEDs on endogenous hormones in PWE compared to healthy controls and drug-naïve PWE. A systematic review and meta-analysis of 33 observational and interventional studies, identified from MEDLINE, EMBASE, SCOPUS, and CENTRAL databases, assessed hormonal parameters, including sex hormone-binding globulin (SHBG) and testosterone (T). Our study found that EIAEDs like phenytoin and carbamazepine significantly increased SHBG levels, with stronger effects in men than women. Weak-EIAED oxcarbazepine also elevated SHBG in men, while non-EIAEDs such as valproic acid and levetiracetam showed no impact on SHBG in men. In contrast, lamotrigine decreased SHBG levels in women. Testosterone levels were reduced with carbamazepine and valproic acid in men. These findings suggest that AED-induced hormonal alterations vary by drug type, sex, and hormone assessed. The results highlight the clinical significance of monitoring reproductive and endocrine health in PWE on AED therapy, particularly those on EIAEDs, to mitigate potential long-term adverse effects. Hormonal profiling in clinical practice is recommended for early detection and management of AED-induced endocrine disruptions.

Keywords: Antiepileptic Drugs, Meta-Analysis, Sex Hormone Binding Globulin, Gonadotropins, Sex Steroid Precursor, Sex Steroid, Gonadal Hormone.

MBPP83

STOML2: The Undercover Driver of Tumor Progression and Chemoresistance

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ABSTRACT

Chemoresistance continues to be a key obstacle in the treatment of cancer, making therapeutic outcomes considerably more difficult for researchers and physicians alike. Recently, the mitochondrial dynamics including processes of mitochondrial fusion, fission, biogenesis, and mitophagy have been studied for maintaining cellular homeostasis as well as their crucial role in chemoresistance. While exploring the factors responsible for altering the mitochondrial dynamics (mainly fission and mitophagy) in cancer cells, the Stomatin-like protein 2 (STOML2), an inner mitochondrial membrane protein is known to be involved in mitochondrial stability. Through its interactions with proteins like PINK1 and PARL, it influences mitophagy and leads to the accumulation of damaged mitochondria and increases the ability of cancer cells to withstand the impact of chemotherapy. Additionally, STOML2 stimulates some pathways that aid in the survival and proliferation of cancer cells. Its role in mitochondrial biogenesis enables cancer cells to meet their high energy needs, and different forms of cancer have been associated with the overexpression of this protein. Thus, STOML2 has emerged as a significant target for increasing the sensitivity of cancer cells against standard drugs by modulating mitochondrial dynamics. Despite its importance, the structural complexity of STOML2 is not well understood, limiting targeted therapies. By providing insights into STOML2's role in cancer and its potential for therapy, this review seeks to bridge this knowledge gap.

Keywords: STOML2; Chemoresistance; Cancer; Therapy; Mitochondria.

MBPP84

Unveiling Emerging Lipid Roles in Mycobacterium-Macrophage Interactions

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ABSTRACT

Tuberculosis (TB) remains a major global health concern, ranking second after COVID-19 and surpassing HIV/AIDS. The survival and pathogenicity of Mycobacterium tuberculosis (M. tb), the causative agent of TB, are closely linked to its lipid-rich cell wall. This distinct layer, made up of complex compounds such as mycolic acids, phenolic glycolipids (PGLs), and phthiocerol dimycocerosates (PDIMs), is critical for immune evasion, intracellular persistence, and disruption of host defensive systems.

Upon infection, M. tb exploits the lipid-rich environment of macrophages, which contain cholesterol, triacylglycerols (TAGs), and phospholipids like phosphatidylcholine, phosphatidylinositol, and phosphatidylserine. This manipulation leads to the accumulation of lipid droplets and the formation of foamy macrophages, creating a nutrient-rich niche filled with TAGs, cholesterol, and bioactive lipids such as prostaglandins. In nutrient-limited conditions, these lipids provide the pathogen with essential energy. M. tb uses mechanisms such as the glyoxylate shunt to metabolize host lipids, which ensures its survival. However, the interactions between mycobacterium and host lipids are still poorly understood. Clarifying these pathways is critical for better understanding pathophysiology and developing lipid-targeted therapies.

Keywords: Mycobacterium Tuberculosis, M. tb, Macrophages, Lipids.

MBPP85

Targeting p38 MAPK in Alzheimer's Disease: A Promising Avenue for Modulating Inflammation and Neurodegeneration

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ABSTRACT

A member of the mitogen-activated protein kinase (MAPK) family of enzymes, p38 controls a number of cellular functions, including inflammation, stress reactions, and cell death. There are several different pathways involved in the intricate interaction between p38 and Alzheimer's disease (AD), especially when it comes to inflammation and neuronal stress. In Alzheimer's, the accumulation of tau tangles and amyloid-beta plaques, two characteristics of AD, triggers the activation of microglia, which are immune cells in the brain. Pro-inflammatory cytokines and other inflammatory chemicals are produced as a result of this activation. This inflammatory process involves p38 MAPK, and elevated AD neuroinflammation has been linked to its activation.

It has been demonstrated that tau, a protein that causes tangles in AD patients, is phosphorylated by p38 MAPK and this hyperphosphorylated tau plays a role in microtubule instability and neuronal cell death. Tau hyperphosphorylation can be encouraged by p38, which makes tau-related neurodegeneration in AD worse. Also, oxidative stress (OS), which is prevalent in AD, is one of the stressors that activates p38 and thus, neuronal damage. The loss of neurons seen in AD can be attributed to p38 MAPK activation, which can cause apoptosis (programmed cell death) in neurons. Therefore, p38 MAPK has been proposed as a possible therapeutic target for Alzheimer's disease due to its pivotal role in inflammation and neurodegeneration.

Keywords: Neuroinflammation; Tau Hyperphosphorylation; Neuronal Degeneration; Inflammatory Cytokines; Amyloid-beta.

MBPP86

Adipose-Derived Stem Cells in Cardiovascular Therapy: Clinical Data and Potential for Myocardial Repair

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ABSTRACT

Cardiovascular diseases (CVDs) remain the foremost cause of mortality globally, traditionally linked to risk factors like obesity and excess adipose tissue, which are associated with inflammation and metabolic dysfunction. Interestingly, adipose-derived stem cells (ADSCs) offer a promising paradox by providing cardioprotective effects despite being sourced from fat tissue—a known risk factor for CVD. ADSCs exhibit potent regenerative capabilities through paracrine signaling, anti-inflammatory action, and angiogenic factor release, which can aid in myocardial repair and support functional recovery in patients with ischemic heart disease (IHD) and heart failure (HF). This review assesses the latest clinical data on ADSC efficacy, where clinical trials have shown notable improvements in cardiac function, including increased left ventricular ejection fraction (LVEF) by an average of 4-8% and infarct size reduction by approximately 10-15%. ADSCs also enhance neovascularization and reduce apoptosis in damaged myocardium, thus supporting tissue regeneration and improving patient quality of life. The paradoxical use of fat derived cells to treat cardiovascular damage opens a novel therapeutic avenue, leveraging ADSCs' reparative effects to potentially counteract obesity-related cardiovascular risks. Challenges such as optimal cell delivery, retention, and long-term safety remain, necessitating further large-scale studies to standardize protocols and improve clinical outcomes. This review underscores the dual role of adipose tissue as both a risk factor and a therapeutic source, reshaping perspectives on regenerative cardiology.

Keywords: Adipose-Derived Stem Cells, Cardiovascular Disease, Myocardial Repair, Ischemic Heart Disease, Left Ventricular Ejection Fraction, Regenerative Cardiology, Paracrine Signaling.

MBOP01

Development of Protein-Based Reagents for the Detection of Carbapenem-Resistant Acinetobacter Baumannii

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ABSTRACT

Multi-drug-resistant (MDR) strains of Acinetobacter baumannii are recognized as major cause of hospital-acquired infections, including bloodstream infections and urinary tract infections worldwide. These infections are associated with high mortality rates, majorly due to the limited treatment options available for MDR strains. Carbapenems have been considered the last line of defense against MDR A. baumannii; however, the emergence of carbapenem-resistant strains has become a major global health challenge. In 2024, the World Health Organization (WHO) published an updated list of antibiotic-resistant priority pathogens and listed carbapenem-resistant Acinetobacter baumannii (CRAB) as a 'critical priority 1' pathogen. This develops an urgent need to develop diagnostic and therapeutic reagents to fight against CRAB infections. The currently available diagnostic methods for detecting CRAB are mostly time-consuming, labor-intensive, and require expensive reagents, making them impractical for clinical use. There is an urgent need for the development of reagents that offer a cost-effective, rapid, reliable, sensitive, and specific method for CRAB detection. In our work, we have focused on a major carbapenemase enzyme expressed by CRAB, and we are using it as a target to develop specific antibodies using phage display technology. Six antibodies have been successfully selected and produced in soluble form, and they are currently undergoing further validation. These antibodies will be used for the development of rapid, point-of-care diagnostic assays that can help manage the spread of CRAB by ensuring timely detection of CRAB-infected patients and controlled use of antibiotics. This work represents a critical step forward in addressing the global challenge of antimicrobial resistance.

Keywords: Carbapenems; Carbapenem-Resistant Acinetobacter Baumannii; Antibody; Phage Display; Antimicrobial Resistance.

MBOP03

Tropical Fruits: From Traditional Practices to Modern Nutraceuticals and Therapeutics

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ABSTRACT

Tropical fruits, a botanically diverse group indigenous to tropical regions, are gaining recognition for their immense potential in addressing global nutritional and health challenges. In India, tropical fruits are very popular and have been integral to traditional dietary practices. Traditionally, these fruits were consumed in various forms, including jellies, murabba, aam papad, jam, candy, pickles, chutney, curries, sauces and fruit juices etc. reflecting their culinary versatility and cultural importance. Recently, their therapeutic potentials have been explored for addressing degenerative diseases, lowering cholesterol, promoting gut health, and improving immunity. Their bioactivities as antioxidants, immunomodulators, and anticancer agents highlight their value as nutraceuticals and functional foods. Additionally, their role as prebiotics & probiotic supports gut microbiota balance and overall digestive health. Nutritionally, tropical fruits are rich sources of essential vitamins (e.g., vitamin C. vitamin B, vitamin A, vitamin E, vitamin K etc.), minerals (e.g., potassium, magnesium. Sodium etc.), and bioactive compounds such as flavonoids, carotenoids, polyphenols, oligosaccharides, polysaccharides, inulin, coumarin etc. These constituents contribute to their multifaceted health benefits. This review summarizes the traditional uses, phytochemical compositions, and therapeutic applications of tropical fruits. It also highlights advancements in fruit production techniques and potential areas for future research, emphasizing the continued relevance of tropical fruits in improving global health and nutrition.

Keywords: Tropical Fruit; Prebiotics; Nutraceuticals; Probiotic; Therapeutics.

MBOP04

Phlorotannin Isolated from the Marine Seaweed as a Translational Strategy to Mitigate the UV-C Induced Damage to Ocular Surface Cells: Translational Strategy

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ABSTRACT

The ocular surface is highly vulnerable to damage caused by environmental and occupational factors. As the eye's primary protective barrier, continuous exposure to harmful agents can lead to irreversible damage to the ocular surface cells. Critical structures such as the cornea, lens, and retina are particularly susceptible, resulting in ocular disorders like corneal damage, corneal dystrophy, cataracts, macular degeneration and UV keratitis. Among these factors, ultraviolet (UV) radiation, particularly natural UVR, significantly contributes to ocular surface damage by generating reactive oxygen species (ROS) and inducing oxidative stress in cells. UV-C radiation (100–280 nm), primarily emitted from welding arcs, poses a major occupational hazard. ROS are unstable molecules such as superoxide anion (O_2^-), hydrogen peroxide (H_2O_2), and hydroxyl radicals (HO), which interact with cellular components, including DNA, RNA and proteins, triggering damage and leading to cell death via various pathways. In this study, ocular surface cells were exposed to UV-C radiation at doses ranging from 1 to 10,000 J/m². The damage assessment was evaluated using various molecular techniques. Notably, pre-treatment with Phlorotannin at 10 µg/mL effectively reversed UV-C-induced damages at doses up to 100 J/m² beyond which the damage could be partially salvaged. The mechanisms involved in seaweed derived phlorotannin salvaging the UVC induced damages in ocular surface cells was via mitigation of ROS induced damages namely, mitochondrial dysfunction, apoptosis, inflammatory pathway proteins, cell cycle regulation and rescuing the DNA damage. These findings, hence, highlight the potential translational application of phlorotannin as a protective therapy against UV-C induced ocular damage.

Keywords: Ocular Disorders; UV-C Radiation; ROS; Oxidative Stress; Phlorotannin.

MBOP05

Arachidonic Acid Activates Intrinsic Skeletal Muscle Stem Cells and Reverses Inflammation to Mitigate Diabetes-Induced Myopathy and Reestablishes Myogenic Differentiation and Regeneration

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ABSTRACT

Skeletal muscles contribute 40% of the body's total body weight and are a metabolic hotspot. Conditions of hyperglycemia like diabetes mellitus and Cushing's syndrome give rise to various consequences, including hyperglycemia-induced myopathy, which translates to the loss of muscle mass referred to as skeletal muscle atrophy. A significant contributing factor to this is inflammation, which has numerous ramifications like increased oxidative stress, DNA damage, loss of protein synthesis, degradation of sarcomeric proteins and a reduction in the activation of muscle stem cells, eventually impairing regeneration. Arachidonic acid (AA), a bioactive lipid, has been shown to have myoprotective effects ranging from alleviating inflammation to restoring the sarcomeric protein repertoire. In this study, in addition to its anti-inflammatory properties, we also recognize AA's potential to mitigate the loss of muscle stem cell niche in diabetic myopathy condition by restoring the population of both muscle-derived stem cells (MDSCs) and skeletal muscle stem cells (satellite cells) thereby restoring the regenerative capacity of skeletal muscles in C57BL/6 mice. Furthermore, through ex-vivo cultures from skeletal muscles, we establish that AA can reverse the loss of nuclear localization of MYOD, a transcription factor required for muscle differentiation. Furthermore, through global proteomic and knock-down studies, we comprehend the association of skeletal muscle stemness restoration with the sarcomeric protein turnover as a function of AA treatment in the diabetic mouse model. These findings reveal the potential of AA as a therapeutic supplement for hyperglycemic patients to combat diabetic myopathy and sarcopenia.

Keywords: Arachidonic Acid; Muscle Stem Cell; Sarcopenia; Diabetes; Muscle Regeneration; Global Proteomics.

MBOP06

Targeting Colorectal Cancer Stem Cells with Vitamin C: In Vitro Cytotoxicity, Cell Cycle Arrest, and Apoptosis, and In Vivo Immunomodulation in a Tumor Allograft Mouse Model

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ABSTRACT

Cancer stem cells (CSCs) are a critical driver of tumor relapse and therapeutic resistance in cancers, including colorectal cancer. These CSCs exhibit self-renewal, proliferative potential, and resistance to conventional therapies. We have previously demonstrated that Vitamin C targets CSCs in breast cancer through apoptotic pathways at pharmacological doses. The present study explores the CSC targeting effects of Vitamin C in targeting colorectal CSCs, with a focus on both direct CSC cytotoxicity and modulation of the immune response in a tumor allograft model. Vitamin C treatment significantly reduced the CD44+ CSC population in a dose-dependent manner. High-dose Vitamin C induced mitochondrial dysfunction, ROS generation, DNA double-strand breaks leading to G2/M cell cycle arrest and apoptosis in HT-29 CSCs. A tumor allograft model was established by injecting sorted CSCs from CT-26 into BALB/c mice, and the immune response was assessed by analysing serum cytokine profiles and immune cell populations. Vitamin C enhanced the immune response, with an increase in CD8+ cytotoxic T cell populations and elevated cytokine levels in treated BALB/c mice, indicating an enhanced anti-tumor immune response. These findings suggest that Vitamin C not only directly targets colorectal CSCs by inducing cytotoxic effects but also enhances the immune system's ability to combat the tumor. This study provides evidence supporting the therapeutic potential of Vitamin C as a dual-target strategy for colorectal cancer, warranting further investigation for clinical application in CSC-targeted therapies.

Keywords: Cancer Stem Cells; Vitamin C; Tumor Allograft Model, Cytotoxicity; Anti-Tumor Immune Response.

MBOP08

Nephroprotective Effects of Natural Compounds

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ABSTRACT

The kidneys are critical organs for fluid balance, electrolyte homeostasis, and waste removal, but they are very vulnerable to damage from oxidative stress, inflammation, fibrosis, and delayed cellular repair. Natural phytocompounds have emerged as promising candidates for maintaining kidney function and reducing renal damage caused by a variety of clinical diseases. Plant-derived phytocompounds are a rich source of bioactive chemicals with nephroprotective characteristics, making them a safer and more sustainable alternative to traditional medicines. Bioactive compounds such as polyphenols, flavonoids, terpenoids, alkaloids, and saponins have demonstrated diverse protective mechanisms in both acute and chronic kidney injuries. These include reducing oxidative stress through increased scavenging of reactive oxygen species (ROS), modulating inflammatory pathways, and inhibiting fibrotic processes that cause irreversible kidney damage.

This review discusses the nephroprotective properties of natural phytocompounds, with a focus on their mechanisms of action and prospective applications in renal health. Future research and clinical validation are critical for optimizing their therapeutic usage and incorporating them into renal health prevention and treatment plans.

Keywords: Bioactive Compounds, Cellular Repair, Fibrosis, Inflammation, Kidneys, Phytocompounds, ROS.

MBOP09

Impact of P-glycoprotein on Anti-Seizure Medication Efflux: An In-Vitro Blood-Brain Barrier Study

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ABSTRACT

Drug-resistant epilepsy (DRE) affects approximately one-third of patients, despite the availability of numerous anti-seizure medications (ASMs). The efflux of ASMs by P-glycoprotein (P-gp) at the blood brain barrier (BBB) is a recognized mechanism contributing to treatment failures. This study investigated the potential of commonly used ASMs as substrates for P-gp utilizing an in-vitro BBB model (hCMEC/D3 cells). Our findings demonstrated that valproic-acid (300µM and 600µM), lamotrigine (30µM, 60µM, and 120µM), and topiramate (120µM) significantly stimulated basal P-gp ATPase activity. Furthermore, a competitive substrate efflux assay using rhodamine123 as a probe revealed that valproic-acid (300µM and 600µM), lamotrigine (15µM and 60µM), and topiramate (15µM and 60µM) significantly increased intracellular rhodamine123 accumulation ($p<0.01$), suggesting competitive interaction for P-gp-mediated efflux. Bidirectional transport assays confirmed these findings, as the efflux ratios of valproic-acid (at 300 µM and 600 µM) and of lamotrigine (at 60 µM), were significantly reduced in the presence of a P-gp inhibitor ($P < 0.01$). These results collectively suggest that valproic-acid and lamotrigine are potential substrates for P-gp-mediated efflux at the BBB. These findings have significant implications for the development of personalized treatment strategies for DRE, particularly for patients experiencing treatment failure with valproic-acid and lamotrigine.

Keywords: Anti-seizure Medications, P-glycoprotein, Drug-resistant Epilepsy, hCMEC/D3 ATPase Assay, Competitive Substrate Efflux Assay, Bidirectional Transport Assay.

MBOP10

Circ_ST6GAL1-Mediated Competing Endogenous RNA Network Regulates TGF-β1-Stimulated Matrix Metalloproteinase-13 Expression via Runx2 Acetylation in Osteoblasts

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ABSTRACT

Transforming growth factor-beta1 (TGF-β1) stimulates matrix metalloproteinase-13 (MMP-13, a bone-remodeling gene) expression, and this effect requires p300-mediated Runx2 (Runt-related transcription factor 2) acetylation in osteoblasts. p300 and Runx2 are transcriptional coactivator and bone transcription factor, respectively, which play key roles in the regulation of bone-remodeling genes. Non-coding ribonucleic acids (ncRNAs), such as long ncRNAs (lncRNAs) and microRNAs (miRNAs), have been linked to both physiological and pathological bone states. In this study, we proposed that TGF-β1-mediated stimulation of MMP-13 expression is due to the downregulation of p300 targeting miRNAs in osteoblasts. We identified miR-130b-5p as one of the miRNAs downregulated by TGF-β1 in osteoblasts. Forced expression of miR-130b-5p decreased p300 expression, Runx2 acetylation, and MMP-13 expression in these cells. Furthermore, TGF-β1 upregulated circ_ST6GAL1, (a circular lncRNA) in osteoblasts; circRNA directly targeted miR-130b-5p. Antisense-mediated knockdown of circ_ST6GAL1 restored the function of miR-130b-5p, resulting in downregulation of p300, Runx2, and MMP-13 in these cells. Hence, our results suggest that TGF-β1 influences circ_ST6GAL1 to sponge and degrade miR-130b-5p, thereby promoting p300-mediated Runx2 acetylation for MMP-13 expression in osteoblasts. Thus, the circ_ST6GAL1/miR-130b-5p/p300 axis has potential significance in the treatment of bone and bone-related disorders.

Keywords: TGF-β1; Runx2; p300; Noncoding RNAs; microRNA; Circular RNA.

MBOP11

A Study on Regulation of Bone Formation: Phytocompound-mediated Runx2 Expression via Micro RNAs

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ABSTRACT

Nuciferine (NF), a plant alkaloid is known to promote osteoblast differentiation in mouse mesenchymal stem cells (mMSCs) by stimulating the expression of Runt-related transcription factor 2 (Runx2), a pivotal regulator of bone formation. However, the precise molecular mechanism underlying NF's osteoinductive effects remains unknown. Recent evidence highlights the critical role of non-coding RNAs (ncRNAs), such as microRNAs (miRNAs) and long ncRNAs (lncRNAs), in regulating osteoblast differentiation. The novelty of this study lies in uncovering the potential involvement of ncRNAs in mediating the effects of NF on Runx2 expression and osteoblast differentiation. In mMSCs, NF stimulated the expression of mmu-mir-466n and mmu-mir-467e that putatively target 3' untranslated region of Runx2. Computational tools predicted the diversified role of mmu-mir-466n and mmu-mir-467e in various tissues and organs. Even though there is a high abundance of these miRNAs, the Runx2 level remained elevated, suggesting the influence of other ncRNAs targeting mmu-mir-466n and mmu-mir-467e. Several lncRNAs were predicted to target mmu-miR-466n-3p and mmu-miR-467e-3p, suggesting the sponging activity of lncRNAs towards them. These findings suggest that NF-regulated lncRNAs, in conjunction with mmu-miR-466n-3p and mmu-miR-467e-3p, modulate Runx2 expression, ultimately influencing osteoblast differentiation, thus, offering novel therapeutic strategies for managing osteopathological conditions.

Keywords: Nuciferine, Non-coding RNA, MicroRNAs, Runx2, Osteoblast Differentiation.

MBOP12

Molecular Docking Studies and In-silico ADMET Profile analysis of E. Cava Constituent's as Potential Inhibitors against Breast Cancer

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ABSTRACT

Cancer is a dreadful genetic disease that is usually caused by changes to genes that help to control the way our cells function, especially the way the cell grows and divides. The absence of programmed cell death or apoptosis leads to uncontrolled division of cells; leads to cancer causing cells. Breast cancer is the aggressive form with its early metastasis and chemo resistance. This can spread to all other parts of the body if not cured earlier. Ecklonia Cava also known as brown algae have many biological activities known for improving immunity. However, the effect of some compounds found in E. Cava constituents on breast cancer has not yet been identified. Present study aimed to evaluate E. Cava extracts' anti-oxidant activities, anti-cancer properties and anti inflammatory activities.

Protein-ligand interaction plays a major role in structural drug design. In this study, the molecular interactions between the estrogen receptor (PDB ID: 2IOK), and the ligands isolated from E. Cava ayurvedic formulation piracetam, oleamide and vigabatrin, an endogenous estrogen receptor ligand, estradiol, and the three economically available breast cancer drug, Anastrozole (Arimidex), exemestane (Aromasin) and raloxifene (Evista), Tamoxifen (Soltamox) using the Autodock Vina software.

In vitro anti-cancer effects of E. Cava powder extracts constituents were evaluated against the MDA MB 231 cell line, cytotoxic MTT assay, cell proliferation, cell cycle, apoptosis assay, and Western blot analysis. Results show the suitable anti-oxidant property, its crude extract, piracetam, oleamide and vigabatrin significantly reduce cell proliferation while also inducing apoptosis in MDA MB231 cells inhibiting and anti-apoptotic Bcl 2 expression, activates caspase 3 dependent pathway which is helpful in eradicating and controlling Breast cancer.

Keywords: Ecklonia Cava; Anti-Oxidant; Piracetam; Oleamide; Vigabatrin, MDA MB 231 cell line.

MBOP15

Clinical and Genetic Profile of Down Syndrome: Insights from 10 years of Experience at a Tertiary Care Center

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ABSTRACT

Down Syndrome (DS) is a genetic disorder characterized by distinct clinical features, predominantly caused by trisomy chromosome 21. This study aimed to conduct a retrospective analysis of clinical features, genetic profiles, and karyotype findings in Down Syndrome patients. We performed a retrospective analysis of cases referred to the Genetic Clinic in the Department of Pediatrics at Maulana Azad Medical College (MAMC) and Lok Nayak Hospital over a ten-year period (2014-2024). Existing case proformas of patients with Down Syndrome phenotype, who underwent cytogenetic evaluation, were systematically reviewed. Analysis included 688 patients with DS, with 375 males and 313 females (M: F ratio 1.2:1). The average age at presentation was 19.4 months (range: 1 day to 26 years). Distinct craniofacial features were present in 97.8% of cases, including mongoloid slant (97.8%), flat facial profile (97%), and protruding tongue (91.7%) and epicanthic folds (62.7%). Cytogenetic findings revealed free trisomy in 95.93%, translocations in 3.05%, mosaics in 0.72%, and rare findings in 0.29%. Among the Robertsonian translocations, 52.4% were t(14;21), 9.5% t(15;21), and 38.1% t(21;21). The findings emphasize the importance of early detection and comprehensive evaluation of Down Syndrome. Understanding the mechanisms of nondisjunction and its implications is vital for genetic counseling and assessing recurrence risks in families.

Keywords: Down Syndrome, Nondisjunction, Translocation, Robertsonian, Mosaic Syndrome.

MBOP16

Circulatory Cytokines: Unveiling their Role in Hypertension and Endothelial Dysfunction

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ABSTRACT

Hypertension, a global cause of morbidity and mortality, poses a heightened risk of serious cardiovascular complications. Although the role of kidney, vasculature, heart, and brain has been defined before, recent research has illuminated the role of immune mechanisms and inflammation in hypertension. To delve into the immune mechanisms of hypertension, we identified association between inflammatory cytokines and incident hypertension in patient populations, assessed their direct vascular effects in mouse blood vessels and probed potential mechanisms of endothelial dysfunction. We identified inflammatory cytokines potentially contributing to incident hypertension using systematic searches, and performed meta-analysis of the relationships between the levels of identified cytokines and incident hypertension. We then undertook mechanistic studies of vasomotor functions in mouse aortas. We further studied the direct effects on transcriptional changes of genes implicated in NO and ROS production by looking at gene expression of eNOS and NADPH oxidases in mouse aortas. Furthermore, we studied eNOS phosphorylation in human endothelial cells for potential mechanisms of endothelial dysfunction. Through our systematic searches we identified IL-6, IL-1β, TNF-α, IL-17a, and IFN-γ among other cytokines. We found that IL-6 is positively associated with incident hypertension, but this association weakens with adjusting for BMI implying a relationship between inflammation and adiposity linked hypertension. Significant impairment of endothelial function induced by IL-1β, IFN-γ and IL-6 suggests a direct link between endothelial dysfunction and inflammation. Further studies are needed to substantiate the results in identifying the mechanisms of inflammatory cytokines in endothelial dysfunction and understand their significance for patho-mechanisms of hypertension.

Keywords: Hypertension; endothelial dysfunction; inflammation; IL-6, IL-1β, IFN-γ.

MBOP18

Unravelling Sulfur Metabolism for Anti-Pseudomonal Drug Discovery

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ABSTRACT

Public health around the world is seriously threatened by the rise of multidrug-resistant (MDR) microorganisms. Acinetobacter baumannii, Pseudomonas aeruginosa, Enterobacter species, Staphylococcus aureus, Enterococcus fecium, and Klebsiella pneumoniae are among the ESKAPE pathogens that pose the greatest threat because of their capacity to develop resistance to several drugs. One of the well-known ESKAPE group members that has developed a concerning degree of resistance is the multipurpose opportunistic pathogen Pseudomonas aeruginosa, forms biofilms that confer increased resistance to antibiotics and disinfectants. The urgent need for new treatments against multidrug-resistant Pseudomonas aeruginosa necessitates exploring novel therapeutic targets. Central metabolic pathways, essential for microbial survival and the production of essential molecules, offer promising avenues. Sulfur-containing amino acids, cysteine, and methionine, are vital for bacterial growth. While most bacteria synthesize cysteine through the de novo (sulfate assimilation) pathway, P. aeruginosa uniquely utilizes both this pathway and the reverse transsulfuration pathway, typically employed by eukaryotes and humans. Furthermore, P. aeruginosa exhibits flexibility in methionine biosynthesis. In addition to the standard transsulfuration pathway, it possesses a unique "direct sulfhydralation" pathway, utilizing homocysteine directly. The presence of multiple pathways for sulfur amino acid synthesis underscores the critical importance of sulfur sources for the growth and survival of P. aeruginosa. This review focuses on the current understanding of the enzymes involved in these pathways, aiming to identify novel drug targets to combat this challenging pathogen.

Keywords: Pseudomonas Aeruginosa; Cysteine; Methionine; Multidrug Resistance; Sulfur Metabolism.

MBOP19

Anti-Psoriatic Potential of Chloroform: Methanol Fractions of Alstonia scholaris Ethanolic Extract: In Vitro and In Vivo Evaluation

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ABSTRACT

Psoriasis, a chronic inflammatory skin disorder characterized by excessive keratinocyte proliferation, aberrant apoptosis, and heightened production of pro-inflammatory cytokines, affects millions globally, posing significant therapeutic challenges. Alstonia scholaris (L.) R.Br, a plant rooted in Ayurvedic and Siddha medicine for treating skin ailments, has emerged as a potential source of anti-psoriatic agents. This study evaluated the anti-psoriatic activity of chloroform:methanol fractions derived from ethanol extracts of A. scholaris using in vitro and in vivo models. In vitro studies on HaCaT keratinocytes demonstrated that the fractions significantly inhibited cell proliferation, induced apoptosis (validated via JC-1 and Annexin V assays), and downregulated key inflammatory mediators, IL-8 and RANTES, in a dose-dependent manner. In vivo, topical application of 80:20 and 60:40 chloroform fractions on an imiquimod (IMQ)-induced psoriasis mouse model led to a substantial reduction in psoriasis-like lesions, as reflected by lower PASI scores, reduced punch biopsy weights, and improved histopathological features, including decreased epidermal thickness and dermal edema. Furthermore, the fractions mitigated the production of psoriasis-related pro-inflammatory cytokines, such as IL-17 and IL-23, in skin homogenates and serum. These findings highlight the anti-proliferative, pro-apoptotic, and anti-inflammatory potential of A. scholaris fractions, establishing their role as promising candidates for the development of novel phytotherapeutics for psoriasis management. This study offers new insights into the molecular mechanisms underlying the anti-psoriatic activity of A. scholaris, emphasizing its potential as a safe and effective natural remedy for psoriasis treatment.

Keywords: Psoriasis; Medicinal Plants; Keratinocytes; Alstonia Scholaris.

MBOP20

Exploring Molecular Mechanism for antihyperglycemia Mediated Through Co-Supplementation of Vitamin D and Metformin

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ABSTRACT

Metformin has been the primary treatment for Type 2 Diabetes (T2DM) for many years, while vitamin D is known to enhance insulin action and improve insulin sensitivity. Preliminary evidence suggests that the combination of metformin and vitamin D may exert a synergistic antihyperglycemic effect, though the underlying mechanisms remain unclear. To address this, the current study primarily aimed to identify the key genes linked to both metformin and vitamin D receptor (VDR) signaling pathways, using systems biology approach. Initially, the metformin-VDR protein-protein interaction (PPI) network was constructed, exhibiting a hierarchical, scale-free structure. The network was statistically analyzed, and the top 5 functional modules were identified based on their M-score. Total 15 key regulators: G0S2, DDIT4, IL6, PRKAA1, EGFR, mTOR, PPARGC1A, SLC2A3, CYBA, CYBB, NCF1, NCF2, NCF4, NOX1, and NOX3 were identified as the potential target genes. As per functional annotations, many of these genes play significant roles in glucose regulation and mitigating hyperglycemia-induced inflammation and oxidative stress. To validate these findings, the differentiated L6 myotubes were grown in hyperglycemic conditions and further treated with vitamin D(10^{-9}M) / metformin (60 μM) /vitamin D(10^{-10}M) + metformin (40 μM). Glucose uptake, antioxidant activity, and mitochondrial metabolism were compared across different sets. As a result, it was observed that co-supplementation of vitamin D with metformin led to improved glucose uptake, enhanced NADH oxidoreductase and catalase activity in treated L6 myotubes. In coordination with the in-silico results, it may be proposed that the identified key genes may be involved in exhibiting the improved antihyperglycemic and antioxidant activity of L6 cells, combinedly treated with vitamin D and metformin. These key genes could be further explored as the potential therapeutic targets for diabetes and related disorders.

Keywords: Protein-protein Interaction, Systems Biology, Hyperglycemia, Vitamin D, Metformin.

MBOP21

Phytochemical Analysis, Antioxidant Properties, and Anticancer Activity of Citrus limetta Peel Extract on Skin Cancer Cell Line

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ABSTRACT

Citrus limetta peel contains diverse polyphenolic compounds, including flavonoids, coumarins, phenolic acids, terpenoids, tannins, sterols, anthocyanins, and quinones. Among these, flavonoids are considered key bioactive components, particularly for their anticancer properties. This study aimed to perform a comprehensive phytochemical screening of C. limetta peel extracts using various solvents and to evaluate their antioxidant and anticancer activities. Quantitative analyses of phenolic compounds, flavonoids, and tannins were conducted, along with antioxidant activity assessments. Advanced analytical techniques, including TLC, HPTLC, HPLC, and FTIR, were employed to characterize the qualitative and quantitative composition of the extracts. The antiproliferative activity of the extracts was evaluated on A431 skin cancer cell lines using the MTT assay. The qualitative analysis revealed that the ethanolic and methanolic extracts contained various phytocompounds compared to extracts obtained using other solvents. The methanolic and ethanolic extracts exhibited significantly higher phenolic and flavonoid contents, with the ethanolic extract demonstrating superior antioxidant activity. In vitro findings suggest that the ethanolic peel extract of C. limetta may serve as a promising source of bioactive compounds with potential anticancer activity.

Keywords: Citrus Limetta Phytochemical Analysis, Quantitative Analyses, Antioxidant Activity, Anticancer Activity.

MBOP22

Phytochemical Characterization, Antioxidant Activity and in-vitro Study of Adhatoda Vasica

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ABSTRACT

Several medicinal plants have multiple bioactive compounds that offer potential therapeutic applications for copious respiratory-associated pathologies. Broadly, phytochemicals have been classified into primary and secondary metabolites. Primary metabolites encompass several components like carbohydrates, proteins, sugar, and amino acids, whereas secondary metabolites contain terpenoids, alkaloids, tannins, phenols, and flavonoids. Like most other plants, Adhatoda vasica contains various secondary metabolites with great potential. The leaves of the selected plants were washed, air-dried, and then powdered. The organic solvents and aqueous extracts of leaf samples were used for the phytochemical analysis to determine the plants' phytochemical constituents. Phytochemical analysis is commercially significant and has gained interest in pharmaceutical companies. The findings from the qualitative screening showed the presence of alkaloids, flavonoids, carbohydrates, triterpenoids, phenols, and tannins. The quantitative evaluation showed that the ethanolic and methanolic extracts exhibited higher phytochemical content and activity compared to aqueous extracts. Further, the study findings revealed that the ethanolic extract showed better antioxidant activity than the other extracts. It is expected that the important phytochemical properties recognized by our study in the plant will be useful for curing several respiratory diseases, such as acute respiratory distress syndrome.

Keywords: Phytochemical, Qualitative, Quantitative, Antioxidant, Respiratory Disorders.

MBOP23

Clinical Utility of Short Tandem Repeats (STRs) Haplotyping for Genetic Diagnosis & Screening of Beta Globin Cluster

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ABSTRACT

Beta- thalassemia is a genetic disorder caused by mutations in the HBB gene, leading to reduced or absent β-globin chain production in hemoglobin. In India, β-thalassemia carrier prevalence ranges from 3% to 10% influenced by ethnic and geographic factors, significantly exceeding the global average reported by WHO. This study highlights the clinical utility of short tandem repeats (STRs) analysis to facilitate the birth of unaffected children. In this research, six short tandem repeat markers closely linked to beta globin gene were analyzed by using 15 couples carrying β thalassemia. A total number of 15 CVS (Chorionic villus sample) tissue were further tested for haplotyping and genetic analysis using Sanger sequencing to confirm a diagnosis. Ultimately, 11 of the 15 couples resulting in healthy or asymptomatic children. This study reveals that STR analysis, verified by Sanger sequencing, offers a reliable and practical approach for detecting β- thalassemia in embryos. This method significantly improves the likelihood of preventing the condition in at- risk pregnancies, thus contributing to reducing the prevalence of β-thalassemia in the population.

Keywords: Beta Thalassemia, Haplotype, STR, Beta Globin Cluster.

ISSN: 2278-9197 © VSRD International Journals: www.vsrdjournals.com

MBOP24

Recombinant Production and Characterization of M. Smegmatis ICL2

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ABSTRACT

Tuberculosis (TB) remains a formidable global health challenge, with Mycobacterium tuberculosis (Mtb) proving to be a resilient and potent pathogen throughout generations. Mycobacterium smegmatis (M.smeg) is a non-pathogenic species commonly used as a model organism for studying mycobacterial biology, particularly metabolic pathways essential for survival in nutrient-limited environments. Isocitrate lyase 2 (ICL2) is a crucial enzyme in the glyoxylate shunt, a metabolic pathway that bypasses the TCA cycle, enabling mycobacteria to utilize lipids as a carbon source under stress conditions. Notably, the CDC1551 strain of Mtb and M.smg share approximately 85% genetic similarity and 77% identity in their genomes. Understanding its structural and functional features is critical for addressing this pathway in pathogenic organisms. This research provides the recombinant production, purification, thermal stability, and size determination of M. smeg ICL2. The gene encoding M. smeg ICL2 was cloned and expressed in E.coli BL21(DE3), and the protein was purified using Ni-NTA affinity chromatography followed by size-exclusion chromatography. Biophysical analysis revealed that M. smeg ICL2 forms a tetramer under physiological conditions. Thermal denaturation studies showed a melting temperature (Tm) of 67°C, indicating significantly higher thermal stability compared to Mtb. This enhanced stability suggests that M. smeg ICL2 can serve as a robust model for studying ICL2 in pathogenic mycobacterium.

Keywords: Mycobacterium Smegmatis, Glyoxylate shunt, ICL2, Purification, SEC.

MBBS01

Therapeutic Potential of Natural Bioactive Compounds for Gene Polymorphism-Driven Pathologies: An Integrative In-Silico and In-Vitro Study Targeting Oxidative Stress and Inflammation in Type 2 Diabetes Mellitus and Cardiovascular Diseases

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ABSTRACT

Type 2 Diabetes Mellitus (T2DM) and cardiovascular diseases (CVD) are complex, multifactorial conditions exacerbated by oxidative stress and chronic inflammation. Polymorphisms in genes like epoxide hydrolase (EPHX) are known to increase susceptibility to these diseases by disrupting normal redox homeostasis and metabolic pathways. This study investigates the therapeutic potential of natural bioactive compounds to mitigate oxidative stress and inflammation caused by gene polymorphisms in T2DM and CVD. Through in-silico analysis, a library of natural compounds, including polyphenols, flavonoids, and carotenoids, was screened for interactions with oxidative stress-related targets such as epoxide hydrolase and pro-inflammatory cytokines. Molecular docking and dynamic simulations identified promising candidates with high binding affinities, good pharmacokinetics, and drug-likeness properties. These candidates were further validated using in-vitro experiments on human cell models exposed to oxidative stress-inducing agents. Results demonstrated that selected compounds significantly reduced oxidative stress markers, including reactive oxygen species (ROS), and inhibited pro-inflammatory pathways via modulation of key signalling molecules. Notably, compounds like C-phycocyanin showed superior efficacy in restoring redox balance and enhancing cell viability under polymorphic conditions. These findings highlight the potential of natural bioactive compounds as adjunct therapeutic agents for managing gene polymorphism-driven pathologies in T2DM and CVD. This integrative approach offers a framework for the development of personalized therapeutic strategies targeting genetic variations and their downstream effects. The study also underscores the importance of natural compounds in drug discovery and the prevention of metabolic and cardiovascular complications.

Keywords: Natural Bioactive Compounds; Gene Polymorphisms; Oxidative Stress; Inflammation; Epoxide Hydrolase; Personalized Therapy.

ISSN: 2278-9197 © VSRD International Journals: www.vsrdjournals.com

MBBS02

Role of Gut Microbiome in Neuro Developmental Disorders

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ABSTRACT

Gut microbiome homeostasis plays an important role in human health. Gut-brain axis refers to complex interrelationship between central nervous system and gastrointestinal system. Recent studies have highlighted the importance of commensal gut microbes to normal gut function and neurobehavioral health especially the Neurodevelopmental disorders (NDD). As per the epidemiological and clinical evidences co-morbid gut dysfunction exists in many individuals with neurodevelopmental disorders. There has been increase in number of cases of NDD especially autism spectrum disorder (ASD) and attention deficit hyperactivity disorder (ADHD). Autism spectrum disorder is of particular interest as a highly prevalent neurodevelopmental disorder in which a significant subset of patients' presents gastrointestinal problems and in which microbial dysbiosis has been highlighted as a potential contributing factor to gastrointestinal and neurodevelopmental abnormalities. Recent case studies suggest that the gut microbiota plays a role in shaping cognitive networks encompassing emotional and social domains in neurodevelopmental disorders. There are several factors that may affect and may alter the gut microbiome like breastfeeding, mode of delivery, use of antibiotics or exposure to other chemicals. Based on pre-clinical and clinical evidences, this work tries to correlate the potential role of the gut microbiota in the origins and development of social and emotional domains related to autism spectrum disorders and also tries to identify if there is a possible role of microbiome in treating NDDs.

Keywords: Microbiota, Autism Spectrum Disorder, Neurobehavioural, Dysbiosis, Neurodevelopmental Disorder.

MBBS03

Microbial Influence: Reducing Harmful Compounds in Tobacco Products

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ABSTRACT

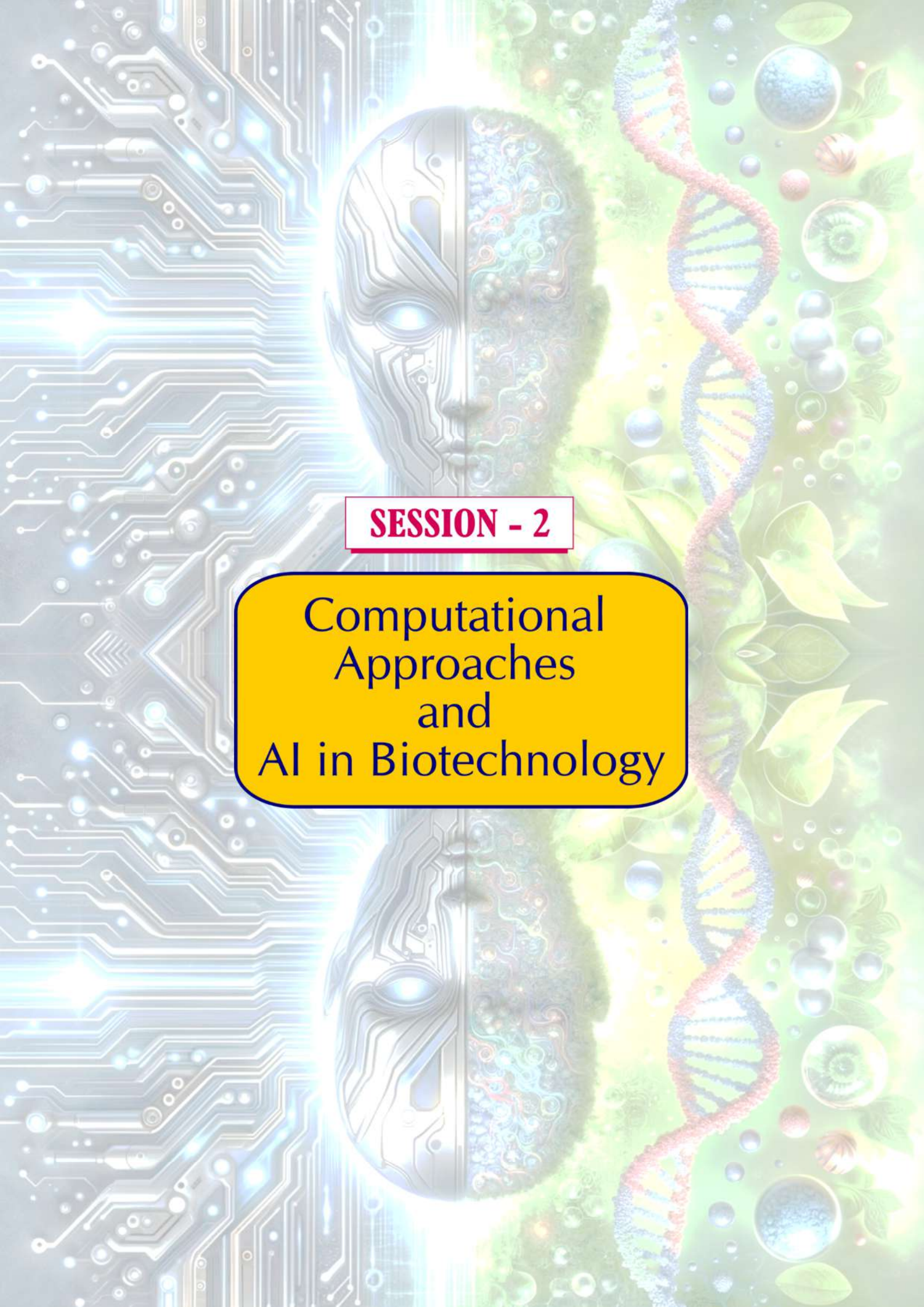
Tobacco products are recognized as highly detrimental to health, contributing significantly to cancer and other health risks. Given the low cessation rates among users, developing strategies to reduce the carcinogenic potential of tobacco products offers a pragmatic alternative.

Microbial communities play a critical role in the formation of carcinogenic tobacco specific nitrosamines (TSNAs) during tobacco curing. Microbial activities elevate TSNA levels in cured tobacco leaves despite their low concentrations in fresh leaves. However, Indian studies exploring the relationship between microbial populations and TSNA formation in tobacco products remain limited.

Many studies investigated the structural and functional diversity of bacterial and fungal communities in tobacco products through both culture-based and culture independent methods. Biochemical and molecular techniques, including 16S/18S rRNA gene sequencing, were employed to characterize microbial populations. Additionally, chemical profiling using GC/HPLC/MS were used to assess the correlation between microbial communities and harmful compounds such as TSNAs, nicotine, and polycyclic aromatic hydrocarbons.

These studies established consistent correlations between microbial diversity and chemical profiles of tobacco products. This relationship between microbial communities and the chemical profile of smokeless tobacco products presents a promising avenue for microbial interventions aimed at reducing harmful chemical concentrations. By manipulating tobacco microflora, the carcinogenicity of tobacco products can be mitigated, improving their safety and reducing public health burdens. The development of such microbial-treated tobacco products offer a novel approach to minimize tobacco-related cancer risks enhancing overall safety of tobacco products.

Keywords: Tobacco, Carcinogens, Microflora, TSNAs.



SESSION - 2

Computational Approaches and AI in Biotechnology

CAPP02

Genome-Wide Identification of Transcriptional Active Intrinsically Disordered Regions in Breast Cancer Patients

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ABSTRACT

Breast cancer is the leading cancer among women in India, representing 13.5% of all cancer diagnoses and 10.6% of cancer-related deaths as of 2020. This study aimed to identify transcriptional active intrinsically disordered regions in breast cancer (IDR). Meta-analysis was performed between four genome-wide transcriptional profiling Indian and Pan cancer BRCA dataset from TCGA. To check the molecular signatures unique to Indian breast cancer patients, Indian studies were compared across different races and ethnicities using the TCGA pan-cancer BRCA datasets with 113 normal and 1106 pan-cancer BRCA samples because other Asian datasets had 175 primary tumor samples while normal sample details was missing in public domain. Comparative analysis among four Indian breast cancer datasets shows that 110 differentially expressed genes (DEGs) were found to be commonly upregulated while 239 DEGs were found to be commonly downregulated. Comparative analysis among four Indian breast cancer and Pan Cancer BRCA datasets shows that 69 DEGs were upregulated while 121 DEGs were downregulated in Indian breast cancer as well as pan cancer BRCA datasets. IDR were found in eleven upregulated and four downregulated genes that were commonly found in tumors of Indian breast cancer patients. Upregulated PRC1 (Protein regulator of cytokinesis 1) and downregulated SORBS1 (Sorbin and SH3 domain-containing protein) were found to have 27.26% and 2 % disordered regions. These candidate IDR in Indian Breast Cancer patients can be further studied to identify their role as potential therapeutic biomarkers in breast cancer.

Keywords: Intrinsically Disordered Regions (IDRs); Differentially Expressed Genes (DEGs); TCGA Pan-Cancer BRCA Data; Gene Ontology; Indian Breast Cancer.

CAPP03

Comparative Gene Interaction Analysis of Electron Transfer Pathways for Efficient Power Generation in Microbial Fuel Cell

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ABSTRACT

Exo-electrogenic bacteria possess the unique ability to transfer electrons to external electrodes, making them vital for microbial fuel cell (MFC) operations. This study investigated the genetic mechanisms underlying exo-electrogenic properties in various bacteria, which have significant potential for applications in MFCs. The study focused on targeting the genes responsible for these capabilities and examining the evolutionary relationships among these bacteria. Phylogenetic analysis assists in connecting Protein-Protein Interaction (PPI) results with the exo electrogenic properties of the bacteria. This research delves into the genetic foundations and phylogenetic connections of various exo-electrogenic bacteria. It was found that some genes (PilT, omcA, mtrA, and mtrB) displayed high connectivity, emphasizing their importance in facilitating extracellular electron transport. These genes were primarily found in species such as Shewanella, Geobacter and are renowned for their effective exo-electrogenic abilities. Comparative analyses KEGG (Kyoto Encyclopedia of Genes and Genomes) & Gene Ontology revealed that organisms with these highly interconnected genes produced higher electrical outputs. A functional and gene expression analysis of these genes was also performed using in silico methods. This study highlights the genetic determinants of bioelectrochemical performance, offering insights for enhancing bacterial strains to boost energy production in microbial fuel cells.

Keywords: Exo-electrogenic Bacteria; Shewanella; Geobacter, Microbial Fuel Cells; Phylogenetic Relationships.

CAPP04

Exploring the Impact of Genetic Variants of Fetuin-A in Disease Predisposition

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ABSTRACT

Fetuin-A, or α2-Heremans-Schmid glycoprotein (AHSG), is a vital plasma protein primarily produced in the liver, playing crucial roles in calcium-phosphate homeostasis, inhibition of ectopic calcification, and regulation of systemic inflammation. Alterations in its structure or function, often due to non-synonymous single nucleotide polymorphisms (nsSNPs), can disrupt these processes, contributing to pathological conditions such as vascular calcification, metabolic disorders, and chronic inflammatory diseases. This study employed a computational framework to identify and prioritize potentially damaging nsSNPs of fetuin-A based on their deleterious effects. A total of 398 nsSNPs were retrieved from Ensembl databases and subjected to a two-step filtration process based on functional impact of amino acid substitution, identifying deleterious variants using PredictSNP tool and then further evaluating using stability prediction tool DynaMut2, I-Mutant 2.0 and DUET for assessing their destabilising effects on protein structure. This integrated approach reduced the candidate pool to seven high-priority variants (I48T, I80S, I82T, E86G, R103S, V142G, F125S) for subsequent structural analysis. Further structural modeling and analysis of these variants will provide insights into their impact on protein conformation and function, potentially linking them to disease mechanisms. By combining computational tools and structural biology, this study offers a systematic approach to understanding the role of genetic variations in fetuin-A dysfunction, paving the way for targeted therapeutic strategies and biomarker development in calcification-related and inflammatory disorders.

Keywords: Fetuin-A; Single Nucleotide Polymorphism; Non-Synonymous SNPs; Computational Biology; Predict SNP.

ISSN: 2278-9197 © VSRD International Journals: www.vsrdjournals.com

CAPP05

Unveiling the Binding Sites of HSC70 Using Computational Approaches

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ABSTRACT

Cellular functions are maintained by continuous replacement of their components. Therefore, the degradation of these components is important and is maintained by various degradation mechanisms. One such degradation mechanism is chaperone-mediated autophagy (CMA). CMA is an essential lysosome-associated degradation mechanism in the realm of cellular homeostasis in mammals. Dysfunction of CMA is related to numerous diseases, including cancers and neurodegenerative disorders. Its structural insights provide a foundation for effective therapeutic development. CMA is well-known for its selectivity, regulated by two key proteins, HSC70 and LAMP2A. HSC70 is the key molecular chaperone of the HSP70 family that recognizes substrate proteins and recruits them for degradation. It is well known that HSC70 recognizes only the protein that contains the KFERQ-like pentapeptide motif. Past studies also reported that HSC70 directly interacts with substrate proteins, but its exact binding site is still under investigation. Here, we have studied the interactions of HSC70 with experimentally verified CMA substrates using integrated computational approaches. Based on structural and thermodynamic analyses at the residue level, we have proposed the substrate binding sites in HSC70. Our current findings indicate that the binding site for CMA substrates is the substrate binding domain (SBDα) of HSC70. Our findings provide a framework for understanding structure-function relationships and open new avenues for new advancements in drug discovery and therapeutics.

Keywords: Autophagy; HSC70; Binding; Substrate; Motif.

CAPP06

Investigation of Valeriana wallichii Plant Phytoconstituents as Potential Inhibitors of MDR - Acinetobacter Baumannii: An In-Silico Approach

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ABSTRACT

Acinetobacter baumanni is one of the multidrug-resistant bacteria that act as an opportunistic pathogen to immune-compromised patients. Till date, there is no validated drug available to treat the infection. In the current study, we have selected a total of nine proteins as a drug target from the microorganism that are essential for survival and pathogenesis. AutoDock vina and iGemdock were used to analyze the interaction of protein and ligands. In AutoDock vina, 12 common ligands were found in the top 30 from each protein. Whereas in iGemdock a total of 9 common ligands were found in the top 30 of each protein. However, to get a better result two proteins (4K0X0 and 5BOH) were excluded from the analysis and a total of 12 common ligands were found in the top 30 of 7 proteins from both software. These two sets of common ligands were further analyzed and a total of 4 common ligands were found. After analyzing the docking score, poses and interaction from two software, it was obtained that these selected ligands can be used as potential molecules for the inhibition of the protein leading to death of the organism.

Keywords: Multidrug-Resistant Acinetobacter Baumannii; Valeriana Wallichii; AutoDock Vina; iGemdock; Microorganism.

CAPP07

Integrative Approach to Assessing the Anticancer Potential of Leaf Extracts on 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. This study aims to evaluate the anticancer properties of leaf extracts on Luminal A breast cancer, using a combination of in silico computational modeling and in vitro experimentation. Using molecular docking and dynamic simulations, bioactive compounds from the extracts are evaluated for their ability to inhibit crucial proteins that play a role in cancer cell growth and survival. The screening results focused on the luminal A biomarker, Estrogen Receptor, revealed that the compounds with the highest affinities were Lupeol, Quercetin, and Globulol, corresponding to mango, guava, papaya and eucalyptus, respectively, among others. 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.

CAPP08

lncRNA-miRNA-TF Interactions: Understanding the Downstream Effector Regulators in the p73 Axis Involved in Cancer Suppression

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ABSTRACT

p73, a member of the p53 tumor suppressor family, shares functional similarities with p53, including a homologous binding site. While p73 can activate many of p53's target genes, it also has unique targets, indicating both similarities and differences in their signaling pathways. Previous studies from our group have shown that p73 has an anti-metastatic role by regulating Navigator-3 and the FER1L4 lncRNA. p73 also transcriptionally modifies non-coding RNAs, including p53-regulated lncRNAs and miRNAs. Notably, p73 regulates the FER1L4 lncRNA, which sponges miR-1273g-3p to enhance PTEN expression and induce cell-cycle arrest. Recently, we identified six additional lncRNAs specifically regulated by p73. In this study, we used the online tool LncBook 2.0 (https://ngdc.cncb.ac.cn/lncbook/home) to identify miRNAs associated with these six specific lncRNAs. The top ten miRNAs, significantly linked to each lncRNAs, were further analyzed using the in-silico tool TransmiR v2.0 (https://www.cuilab.cn/transmir) for miRNA target prediction and to explore their biological functions. Preference was given to targets showing strong complementarity to the lncRNAs. After identifying the miRNAs, we used miRDB (https://mirdb.org/) to find the target genes of each miRNA. We observed that each miRNA regulates multiple target mRNAs. Based on the significance of these genes in cancer progression and their Target scores, the top 15 target genes for each miRNA were selected. Ongoing work aims to identify the transcription factors associated with the top miRNAs using TransmiR v2.0 and validate their expression in cancer patients to understand their functional relevance.

Keywords: p53 Tumor Suppressor Family; Navigator-3; FER1L4 lncRNA; LncBook 2.0; TransmiR v2.0.

CAPP09

Optimizing Wastewater Treatment Through Artificial Intelligence

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ABSTRACT

Effective treatment of wastewater, which contains a range of organic pollutants, heavy metals, and excess nutrients, has been achieved using microbial bioremediation. The traditional optimization techniques for the microbial bioremediation process are tedious and sometimes imprecise. The application of AI-driven optimization techniques would make microbial bioremediation in wastewater treatment more effective and sustainable. Merging algorithms of machine learning with data acquisition systems in real-time allows the AI model to predict ideal microbial consortia, nutrient levels, and environmental conditions for enhancing the degradation of pollutants. With such a large dataset training myriad species of microbes, compositions of wastewater, and outcomes of treatment, such algorithms will continue to enhance and fine-tune the parameters of bioremediation. AI-based predictive analytics will also be able to detect fluctuations in water quality early, allowing for proactive intervention and achieving regulatory compliance. AI can optimize treatment processes by automating real-time monitoring, adjusting parameters based on data analysis, and enabling adaptive responses to changing environmental conditions. This not only enhances the efficiency of bioremediation but also helps improve nutrient recovery, energy efficiency, minimizing treatment costs, boosting microbial efficiency and system performance, and ensuring the long-term sustainability of operations. This review explores the role of AI in optimizing wastewater treatment, addressing bioremediation limitations, and fostering more eco-friendly wastewater treatment operations.

Keywords: Microbial Bioremediation; AI-Driven Optimization; Wastewater Treatment; Machine Learning; Environmental Sustainability.

CAPP10

Emerging Artificial Intelligence Techniques for Air Pollution Forecasting: Fundamentals, Applications, and Performance

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ABSTRACT

The Air Quality Index (AQI) is a crucial figure to inform the public about the air quality that relies on several factors such as PM2, RSPM/PM10, SO2, NO2, and O3. These air pollutants have a range of harmful effects on public health, including respiratory and cardiovascular diseases, as well as premature mortality. Therefore, it is crucial to enhance accurate air quality forecasting to mitigate these risks. Although various environmental agencies have developed several methods over time for determining the AQI, but no universally accepted method exists that is suitable for all situations. The complex, dynamic, and nonlinear nature of air pollutants makes traditional forecasting methods inadequate, as they struggle to provide reliable predictions due to the influence of various factors, including weather conditions, traffic emissions, and industrial activities. Air pollution varies significantly by region, with urban areas facing high levels of pollutants from traffic and industries, while rural areas deal with dust and agricultural emissions, making accurate forecasting challenging on a broad scale. In this regard, machine learning-based technologies have been shown to be the most effective means of researching such contemporary threats when compared to more conventional approaches. Therefore, this review primarily focuses on Machine Learning and Artificial Intelligence (AI), particularly Deep Neural Networks (DNN), which provide a powerful solution for predicting air pollution and overcoming the limitations of traditional methods. Moreover, the present study focuses on how Artificial Intelligence and Machine Learning, with a particular emphasis on AI techniques, can effectively forecast major pollutants such as PM2.5, PM10, O3, CO, SO2, NO2, and CO2.

Keywords: Machine Learning; Artificial Intelligence; Air Pollutants; Air Quality Index.

CAPP11

Exploring Phytocompounds for Multi-Protein Targeting in Neurodegenerative Diseases: An Integrative Analysis

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ABSTRACT

Neurodegenerative diseases, including Alzheimer's, Parkinson's, and Huntington's, represent a global health challenge due to their complex mechanism and progressive nature, leading to severe cognitive and motor impairments. Despite advancements in medical science, effective treatments remain scarce. This study explores the integration of computational drug discovery techniques and bioinformatics tools to address this pressing issue. By identifying key protein targets involved in neurodegenerative pathways and leveraging molecular docking, pharmacophore modelling, and ADMET (absorption, distribution, metabolism, excretion, and toxicity) predictions, we aim to streamline the identification of potential therapeutic agents.

Additionally, the neuroprotective potential of phytocompounds such as berberine, withaferin A, and quercetin is investigated, emphasizing their promising role in disease prevention and treatment. This approach not only accelerates the drug discovery process but also highlights the importance of combining computational and experimental methodologies to develop effective therapies. Ultimately, this research contributes to the growing efforts to meet the unmet medical needs of individuals suffering from neurodegenerative diseases, while considering the impact of modifiable lifestyle factors and exploit the therapeutic potential of natural compounds.

Keywords: Neurodegenerative Disease; Phytocompounds; Protein Targets; Therapeutic Agents; Drug Discovery; ADMET.

ISSN: 2278-9197 © VSRD International Journals: www.vsrdjournals.com

CAPP12

Exploring the Potential of Phytocompounds in Parkinson's Disease: An In-Silico Approach

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ABSTRACT

Parkinson's disease (PD) is the second most common neurodegenerative disorder and is produced by human physiological function. Among the current treatments available, dopamine agonists play a significant role by mimicking dopamine's natural activity and directly stimulating dopamine receptors in the brain. However, presently available drugs only offer temporary symptomatic relief and are associated with high risk of side effects. Phytocompounds have emerged as a promising avenue in the search for novel therapeutic agents due to their ability to produce secondary metabolites with unique chemical structures.

The present study focuses on the natural compounds for Parkinson disease by using computational approach to design novel candidate for the treatment of PD. Further, identification of potential therapeutic agents for Parkinson's disease involves in-silico approach such as molecular modelling, molecular docking and prediction of ADME/Tox properties. Molecular docking shows the interaction with the active site of protein and ADME/Tox properties assessing the pharmacokinetics and overall viability of a compound as a therapeutic agent.

Keywords: Neurodegenerative; Parkinson's Disease (PD); Phytocompounds; In-silico; Molecular Modelling; Docking; ADME/Tox.

CAPP13

Biosensors and 5G Technology: A Powerful Combination for Real-Time Environmental Monitoring and Sustainable Ecosystems

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ABSTRACT

Increasing industrialization and urbanization lead to a wide range of environmental contaminants such as Heavy metals, pharmaceutical drugs, Microplastics, Persistent organic pollutant etc. These pollutants pose a serious risk to both the environment and human health, making their detection and removal from the environment crucial in the present scenario. Monitoring the environment is crucial to safeguard public health and ensure ecosystem sustainability, as rapid detection of pollutants in the air, water, and soil is essential to mitigate the adverse effects of environmental contamination. The conventional approaches for effectively removing emerging pollutants are costly, time-consuming, labour-intensive, and inefficient. In this respect, biosensors are increasingly used to detect pollutants due to their high specificity and sensitivity, enabling real-time, on-site analysis with minimal environmental impact. When combined with the advanced capabilities of 5G technology, biosensors operate within highly interconnected networks, transmitting large volumes of data over long distances at very high speeds. The low latency and high-speed communication by 5G networks improve the functioning of biosensors by providing timely responses to environmental threats. This article discusses the role of biosensors in detecting environmental pollutants and explores how 5G technology can enhance the efficiency of biosensor-based environmental monitoring systems. This review also documents the use of biosensors for detecting various pollutants, such as heavy metals and organics, and highlights their application in achieving the SDGs. It also summarizes the current advantages and future research directions in this field.

Keywords: Biosensors; 5G; Heavy Metals; Organic Pollutants; Sustainable Development Goals; Microplastics.

CAPP14

Application of "Omics" in Biotechnology

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ABSTRACT

High-throughput technologies have revolutionised our understanding of biological systems, enabling researchers to delve deeper into the complexities of life. This presentation explores the applications of four key omics technologies: transcriptomics, secretomics, Metabolomics, and genomics. Transcriptomics, by analysing gene expression patterns, provides insights into cellular processes, disease mechanisms, and the effects of environmental factors. Secretomics focuses on the proteins secreted by cells, revealing their role in cell-to-cell communication, signalling pathways, and disease progression. Proteomics investigates the protein composition and interactions within cells, offering a comprehensive view of cellular functions, protein networks, and metabolic pathways. Genomics analyses the complete genetic makeup of an organism, uncovering genetic variations associated with diseases, traits, and individual responses to treatments. By integrating these omics technologies, researchers can make significant strides in various fields of life sciences. For example, in the field of medicine, omics technologies can be used to identify novel biomarkers for early disease diagnosis, understand the molecular mechanisms underlying diseases, and develop targeted therapies. In agricultural biotechnology, omics technologies can be used to improve crop yields, resistance to pests and diseases, and nutritional content. In environment. science, omics technologies can be used to study microbial communities, ecosystem dynamics, and the impact of environmental pollutants. Moreover, the integration of omics technologies has the potential to revolutionise personalised medicine. By analysing an individual's genetic makeup and molecular profile, researchers can tailor treatments to their specific needs, leading to more effective and personalised healthcare.

Keywords: Transcriptomics; Secretomics; Proteomics; Genomics; Metabolomics.

CAPP15

AI in Lung Cancer: Enhancing Early Detection, Treatment Planning, and Prognosis

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ABSTRACT

Lung cancer is the leading cause of cancer death with high morbidity and mortality, especially late presentation which remains the primary setback for early detection. Mostly, pulmonary nodules present in an early stage but most cases go undiagnosed with a poor prognosis and poor treatment options.

The conventional approaches to diagnosis, such as imaging modalities and biopsies, have major limitations regarding sensitivity, specificity, and predictive validity. These methods often cannot distinguish between benign and malignant nodules, leading to unwarranted interventions and a delay in diagnosis. Furthermore, the reliance on manual analysis of medical images and unstructured clinical data introduces variability in diagnostic outcomes.

Artificial intelligence has revolutionized lung cancer diagnosis with the application of machine learning algorithms, convolutional neural networks (CNNs), and natural language processing (NLPs). CNNs enhance image accuracies taken to separate nodules from benign and malignant. It reduces unnecessary intervention without a cause. It helps in meaningful insights coming from unstructured medical records; hence, it aids in better patient history analysis and improved treatment planning. The AI models outperform the conventional techniques with better predictive accuracy, easy integration of multi-omics data, and support for personalized healthcare through Clinical Decision Support Systems (CDSS).

These AI-based diagnostic tools accelerate the pace of early detection, simplify clinical workflows, and minimize diagnostic variability.

Keywords: Lung Cancer; Pulmonary Nodules; Artificial Intelligence (AI); Machine Learning (ML); Convolutional Neural Networks (CNNs); Natural Language Processing (NLP); Imaging Modalities; Clinical Decision Support Systems (CDSS); Multi-omics Data Integration; Prognosis Improvement.

CAPP16

Single-Cell RNA Sequencing in Cancer Immunotherapy

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ABSTRACT

Single-cell sequencing utilizes advanced next-generation sequencing technologies to analyze nucleic acid sequences at the level of individual cells. Over recent decades, single-cell RNA sequencing (scRNA-seq) has emerged as a crucial and transformative tool in cancer research. By examining gene expression on a single-cell scale, scRNA-seq facilitates in-depth analysis of immune, stromal, and tumor cell populations, uncovering their complex interactions and contributions within the tumor microenvironment (TME).

This review highlights the significant impact of scRNA-seq in identifying various immune cell types and pathways. This has led to the discovery of novel biomarkers that could enable more precise and effective personalized cancer treatments. Furthermore, scRNA-seq has enhanced the understanding of how immune cells behave within the TME by capturing subtle transcriptional changes and pinpointing essential pathways that influence therapeutic responses and resistance. It has also facilitated the identification of rare and previously uncharacterized cell subpopulations, offering new avenues for therapeutic targeting.

While scRNA-seq has transformed cancer research, it poses challenges such as managing large datasets, studying infrequent cell populations, and bridging the gap between preclinical findings and clinical applications. Overcoming these issues will require progress in computational tools, standardized data analysis techniques, and scalable strategies to widen the scope of scRNA-seq applications. By addressing these challenges, scRNA-seq could revolutionize cancer research and immunotherapy, leading to groundbreaking advancements in precision medicine and improved patient outcomes.

Keywords: Next-generation Sequencing, Single-Cell RNA Sequencing (scRNA-seq); Tumor Microenvironment (TME); Immune Cells, Stromal Cells; Tumor Cells; Gene Expression; Biomarkers; Personalized Cancer Treatments; Immune Cell Dynamics; Transcriptional Changes; Therapeutic Responses; Therapy Resistance; Therapeutic Targeting; Computational Tools; Data Analysis Techniques; Immunotherapy; Precision Medicine.

CAPP17

Natural GPCR Agonists in Focus: A Combinatorial Library Design for Gut-Immune axis Regulation

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ABSTRACT

The growing prevalence of antimicrobial resistance (AMR) poses a critical global health challenge, exacerbating the ineffectiveness of conventional antibiotics. Simultaneously, gut dysbiosis (a disruption in the balance of the gut microbiota) has been linked to various chronic diseases, including inflammatory bowel conditions and metabolic disorders, necessitating the development of novel therapeutic strategies. Current therapeutics, primarily antibiotics are limited in their scope and effectiveness, often failing to address the complex gut-immune interactions and the rising AMR concerns. G-protein-coupled receptors (GPCRs) play a pivotal role in regulating immune responses and gut microbiota balance, offering a promising target for addressing these challenges. Despite their potential, the systematic identification of natural GPCR agonists capable of inducing antimicrobial peptides (AMPs) remains underexplored. This study proposes a novel approach to design a combinatorial library of natural G-protein coupled receptor (GPCR) agonists using in silico approaches, offering dual solution for restoring gut microbiota balance and mitigating AMR, both are pivotal in regulating the gut immune axis. The current study will evaluate the binding affinities and specificities of these natural GPCR agonists through molecular docking. This approach introduces a novel strategy to identify natural GPCR agonists with AMP-inducing properties, paving the way for innovative therapies to combat AMR and restore gut health, offering a sustainable alternative to antibiotics.

Keywords: GPCR; Natural Agonists; Gut Dysbiosis; AMR; Combinatorial Library Design; AMPs; Gut-Immune Axis.

CAPP18

In Silico Docking of Phytocompounds Against Biofilm-Forming Protein Targets of Microorganism Causing Chronic Wound Infection

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ABSTRACT

Biofilm formation is a crucial factor in the persistence and pathogenicity of chronic wounds, which significantly enhances the challenges in the treatment of chronic wounds. Biofilm formation also increases the level of antibiotic resistance leading to the evasion of the host immune system. Targeting the mechanisms of biofilm formation including quorum sensing, adhesion, and extracellular matrix production, creates an opportunity to develop novel therapeutic strategies for the treatment. In this study, an in-silico analysis using molecular docking techniques is carried out to evaluate the efficacy of phytocompounds as inhibitors of key proteins that are involved in the formation of biofilm and to assess the binding interaction of selected phytocompounds to key target proteins. Target biofilm-related proteins include quorum-sensing regulators such as LasR in Pseudomonas. aeruginosa, adhesins like PilA in Acinetobacter. baumannii, and extracellular matrix components such as PIA in Staphylococcus. aureus. This study addresses the challenges posed by biofilm-associated infection and highlights the promising role of phytocompounds in developing novel therapeutic strategies against multidrug-resistant bacterial infections.

Keywords: Biofilm, Docking, Inhibitor, Phytocompounds, Resistance.

CAPP19

Artificial Intelligence in Healthcare: A New Era of Precision and Efficiency

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ABSTRACT

Healthcare is one of the world's largest and fastest-growing sectors but it faces certain challenges. Artificial intelligence (AI) lies in the computer science department, which stresses the creation of intelligent machines that work and react just like humans. AI can address traditional healthcare challenges, driving transformative changes in the healthcare sector. From early disease diagnosis to robotic surgery, AI has the potential to make these processes more efficient & less time-consuming with the help of different machine learning algorithms, neural networks, natural language processing, and computer vision.

AI uses ML and deep learning algorithms to analyze complex genetic data and identify genetic markers and complex interactions between genetic factors and medication responses. It can also uncover various patterns and outperform humans in several areas by offering greater accuracy, cost efficiency, and wide-ranging applications while reducing human errors. It also focuses on developing innovative technologies to improve patient care like Virtual Health Assistants. This text provides a holistic understanding of how models such as conventional neural networks, computer vision, and deep learning mechanisms with the help of various case studies. Reporting AI's role in clinical practice is crucial for successful implementation by equipping healthcare providers with essential knowledge and reliable tools.

Keywords: AI-Driven Technologies, Machine Learning, Healthcare, Disease Monitoring and Management, Personalised Medicine, Algorithmic Bias, Diagnostics, Patient Management, Treatment Planning, Early Disease Detection, Neural Networks.

CAPP20

Predicting the Effect of Bioactive Compounds of Mushroom as Novel Therapeutic Agents Against Skin Cancers Using Computational Biology

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ABSTRACT

Mushrooms have long been recognized for their rich array of bioactive compounds, including polysaccharides, terpenoids, and phenolic substances, which have been shown to present promising potential as cosmeceutical or nutricosmetic ingredient due to their antioxidant, anti-inflammatory, antimicrobial, wound-healing capabilities, photoprotective, anti-tyrosinase, anti-elastase, and anti-collagenase activities. These metabolites can be used to suppress the severity of Inflammatory Skin Diseases, offer photoprotection to the skin, and correct hyperpigmentation showing diverse therapeutic properties against skin conditions. In the context of oncology, certain mushroom-derived compounds have demonstrated promising anti-cancer activities. For instance, polysaccharide-K (PSK), isolated from Trametes versicolor, has been extensively studied for its immunomodulatory and anti-tumor properties. Despite these advancements, applying mushroom bioactive compounds in treating skin cancers remains an emerging field. The current study aims to identify the potential biomarkers associated with skin cancers and the effects of mushroom's bioactive compounds on these biomarkers as a potential therapeutic strategy for treating skin cancers. By employing molecular modelling and docking studies, we intend to predict and analyze the binding affinity of these bioactive compounds against cancer-specific biomarkers, potentially leading to the development of more effective therapeutic agents.

Keywords: Skin Cancer, Bioactive Compounds, Biomarkers, Mushroom, Computational Biology, Novel Therapeutic Agents.

CAPP21

An In-Silico Approach to Understand the Co-Existential Nature of T2dm (Type 2 Diabetes Mellitus) and NAFLD (Non-Alcoholic Fatty Liver Disease)

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ABSTRACT

T2DM and NAFLD are interlinked metabolic disorders that affect more than 197 million people in India alone. T2DM arises due to impaired insulin utilization, leading to dysregulated blood sugar levels, while NAFLD is a result of triglyceride accumulation in the liver. The two diseases share a striking connection where one seems to predispose to the other. This study aims to find complex links between these two metabolic disorders by utilizing RNA sequence datasets of 34 patients divided into 5 cohorts with sub-cohorts, to examine the complex link between T2DM and NAFLD. Each sub-cohort had 3 replicates and performed DGE analysis where we identified 408 genes that were significantly upregulated or downregulated in all cohorts. The pathway enrichment analysis later revealed pathways like the AGE-RAGE signaling pathway to be elevated, liking the two conditions. Additionally, we performed network analysis, where we constructed a network based on curated literature and the gene products of DGE analysis. An extensive network of 750 nodes was constructed. Later, the genes identified via DGE analysis and literature curation were intersected against DisGeNet disease database, which revealed a total of 12 genes, which came out to be significantly implicated in both T2DM and NAFLD. These genes provide insight into the interlinked molecular pathways of T2DM and NAFLD and may serve as potential therapeutic targets for future research. The study enhances our understanding of the molecular crosstalk between T2DM and NAFLD, paving the path for further novel therapeutic interventions against co-occurring metabolic disorders.

Keywords: Differential Gene Expression Analysis, Network Analysis, Hub Node, Expression, DESeq2, Metabolic Disorders.

CAPP22

Computational Approaches to Protein-Protein Interaction Prediction: Methods, Challenges, and Implications for Disease Mechanisms and Drug Discovery

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ABSTRACT

Protein-protein interactions (PPIs) are critical for cellular function and disease progression, making their accurate prediction essential for biomedical research. Recent advancements in computational methods have improved PPI prediction by integrating sequence and structural data from databases such as STRING, BioGRID, DIP, and BIND. While these approaches have shown promise in understanding disease mechanisms and identifying drug targets, discrepancies in prediction accuracy remain. Contradictory results across studies highlight the challenges in choosing optimal methods, with some models favoring sequence-based approaches, while others emphasize structural or hybrid methods. Ongoing analysis aims to address these inconsistencies and evaluate the applicability of these models across various diseases, including cancer, neurodegenerative disorders, and antibiotic resistance. Although progress has been made, further refinement of computational models is necessary to enhance their reliability and utility in drug discovery and disease research.

Keywords: Protein-Protein Interactions (PPIs); Computational Prediction; Bioinformatics, Structural Data; Sequence Data.

CAPP23

Computational Drug Designing for Validating Ayurvedic Practices

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ABSTRACT

The incorporation of computational methodologies with traditional Ayurvedic knowledge represents a promising paradigm in drug discovery. Ayurveda, an ancient Indian medicinal system, offers a vast repository of bioactive compounds with therapeutic potential. However, leveraging this knowledge for modern drug development requires robust validation. Computational methods, such as molecular docking, pharmacokinetics studies, and reverse pharmacology, play a pivotal role in bridging traditional practices with contemporary medicine. These technologies facilitate the identification and optimization of bioactive compounds, streamlining drug discovery by saving time and costs. For example, molecular docking studies can analyze vast databases like the Traditional Knowledge Digital Library (TKDL) to prioritize leads for experimental validation. Reverse pharmacology, a key strategy, employs a "clinics-to-laboratories" approach, translating centuries of empirical Ayurvedic practices into potential therapeutic agents. Notable examples include the discovery of Rauwolfia alkaloids and the repurposing of Ayush-64 as a therapeutic formulation. Additionally, computational tools with advanced computer aided ligand based drug discovery assist in designing synergistic polyherbal formulations targeting complex diseases such as cancer and diabetes, which require multi-target approaches. This confluence of Ayurveda and advanced computational drug designing accelerates drug discovery and provides a scientific foundation for integrating traditional medicine into global healthcare systems, with an emphasis on safety, efficacy, and standardization.

Keywords: Computational Drug Designing, Ayurvedic Medicine, Molecular Docking, Reverse Pharmacology, Bioactive Compounds.

CAPP24

Computational Identification of DENV-2 serotype Inhibitors Targeting the Allosteric Pocket of NS2B/NS3 Protease through Molecular Docking and Molecular Dynamics Simulation Studies

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ABSTRACT

Dengue is one of the most common vector-borne viral diseases in tropical countries like India. Four different serotypes of dengue viruses are responsible for dengue viral infection. This means every individual in the dengue epidemic region is four times susceptible to the dengue viral infection. India is also one of the dengue epidemic regions facing the same risk. One recent study conducted in Jaipur, India, revealed that Dengue virus serotype-2 (DENV-2), is causing severe viral infection when compared to the other three serotypes. Hence, even though there is a need to find dengue virus inhibitors for all four serotypes, finding the dengue virus inhibitors for the DENV-2 serotype will be a priority. The NS2B/NS3 protease enzyme of the Dengue virus is responsible for its infectivity and maturity. The inhibitors that inhibit the allosteric activity of NS2B/NS3 protease can be identified as Dengue virus inhibitors and taken for further studies. In this study, we took 12 different compounds known to have antiviral properties and checked for their inhibitory activity in the allosteric pocket of NS2B/NS3 protease using molecular docking and dynamics simulation studies. As a result, we have identified one natural compound Carvacrol binding well in the allosteric pocket and inhibits the allosteric activity of NS2B/NS3 protease through molecular docking and dynamics simulation studies. This suggests that it can be taken for further studies in the drug discovery process.

Keywords: Dengue Virus; DENV-2 serotype Inhibitors; NS2B/NS3 Protease; Allosteric Inhibition; Molecular Docking; Molecular Dynamics Simulation.

CAPP25

Leveraging Bioinformatics to Decipher Molecular Mechanisms and Therapeutic Pathways in Hutchinson-Gilford Progeria Syndrome

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ABSTRACT

Hutchinson-Gilford Progeria Syndrome (HGPS), a rare genetic condition stemming from mutations in the LMNA gene, serves as a model for understanding accelerated aging and its interplay with genetic and molecular mechanisms. Despite its rarity, HGPS exemplifies premature senescence, presenting with hallmark aging symptoms such as alopecia, osteoporosis, and cardiovascular complications, leading to an average lifespan of 13 years. These features, alongside its molecular underpinnings, position HGPS as a critical focal point for aging and therapeutic research. Addressing HGPS is complicated by its molecular basis, driven by the accumulation of progerin, a defective lamin A variant that disrupts nuclear architecture, chromatin organization, and signaling pathways. These disruptions accelerate cellular aging and pose significant barriers to targeted therapeutic interventions. Current treatment ef orts, including small-molecule inhibitors and gene-editing approaches, demonstrate limited ef icacy and underscore the need for innovative solutions. Bioinformatics emerges as a transformative tool in this landscape, of ering robust platforms for analyzing omics data, elucidating pathways, and identifying potential therapeutic targets. The integration of RNA sequencing and proteomics has revealed shared and distinct pathways in natural and pathological aging, implicating genes such as WNT16 and IGFBP2. These insights pave the way for designing miRNA-based interventions and drug discovery pipelines tailored to mitigate progerin toxicity. Predictive models using bioinformatics have shown promise in distinguishing between age-related transcriptional changes and HGPS-specific alterations, enabling precise stratification for therapeutic studies. The following review will include a detailed exploration of the challenges posed by HGPS, the potential of bioinformatics in advancing therapeutic strategies, and its broader implications for understanding aging. By bridging the gap between molecular data and clinical application, bioinformatics provides a pathway toward unraveling the complexities of progeria and its relevance to broader aging processes.

Keywords: Hutchinson-Gilford Progeria Syndrome (HGPS), LMNA gene, Progerin Toxicity, Accelerated Aging, Bioinformatics, Multi-omics Analysis.

CAPP26

Diagno Plus+ - Accurate Disease Diagnosis in Just One Click

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ABSTRACT

Diagno Plus+ is a revolutionary start-up dedicated to reshaping the medical diagnostics landscape through advanced AI-based solutions. Leveraging cutting-edge artificial intelligence and machine learning, our diagnostic models are designed to provide precise, efficient, and non-invasive disease detection. These models utilize extensive parameters and sophisticated image analysis techniques to accurately diagnose conditions such as lung cancer, skin cancer, pneumonia, breast cancer, and brain tumors.

Our innovation caters to both clinical laboratories and healthcare professionals by significantly reducing diagnostic workloads while maintaining high accuracy. By streamlining the diagnostic process, we enable early intervention and personalized treatment plans, enhancing patient care and improving healthcare outcomes.

With a steadfast commitment to innovation, Diagno Plus+ aims to emerge as a leader in medical diagnostics. Our solutions empower clinical labs to optimize efficiency and healthcare professionals to deliver timely and precise medical interventions. Together, we are shaping the future of global healthcare by making accurate disease diagnosis accessible and efficient for all.

Keywords: AI Diagnostics; Medical Innovation; Disease Detection; Healthcare Optimization; Machine Learning.

CAPP27

Structural and Functional Implications of SHANK3 Mutations in Autism Spectrum Disorder: Insights from Molecular Dynamics Simulations and Gene Expression Analysis

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ABSTRACT

Autism Spectrum Disorder (ASD) is a complex neurodevelopmental condition marked by diverse clinical symptoms, including social communication deficits and repetitive behaviors. Genetic factors, particularly mutations in the SHANK3 gene, play a significant role in ASD pathogenesis. This study investigates the structural and functional consequences of specific SHANK3 mutations (E71S, N52R, P141A, and L270M) using molecular dynamics simulations. Results indicate that E71S and N52R mutations disrupt the stability and folding of SHANK3, affecting interactions with key proteins like αCaMKII and α-Fodrin.

The P141A mutation leads to increased distance between the SPN and ARR domains, suggesting a less compact structure that may enhance α-Fodrin binding while impairing αCaMKII interactions. Conversely, L270M maintains moderate stability without significant unfolding. Additionally, a comprehensive bioinformatic analysis of gene expression profiles in ASD patients revealed 581 differentially expressed genes (DEGs), with notable upregulation of pro-inflammatory cytokines linked to immune dysregulation in ASD. Eight common DEGs were identified as potential biomarkers for early diagnosis and therapeutic targets. These findings underscore the intricate relationship between SHANK3 mutations and neuroinflammation, offering insights into the molecular underpinnings of ASD.

Keywords: Autism Spectrum Disorder, SHANK3 Mutations, Molecular Dynamics Simulations, Neuroinflammation, Biomarkers.

CAOP03

Targeting the Achilles Heel of Cancer: A Structure-Guided Drug Design Approach to Identify Novel Lead Compounds and Repurpose FDA-Approved Drugs as Telomerase Inhibitors

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ABSTRACT

Replicative immortality driven by increased telomerase activity is a hallmark of cancer, making telomerase an attractive anti-cancer drug target. However, the lack of a high-resolution hTERT structure and narrow therapeutic windows have hindered the development and approval of small-molecule inhibitors. This study adopts a structure guided drug design approach to repurpose FDA approved drugs and identify novel telomerase inhibitors followed by experimental validation using an in-vitro TRAP assay.

Due to the absence of a co-crystal structure of BIBR1532 with the hTERT thumb domain, MD simulations were employed to accurately identify its binding site. Two pharmacophore models, corresponding to the putative and newly identified binding pockets, were developed and screened against Drug Bank and novel libraries. The models were validated based on the fit value of BIBR1532 and selectivity scores, highlighting key features required for inhibition. High-ranking hits were filtered using drug-likeness criteria, including Lipinski's rule, ADME, and TOPKAT, followed by redocking into the identified pockets. MD simulations of selected compounds confirmed their stability, while binding free energy calculations (MM-PB(GB)SA), PCA, and FEL characterization revealed key interactions.

Our findings indicate that the BIBR1532 binding site lies 8.4 Å away from the reported putative FVYL pocket, exhibiting conserved interactions essential for its activity. Five lead drugs and four novel compounds demonstrated remarkable stability in the new binding pocket, as revealed by trajectory analysis metrics (RMSD, RMSF, H-bonds, radius of gyration). Two FDA approved drugs and five novel leads have been identified after in-vitro evaluation, highlighting their potential for future clinical development in cancer therapeutics.

Keywords: MD Simulation; Pharmacophore Models; Drug Repurposing; FDA Approved Drugs; Cancer Therapeutics.

CAOP04

Deciphering the Role of p73 in the Regulation of Angiogenesis in Colorectal Cancer Using Bioinformatic and in-vitro Analyses

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ABSTRACT

This study aimed to identify key genes involved in colorectal cancer angiogenesis and prognosis. We included GEO datasets where p73 was either downregulated or absent to mimic our cell line model. Three Gene Expression Omnibus (GEO) datasets and the MSigDB (GSEA) database were used to extract angiogenesis-related genes, intersecting genes were harnessed using Venny2.1. A total of 70 DEGs were identified, consisting of 18 downregulated genes and 52 upregulated genes. We constructed a protein-protein interaction (PPI) network using STRING followed by the extraction of 20 hub genes using the Cytoscape software. Prognostic values of hub genes were evaluated using KM Plotter. Various genes showed significant upregulation upon expression analysis by UALCAN, and showed significant variation in the expression among different stages of the tumor and significant in the prognosis of CRC patients. Further, expression of few genes was validated by real time PCR in HCT116p73wt and p73kd cells and MMP2 and MMP9 expression was found to be elevated in the spheroid samples of the HCT116 $p53^{-/-}$ p73kd cell line also migratory rates were high in HCT116p73kd cells as checked through wound healing and spheroid migration assays. In a nutshell, this study sheds light on the regulation by p73 over the hallmark genes involved in angiogenesis and their relation to carcinogenesis which might contribute to the discovery of new treatment targets.

Keywords: p73; Bioinformatics; Angiogenesis; Hub Genes; Carcinogenesis.

CAOP06

Identification and Validation of a Metabolic-Related Gene Risk Model Predicting the Prognosis of Lung, Colon, and Breast Cancers

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ABSTRACT

Metabolic reprogramming, vital for cancer cells to adapt to the altered microenvironment, remains a topic requiring further investigation for different tumor types. Our study aims to elucidate shared metabolic reprogramming across breast (BRC), colorectal (CRC), and lung (LUC) cancers. Leveraging gene expression data from the Gene Expression Omnibus and various bioinformatics tools like MSigDB, WebGestalt, String, and Cytoscape, we identified key/hub metabolism-related genes (MRGs) and their interactions. The functional characteristics including survival parameters and expression of the key MRGs were analyzed and validated through Gene Expression Profiling Interactive Analysis 2 and qRT-PCR. In addition, we employed machine learning algorithms such as k-nearest neighbours (KNN), support vector regressor (SVR), and extreme gradient boosting (XGBoost) to assess MRGs' effectiveness in predicting overall patient survival. Among 11,384 DEGs analyzed, 540 overlapped across BRC, CRC, and LUC, with 46 MRGs and 20 key/hub MRGs involved in all studied cancer types. Of these, 11 key MRGs were prognostically significant. qRT-PCR validation of key MRGs in specific cancer cell lines confirmed their expression profiles, with some showing cell-type-specific patterns. SVR exhibited remarkable accuracy in predicting overall survival, emphasizing its clinical utility. Our integrated approach combining bioinformatics analyses and experimental validations underscores the potential of MRGs as biomarkers for metabolic therapies, with machine learning models enhancing predictive capabilities for patient outcomes.

Keywords: Cancer Metabolism; Metabolism-Related Genes; Machine Learning; Overall Survival; qRT-PCR.

CAOP07

Harnessing Geospatial Artificial Intelligence (GeoAI) for Global Health Advancements: Applications in Precision Public Health, Environmental Health, and Sustainable Development

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ABSTRACT

Geospatial Artificial Intelligence (GeoAI) is transforming health research and management utilizing geospatial information alongside artificial intelligence. GeoAI combines GIS, machine learning, and big data to solve global health problems like communicable and non-communicable diseases and environmental health. GeoAI, with applications of EpiDMS, helps in modelling, monitoring, and allocating the resources for diseases carried by vectors like malaria or any predictive pandemic like COVID 19. It also strengthens environmental health by mapping the sources of pollution including the contribution agribusiness made to the PM2.5 emissions in Italy, as well as addressing upstream determinant factors like air quality, walkability, food access to premature death causes including obesity and type-2 diabetes. GeoAI in Precision Public Health uses genetic, behavioural and spatial data to work on health disparities, aid disaster management and enhance the urban and sustainable development goals. Despite the issues such as data privacy and interoperability, GeoAI presents possibilities for innovative solutions, evidence-based decisions and policies that would have long term positive impacts on the health of individuals and quality of life around the world.

Keywords: Geospatial Artificial Intelligence (GeoAI); Precision Public Health; Disease Modeling and Tracking; Environmental Health; Sustainable Development Goals (SDGs).

CAOP08

Ketal Pyruvyltransferases as Novel Catalysts in Pyruvylation: A Key to Enzyme Evolution

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ABSTRACT

Ketal pyruvyltransferases (KPTs), a subclass of pyruvyltransferase, transfer a pyruvate group onto saccharides. These enzymes are found in diverse organisms ranging from bacteria, yeast, algae and humans. These ubiquitous enzymes play essential biosynthetic roles and mediate cellular processes including adhesion and biofilm formation. This study characterizes the evolutionary and functional features of KPTs by investigating their structural and sequence conservation from bacteria to yeast and algae. By using the MUSCLE algorithm for multiple sequence alignment (MSA) and phylogenetic analysis with the maximum likelihood method, we identified conserved residues, particularly histidine (H) and arginine (R), likely involved in phosphoenolpyruvate (PEP) binding. Structural analysis revealed a conserved PEP-binding site and classified KPTs into GT-A and GT-B subcategories within the glycosyltransferase superfamily. These observations underpin a conserved nature of donor (PEP) and acceptor (saccharides) substrate, with implications for virulence. This work offers novel insights into KPTs' conserved biochemical mechanism and sets the foundation for new development of antibacterial strategies. This study facilitates the importance of KPTs as a gateway to reveal the complexities of pyruvylation and its biological significance.

Keywords: Pyruvylation; Ketal pyruvyltransferase; Phosphoenolpyruvate (PEP); MSA; Phylogenetic Analysis; MUSCLE; Maximum Likelihood; Secondary Structures; Glycosyltransferase (GT).

CAOP09

Drug Repurposing for Antimicrobial Resistance: Identification of Ketal Pyruvyl Transferase Inhibitors

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ABSTRACT

Antimicrobial resistance (AMR) has emerged as a critical global health threat, underscoring the need for the development of novel therapeutic strategies and pharmacological targets. We propose ketal pyruvyl transferase, an enzyme involved in the biosynthesis of exopolysaccharides (EPS), as a potential target for therapeutic intervention. A pyruvyl group is transferred from phosphoenolpyruvate (PEP) to a hydroxyl group within EPS by EPSO, a gene that encodes KPT in Bacillus subtilis. This mechanism impacts cell-cell communication, pathogenicity, and biofilm formation. We identified potential inhibitors of EPSO by performing high-throughput virtual screening with PyRx, focusing on a library of 2,308 FDA-approved drugs. After discovering several promising compounds, we refined their binding predictions through re-docking. Top three compounds identified were, Pyridoxal phosphate with binding affinity of -11.4 kcal/mol, Ademetionine and Pyruvic acid, with binding affinities of -10.6 kcal/mol, and -10.4 kcal/mol, respectively. We conducted molecular dynamics (MD) simulations using GROMACS for validation of these interactions. MM-PBSA (Molecular Mechanics Poisson-Boltzmann Surface Area), RMSF (root mean square fluctuation), SASA (solvent-accessible surface area), radius of gyration, RMSD (root mean square deviation), and H Bonding, these parameters were considered for the assessment of interactions. ADMET analysis further indicates that these compounds hold promise for drug repurposing. This study underscores the potential of ketal pyruvyl transferase as a new target in the fight against antimicrobial resistance, providing important insights into its therapeutic applications.

Keywords: Antimicrobial Resistance; MM-PBSA; Molecular Dynamics; Molecular Docking; Exopolysaccharides; Ketal-pyruvyl Transferase; EPSO; Bacillus Subtilis.

ISSN: 2278-9197 © VSRD International Journals: www.vsrdjournals.com

CAOP10

Revolutionizing Healthcare with an Automated Framework for Medical Document Analysis to Enhance Efficiency and Accuracy Using Deep Learning and NLP

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ABSTRACT

This paper presents a cutting-edge automated framework for efficiently processing unstructured medical documents, addressing critical challenges faced by healthcare institutions and insurance companies handling vast amounts of multi-format data. The proposed system integrates state-of-the-art deep learning, natural language processing (NLP), and advanced large language models LLaMA to extract structured data with high accuracy and scalability. With over 95% precision, 92% recall, and the ability to process up to 100 documents per minute, the framework demonstrates 98% accuracy in table extraction and a 70% reduction in manual effort. Key features include accurate identification and extraction of patient details, billing summaries, diagnosis codes, and treatment costs from complex, multi-page documents. Preprocessing techniques such as noise reduction and skew correction enhance OCR performance by 15%, enabling better handling of low-resolution and noisy inputs. Semantic search models and LLaMA-based prompting mechanisms enable precise and rapid retrieval of relevant sections, reducing query time by 30%. Additionally, a user-friendly interface powered by Gradio facilitates interactive querying and visualization of extracted data. Tested on a dataset of 10,000 scanned medical reports and bills, the framework significantly improves healthcare workflows, streamlining billing processes, accelerating claims processing, and enhancing record-keeping. This approach not only ensures operational efficiency but also contributes to reducing labor-intensive, error-prone tasks, making it a valuable tool for modern healthcare institutions.

Keywords: Multi-Format Data; Natural Language Processing (NLP); OCR; LLaMA-Based Mechanisms.

CAOP11

Unravelling Microbiome-GPCR Interactions: Insights into Antibiotic Impact and Gut-Brain Axis Dynamics

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ABSTRACT

The human gut microbiome plays a critical role in metabolism, immune regulation, and host defense. Its disruption has been implicated in various diseases, including obesity, diabetes, inflammatory bowel syndrome (IBS), and certain cancers. G-protein-coupled receptors (GPCRs), central to cellular functions and drug discovery, mediate interactions between microbiota-derived metabolites and host signaling pathways, particularly within the Gut-Brain Axis. Antibiotics, while essential for managing infections, disrupt microbiota composition and function, leading to decreased bacterial diversity, altered metabolite production, and emergence of multidrug-resistant organisms (MDROs). These disruptions impact GPCR-mediated signaling, potentially altering gut-brain communication and associated physiological processes.

Despite the growing recognition of microbiome-GPCR-antibiotic interactions, significant gaps persist. The specific conformational changes induced by metabolite-GPCR interactions and the downstream effects on cellular pathways remain poorly understood. Additionally, current computational models inadequately address GPCR dynamics within microbiome resilience and Gut-Brain Axis signaling. GPCR-targeted drug development has largely overlooked microbiome protection during antibiotic use.

This review highlights these gaps in the current literature, focusing on the limited understanding of microbiome-GPCR-antibiotic interactions and their implications for Gut Brain Axis signaling. It emphasizes the need for studies on GPCR conformational changes, computational models integrating microbiome and GPCR dynamics, and strategies for developing GPCR-targeting compounds to safeguard the microbiome. Addressing these gaps will provide a foundation for future research and therapeutic advancements aimed at mitigating antibiotic-induced disruptions and enhancing gastrointestinal and neurological health.

Keywords: Gut Microbiome; Microbiome-GPCR Interactions; Gut-Brain Axis; Multidrug Resistant Organisms (MDROs).

CAOP12

Sudden Cardiac Arrest and Its Global Impact in Young Population: A Focus on India's Rising Mortality Rates

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ABSTRACT

Cardiovascular diseases (CVD) continue to be the leading cause of death worldwide, claiming approximately 17.9 million lives each year. Among these, sudden cardiac arrest (SCA) is a major contributor, particularly in younger individuals. The review draws on data from scientific studies and global health organizations, with a particular emphasis on India, where approximately 5–6 lakh sudden cardiac deaths occur annually, a significant number of which involve individuals under the age of 50. The survival rate for SCA is critically low, ranging between 1–2% where conditions like arrhythmias and hypertrophic cardiomyopathy (HCM) play a significant role. In contrast, coronary artery disease is the predominant cause in older age groups. The risk of SCA remains a significant concern for young individuals. Early detection through family screening and genetic testing, combined with increased awareness of the condition, are crucial steps toward improving outcomes. This review consolidates existing research on the underlying causes of SCA, highlighting differences across age groups and emerging trends. The findings emphasize the urgent need for targeted preventive measures and greater awareness to combat the rising prevalence of SCA.

Keywords: Cardiovascular Diseases; Hypertrophic Cardiomyopathy; Arrhythmias; Sudden Cardiac Arrest; Sudden Cardiac Death.

CAOP15

In-silico Study of Salt/Salinity Stress in Chickpea (Cicer Arietinum) Through Transcriptomic Analysis

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ABSTRACT

Salinity is a major abiotic stress causing significant agricultural losses worldwide. Chickpea (Cicer arietinum), an essential legume crop, is particularly sensitive to salt stress. As the second most important cool-season grain legume, chickpea is cultivated primarily in arid and semi-arid regions and belongs to the Fabaceae family. Renowned for its high protein content and rich nutrient profile, it also enhances soil fertility through nitrogen fixation. However, abiotic stress factors, especially salinity stress, severely constrain chickpea production by disrupting key processes such as photosynthesis and metabolism, ultimately impairing plant growth and reproduction. This study aimed to identify key genes associated with salinity stress tolerance through meta-analysis of transcriptomics data. A total of 1,294 million reads were collected from root and shoot samples of seven genotypes from the NCBI SRA database to identify differentially expressed genes. Analysis revealed 1,310 DEGs linked to critical metabolic pathways, including hormone signaling, photosynthesis, lipid and carbohydrate metabolism, and cell wall biogenesis. Gene ontology analysis highlighted an enrichment of transcripts involved in salinity response. Notably, we identified key genes associated with cell wall modification and root morphogenesis, such as dirigent proteins, expansin, and casparian strip membrane proteins, which are potentially involved in salt tolerance. Gene set enrichment analysis and functional annotation of these genes suggest their potential as candidates for improving salt tolerance in chickpea.

Keywords: Differential Gene Expression; Salinity; Transcriptomics; Gene Ontolog.

CAOP16

Integrating Bioinformatics and Machine Learning to Elucidate the Genetic and Molecular Basis of Drug-Induced Kidney Injury

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ABSTRACT

Drug-induced nephrotoxicity accounts for approximately 20% of acute kidney injury (AKI) cases and is a significant cause of chronic kidney impairment. This study investigates the molecular mechanisms behind nephrotoxicity using gene expression datasets from human and rat kidney models exposed to nephrotoxic drugs. A dataset encompassing 10,000+ gene expression profiles from 50+ nephrotoxic drugs was analyzed. Advanced bioinformatics tools and deep learning algorithms, including convolutional neural networks and autoencoders, were applied for differential expression analysis and pathway enrichment. Key biomarkers, such as specific upregulated genes with log2 fold change >2 and statistically significant p-values (<0.01), were identified. Integrating data across species, the models achieved >90% accuracy in predicting gene-drug associations. This comprehensive approach uncovers critical molecular pathways and novel therapeutic targets, advancing our understanding of nephrotoxicity. The findings provide a quantitative and mechanistic foundation for developing targeted interventions to prevent or treat kidney damage caused by nephrotoxic drugs.

Keywords: Chronic Kidney Toxicity; Nephrotoxicity; Neural Network; Therapeutic Target.

CAOP17

Exploring ROCK Protein Targeting Ability of Natural Phytocompounds: A Promising Approach to Manage Neurological Disorders

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ABSTRACT

Neurodegenerative diseases (NDDs) pose a significant global health challenge due to their progressive nature and lack of effective treatments. Among the various underlying causes, mitochondrial dysfunction has emerged as a critical factor, contributing to oxidative stress, energy deficits, and neuronal degeneration. Mitochondrial dynamics, including fission and fusion, facilitate organelle repair, while mitophagy selectively degrades damaged mitochondria via autophagy. Dysregulation of these processes in neuronal cells exacerbates oxidative damage and promotes cell death. Recent studies highlight that mitochondrial dynamics and mitophagy are tightly regulated by Rho-associated protein kinases (ROCK1 and ROCK2). ROCK1 promotes mitochondrial fission by phosphorylating Drp1, while ROCK2 inhibits Parkin-dependent mitophagy by phosphorylating PTEN, making them promising therapeutic targets for NDDs.

To explore potential therapeutic options, this study investigated natural compounds to target ROCK proteins. Based on ancient Indian medicinal literature, 11 neuroprotective plants were selected, yielding 1,223 natural phytocompounds (NPCs) from the IMPPAT database. In silico analyses using Schrodinger identified 143 NPCs with strong binding energy to ROCK1 and 169 to ROCK2 proteins. After ADME and toxicity analyses, 54 NPCs for ROCK1 and 85 for ROCK2 were shortlisted. MM-GBSA analysis further refined the selection, identifying five NPCs from Evolvulus alsinoides, Dendrobium nobile, Leucojum aestivum, and Setaria italica that inhibited ROCK1, and six NPCs from Setaria italica, Desmodium gangeticum, Alpinia galanga, and Cannabis sativa that inhibited ROCK2. Molecular dynamics simulations validated the stability and binding efficiency of these compounds, with P3-CID1 and P9-CID1 emerging as top candidates for ROCK1, and P4-CID34 and P11-CID3 for ROCK2. Furthermore, P10-CID12 demonstrated dual inhibition of both ROCK1 and ROCK2, making it the most promising candidate. These findings suggest that the identified NPCs, particularly P10-CID12, hold significant therapeutic potential for targeting mitochondrial dysfunction in NDDs and warrant further validation through in vitro and in vivo studies.

Keywords: Neurodegenerative Diseases, Mitophagy, Mitochondrial Dynamics, Indian Medicinal Plants, Rho-Associated Protein Kinases.

CAOP18

Exploring Indian Medicinal Plants for Mitophagy Modulation in Chemotherapy Resistance: An In-Silico Study

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ABSTRACT

Cancer has been one of the leading causes of death globally. Being the organelle involved in the energy production, quality control of mitochondria via mitophagy is important for its functioning. Dysregulated mitophagy leads to mitochondrial accumulation, promoting tumor progression in cancer cells. Increased mitophagy also triggers metabolic reprogramming, leading to resistance against standard treatments. Therefore, inhibiting mitophagy presents a promising therapeutic approach to overcome chemoresistance. However, studies using natural phytocompounds (NPCs) for this purpose are limited.

To address this gap, our study investigates the impact of NPCs on mitophagy-inducing proteins and their effects on tumor growth and chemoresistance. We reviewed literature and online databases, identifying 327 Indian anti-cancer plants with 31,708 phytocompounds. After removing duplicates and applying Lipinski's rule of five using Swiss ADME, we selected 878 phytocompounds for molecular docking.

A STRING network and CYTOSCAPE analysis identified 12 key mitophagy-related proteins for molecular docking, with active sites determined using the CASTp3.0 server. We conducted molecular docking to assess binding affinities between these proteins and the selected NPCs, 240 complexes were shortlisted based on Glide Gscore for post prediction studies. Further analysis via ADME properties using Swiss ADME and ADMETLab3.0 and toxicity analysis using PROTOX3.0 shortlisted 10 compounds. This was succeeded by MMGBSA of 10 compounds that narrowed down to 5 NPCs. These selected compounds seem to be the most promising NPCs inhibiting the mechanism of mitophagy. After running the MD Simulation of the 7 complexes obtained, based on RMSD, RMSF and ligand- proteins interactions we concluded that NPC5-AMBRA complex proved to be the most promising result and was most stable in the system.

Keywords- Mitophagy, Chemoresistance, Indian Medicinal Plants, In-silico Screening, Network Analysis.

CAOP19

In silico screening of anti-inflammatory Activity of phytocompounds from Adhatoda vasica as Potential Inhibitors against ARDS: Molecular Docking and MD Simulation

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ABSTRACT

ARDS is characterized by the rapid onset of non-cardiogenic pulmonary edema and impaired gas exchange, primarily due to a severe inflammatory response, which is often referred to as a cytokine storm. As inflammation pathways can be the major target to deal with ARDS, current study demonstrates the molecular docking of phytocompounds derived from Adhatoda vasica against the three different proteins in the pro-inflammatory cytokines cascade - IL8 receptor - CXCR1, MPO, and TLR4. The study investigates the possibility of targeting and inhibiting these proteins via selected phytocompounds to circumvent lung inflammation. Eleven bioactive compounds from AV were pharmacologically analyzed using Protox II and Swiss ADME. They were further docked using the docking software AutoDock Vina and compared with the anti-inflammatory standard drugs. In silico, ADMET properties prediction shows that quercetin and vasicine indicated adequate values for solubility and absorption characteristics with minimal toxic effects. In docking, Vasicine and quercetin showed the most favorable binding energy towards the receptor proteins. MD simulation study suggests that quercetin and vasicine could be promising alternatives to commonly used synthetic drugs for the treatment of ARDS. These compounds may offer potential for reduced side effects while effectively targeting the inflammatory pathways involved in the condition.

Keywords: ARDS; Proteins; Pro-inflammatory Cytokines; Docking; Bioactive Compounds.

CAOP20

Datura Metel in Developing Novel Biopesticide using Computational Approach

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ABSTRACT

Current global population demands an increase in agricultural yields to meet the food requirement, where pesticides play a very crucial role. However, their uncontrolled uses led to significant environmental pollution causing various human health issues. On exposure to pesticides, pests develop resistance as a result of which, their effectiveness declines, demanding an increase in doses and frequency. To this respect, biopesticides, derived from natural sources can be an alternative for sustainable agriculture and environmental- friendly solutions to human health and ecosystems. Datura metel, a plant with insecticidal properties and a phytochemical composition, has potential as a biopesticide due to its biological activity against insects. The aim of the present study is to investigate the pesticidal potential of Datura metel using computational methods. In pest species, EGFR, AKT1, and PI3K, known to be —highly involved in cellular processes as well as glucose metabolism were selected as targets and their plant-based inhibitors were explored through molecular docking analysis. Known phytochemicals of Datura metel were extracted, and docked against the targets to identify the most stable target-inhibitor complex. On the basis of the lowest binding energy, few compounds are shortlisted. Ramachandran Plot of the targeted gene, Hydrophobicity Plot of the genes, and ADMET analysis are done to assess the structural stability and secondary structure conformation, predict potential transmembrane domains, and determine their drug-like potential, respectively. This study highlights the potential of phytochemicals from Datura metel as effective inhibitors of targeted pest genes, offering a promising approach for Sustainable pest management.

Keywords: Plant-based Inhibitors, Insect Targets, Sustainable Agriculture, Computational Methods, Datura Metel.

CAOP21

The Role of Deep Learning-based Automation in Identifying the Onset of Cognitive Impairments through Revolutionized Evaluation of Cognitive Function Tests for Subjects in Remote Geographic Locations

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ABSTRACT

Early diagnosis of cognitive impairments, particularly Mild Cognitive Impairment (MCI) and dementia, is crucial in healthcare. Effective screening tools like the Verbal Fluency Test, Mini-Cog Test, and language assessments allow for remote administration, minimizing the need for healthcare professionals' involvement. Research highlights the variability in the sensitivity and specificity of these tests, necessitating careful selection based on diagnostic capabilities. An ideal evaluation tool should analyze speech samples for hesitations and flaws while using image description tasks to assess cognitive understanding. Verbal fluency tests are essential in both research and clinical settings, assessing cognitive domains such as executive function and semantic memory. Performance changes may indicate cognitive decline or neurological disorders like Alzheimer's disease. The Mini-Cog test effectively screens for neurodegenerative diseases by evaluating memory and visuospatial skills, facilitating early detection of conditions like Alzheimer's. It comprises the Item Recall Test and Clock Drawing Test, alongside assessments that gauge environmental awareness. Advancements in computational techniques enable remote administration of cognitive tests, allowing individuals in underserved areas to participate without visiting healthcare facilities. Automated analysis enhances accuracy in scoring and interpretation, providing immediate feedback while ensuring secure data storage. Integrating cognitive test results with other health data offers a comprehensive understanding of an individual's cognitive health, supporting personalized treatment plans and promoting timely interventions for at-risk people.

Keywords: Mild Cognitive Impairment (MCI); Alzheimer's; Item Recall Test; Clock Drawing Test.

ISSN: 2278-9197 © VSRD International Journals: www.vsrdjournals.com

CAOP22

Computational Approaches for Gene Signature Identification in Meningiomas

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ABSTRACT

Gene signatures in meningiomas represent a fundamental area of emphasis in understanding these tumors' behavior, recurrence, and response to therapies. Among the most frequent primary tumors in the central nervous system, meningiomas represent a highly diverse group of cancers at the molecular level, where traditional methods for classification and therapy are challenged by this diversity. Computational analyses in the form of transcriptomic and proteomic data have been at the forefront in identifying gene signatures associated with clinical outcomes. Molecular profiling demonstrated superior predictive values over histologic grading in assessing tumor recurrence and aggressiveness, the gene expression signatures distinguishing different types of tumors. FOXM1, PTTG1, and LEPR are some identified biomarkers. Advanced machine learning tools, especially MPscore that integrates non-coding RNA, and DNA methylation data enhance the identification of biomarkers further. Studies using deep molecular characterizations have elucidated critical pathways and genetic changes, including the recurrent POLR2A mutation and the oncogenic role of FOXM1 in tumor development. The investigations into the tumor microenvironment and interactions with the immune system have opened up new avenues for immunotherapy, while transcriptomic analyses have identified novel mutations crucial to tumor development. Repurposing existing drugs based on gene expression data demonstrates the potential of computational techniques in guiding targeted therapeutic strategies. These studies underscore the increasing role of molecular research in the management and treatment of meningiomas. The applications of transcriptomic, proteomic, and machine learning techniques have advanced personalized medicine, providing more accurate prognostic tools and more effective treatments for patients with meningiomas.

Keywords: Gene Signatures, Meningiomas, Transcriptomic Analysis, Biomarker Identification, Machine Learning.

CAOP23

Next-Gen Psychometric Testing: An Automated Data-Driven AI-ML Tool for Mental Health Professionals

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ABSTRACT

Subjectivity, static methodologies, and the lack of real-time insights into patient behavior often hinder the accuracy and reliability of psychometric tests. To address these limitations, we conducted a comprehensive research study to develop an AI-powered tool that enhances the precision and objectivity of psychometric assessments. This tool integrates advanced facial emotion analysis, response dynamics, and behavioral pattern recognition to provide mental health professionals with actionable, data-driven insights. Our research focuses on leveraging live video feeds to analyze patient emotions, tracking response times for each question, and evaluating certainty by monitoring the frequency of answer revisions. These capabilities address critical challenges in traditional psychometric evaluations, including human bias, the absence of real-time models, poor image quality, and the general neglect of routine mental health assessments. The tool was developed using HTML, CSS, JavaScript, and Python to create a robust system that processes data and generates detailed, interactive reports in PDF format. These reports are tailored for counselors and psychiatrists and include comprehensive visualizations of response times, chosen answers, changes in emotions per question, and behavioral inconsistencies. Additionally, the tool provides preliminary interpretations of psychological tendencies such as indecisiveness, stress, or trauma, aiding practitioners in identifying key areas of concern. By utilizing artificial intelligence, machine learning, and computational biology, our tool predicts the validity of psychometric test responses with high accuracy. Deep learning algorithms ensure robust emotional analysis, identifying subtle, real-time changes in facial expressions to enhance reliability. This research represents a multidisciplinary approach to reimagining psychometric assessments, transforming them into dynamic and objective processes. By addressing the gaps in traditional evaluations, our work empowers mental health professionals to make data-informed decisions, thereby advancing the field of mental health assessments and improving patient care.

Keywords: Facial Emotion Recognition, AI-driven Analysis, Subjective Data Analysis, Psychometric Evaluation, Psychological Disorders.

CAOP24

Virtual Screening of phytocompounds from Peel of Citrus limetta to Combat Skin Cancer Targets: Molecular Docking and Molecular Dynamic Simulation Analysis

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ABSTRACT

Skin cancer remains a significant global health challenge, necessitating the development of effective and safer therapeutic options. MEK1, CDK4, and IL1 are key targets in skin cancer treatment due to their pivotal roles in the MAPK, CDK4, and IL1 signaling pathways. This study evaluated the inhibitory potential of Citrus limetta peel-derived phytocompounds against these targets using computational approaches. Molecular docking was performed to compare the binding affinities of phytocompounds with known inhibitors. ADMET analysis was conducted to assess the pharmacokinetic and toxicity profiles of the phytocompounds, while molecular dynamics simulations and MM-GBSA calculations were used to evaluate binding stability and free energy. Docking results revealed that ellagic acid, hesperidin, and quercetin exhibited stronger binding affinities toward MEK1, CDK4, and IL1, respectively, compared to reference drugs. ADMET predictions confirmed the drug-like properties and non-toxic nature of all phytocompounds. Molecular dynamics simulations indicated stable interactions for ellagic acid with MEK1 and quercetin with IL1, while hesperidin showed minor conformational changes with CDK4 during the simulation. These findings suggest that ellagic acid, hesperidin, and quercetin hold promise as natural inhibitors targeting MEK1, CDK4, and IL1, offering potential alternatives to synthetic drugs in skin cancer treatment. Further in vitro and in vivo studies are necessary to validate their therapeutic efficacy.

Keywords: Skin Cancer; Target Proteins; Citrus Limetta; Phytocompounds; ADME-T; Molecular Docking Simulation.

CABS01

Navigating the Structural Landscape of Autophagic Proteins Post Alpha Fold Era

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ABSTRACT

AlphaFold, a groundbreaking AI-based protein structure prediction algorithm, has transformed structural biology by accurately predicting the structures of over two million proteins. This unprecedented achievement has provided researchers with a vast repository of structural information, enabling new avenues of exploration in protein function and interactions. Building on this success, the advanced AlphaFold3 now facilitates the prediction of protein complexes. Harnessing these innovations, we have focused on one of the key pathways of cellular homeostasis, autophagy, which holds immense therapeutic potential in addressing various diseases. In our work, AlphaFold enabled the identification of novel motifs in multiple autophagy-related proteins. To ensure this discovery benefits the broader scientific community, we developed a user-friendly web resource, making our motif prediction pipeline publicly accessible. Furthermore, by integrating AlphaFold3 predictions with molecular dynamics simulations, we investigated fundamental complexes critical to chaperone-mediated autophagy. These analyses provide insights into protein protein interactions and structural mechanisms within this pathway. The robustness of our approach is validated through experimental evidence, highlighting its reliability and scalability for studying other proteins and complexes. By combining cutting-edge AI tools with computational and experimental methods, our work not only leverages the transformative power of AlphaFold but also paves the way for new discoveries in structural biology and cellular pathway analysis, setting a strong precedent for the post-AlphaFold era.

Keywords: AlphaFold; Autophagy; Web-Resource; Molecular Dynamics Simulations.

CABS02

Novel Curcumin Derivative Can Interfere with MurC Ligase-Dependent Peptidoglycan Biosynthesis in Multi-Drug-Resistant Salmonella Typhi: Evidence from Molecular Docking and Dynamics Simulations

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ABSTRACT

The emergence of multi-drug resistance in recent Salmonella Typhi isolates, causative agent of enteric Typhoid fever, have compelled us to evaluate for alternative therapeutic strategies. The World Health Organization reported 11-20 million cases with 128,000–161,000 deaths per year due to typhoid fever globally. Higher incidence of typhoid fever is seen in children (2-5 years), which is aggravated by elevating antimicrobial resistance in Salmonella strains towards first-line antibiotics. The current study amalgamated ligand-based virtual screening, ADMET screening and antibacterial activity prediction to screen out potent lead molecules whose binding affinities (BAs) were recorded against major druggable S. Typhi protein targets, and were compared with that of standard anti-Typhi drugs. The top-docked complexes possessing superior intermolecular affinities were checked for residual-fluctuations through course-grained dynamics simulations. BA assessment revealed deoxy-tetradeutero- curcumin derivative to be a novel bioactive compound having low binding energy (BE) towards UDP-N-acetylmuramate–L-alanine ligase (MurC) protein, one of the major enzymes contributing towards peptidoglycan biosynthesis. From docking and dynamics simulations, it was interpreted that the curcumin derivative (BE with MurC= -8.00±0.02kcal/mol) can be a potent competitive inhibitor of ATP (BE= -7.65±0.19kcal/mol) for MurC-catalytic domain (contributed by Hydrogen bonds and non-canonical interactions) having low relative RMSF (0.59Å) to inhibit MurC-induced peptidoglycan biosynthesis. The lead molecule additionally showed better binding and inhibition profile against MurC than other commercial antibiotics against their corresponding protein targets. The present findings can pave new paths for designing potential therapeutic strategies against S. Typhi.

Keywords: ADMET Screening; Binding Affinity; Binding Energy; Coarse-grained Dynamics Simulation; Typhoid Fever; Virtual Screening.

SESSION - 3

Nanotechnology

NBPP01

Degradation of Phenol Red using Ag-Cu-Zn Tri-Metallic Nanoparticles Derived from Citrus Limetta Peels

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ABSTRACT

The present work proposes a new and eco-friendly methodology of degradation of phenol red through Citrus limetta peel-derived Ag-Cu-Zn tri-metallic nanoparticles. The process for the preparation of the nanoparticles was achieved by using presence of bioactive compounds that are present in the peel extract. Alkaloids and many more available in the peel extract of Citrus limetta, which also acts as reducing and stabilizing agents for the metallic nanoparticles. The synthesized nanoparticles were characterized using UV-visible spectroscopy and FTIR spectroscopy. Based on this study, it can be, therefore, inferred that these nanoparticles can be used as catalysts. Tri-metallic nanoparticles offer superior catalytic activity to single-metal counterparts and offer promising pathways for the treatment of effluent wastewater by organic pollutant removal. In this study,96.59% of phenol red were degraded in 1hr. The green synthesis method presented in this study provides a sustainable and non-toxic synthesis route while simultaneously remediating the environment.

Keywords: Phenol Red Degradation; Citrus limetta peel; Ag-Cu-Zn tri-metallic nanoparticles; Bioactive Compounds; Non-Toxic Synthesis.

NBPP02

Phenol Red degradation using tri-metallic Ag-Cu-Ti Nanoparticles Synthesized using Leaf Extract of Pongamia Pinnata

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ABSTRACT

Pongamia Pinnata is a multipurpose leguminous tree containing a wide range of biologically active compounds rich in flavonoids, terpenoids, phenols, saponins, alkaloids, and vitamins. It has various functional properties such as dye-degradation, anti-inflammatory, antioxidant, antifungal, antimicrobial, anti-lipid oxidative, anti-diarrhoeal, anti-ulcer, and anti-hyperammonic. The plant extract can be used for the synthesis of natural, renewable and low-cost materials. P. pinnata leaf extract can produce metal oxide nanoparticles by using aqueous extract in order to avoid the presence of hazardous substances and toxic solvents that are generally used in case of chemical methods. In this work an eco-friendly methodology of phenol red dye degradation using tri-metallic nanoparticles that were derived from Pongamia Pinnata leaf extract has been reported. The bioactive compounds that are present in the leaf extract were employed in the synthesis of nanoparticles which acts as reducing and stabilizing agents. The synthesized nanoparticles were characterized using UV-visible and FTIR spectroscopic techniques. Further tri-metallic nanoparticles were evaluated for degradation for phenol red dye. It was found that tri-metallic nanoparticles showed 94.60% in an hour degradation of phenol red dye in 1 hour. The green synthesis method presented in this study offers a sustainable and environmentally non-toxic approach.

Keywords: Pongamia Pinnata; Multipurpose Leguminous Tree; Biologically Active Compounds; Dye-Degradation; Tri-Metallic Nanoparticles.

NBPP03

Development and Toxicological Analysis of Metallo-Polyester Hybrid Nanomaterial for Possible Biomedical Use

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ABSTRACT

Metallo-polymer nanocomposites are hybrid nanomaterials, i.e., made up of polymers and metal/metal oxides. These nanomaterials possess polymer (flexibility, processability, solubility, biodegradability, biocompatibility) and metal properties (thermostability, electrical, optical, and catalytic). Due to improved properties, metallopolymer nanocomposites have been extensively used in drug delivery, tissue engineering, biosensing, bioelectronic, bioimaging, and portable bioelectronic applications. In the present study, we have developed a $ZnFe_2O_4$@poly(tBGE-alt-PA) composite by physical method. The obtained nanocomposite was characterized by different physicochemical techniques. FTIR confirmed nanocomposite formation by functional groups of both copolymer and zinc ferrite nanoparticles. XRD showed the crystalline nature of nanocomposite due to the presence of zinc ferrite. TGA displayed the thermostable nature of the composite, while DSC presented no evidence of chemical interactions between the zinc ferrite nanoparticles and the copolymer. Next, the nanocomposite was nontoxic to mouse fibroblast cells and showed no hemolysis at greater concentrations. Further, before their use in healthcare, the nanocomposite was tested for their behavioral, developmental, and morphological impacts on Drosophila melanogaster. The treatment of different doses of nanocomposite was given to both larvae and adult flies, who were permitted to go through their whole life cycle. The treated larvae showed no changes in crawling patterns, suggesting no neurotoxicity produced by the composite. Next, the lesser production of ROS was seen in the nanocomposite-treated larvae's gut during oxidative stress. The treated adult flies showed no changes in their climbing behaviour. Furthermore, no significant deformities were seen in the morphology of adult flies, suggesting the $ZnFe_2O_4$@poly(tBGE-alt-PA) nanocomposite is significantly less or non-toxic to fruit flies. Based on these results, the nanocomposite is currently being used to develop nanocarriers for targeted drug delivery to cancer cells.

Keywords: Metallo-Polymer Nanocomposites; Hybrid Nanomaterials; Metal/Metal Oxides; Thermostability; Biocompatibility.

NBPP04

Ultra-Sensitive Colorimetric Detection of Glutathione in Human Serum Using Peroxidase-Mimic Nanozyme

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ABSTRACT

Glutathione (GSH) is a necessary antioxidant for detoxification and preventing cellular damage to biological components. Abnormal GSH levels are associated with various diseases, such as psoriasis, cardiovascular disease, Parkinson's disease, and cancer. Therefore, developing a sensitive and selective GSH detection method to diagnose these associated disorders is crucial. In this study, we synthesized Cu/SiO2 nanozyme which shows excellent peroxidase mimetic activity to establish a highly precise, inexpensive approach for colorimetric GSH detection. In the presence of hydrogen peroxide (H_2O_2), the nanozyme effectively oxidized the chromogenic substrate 3,3', 5,5'-tetramethylbenzidine (TMB) to produce oxidized TMB (oxTMB), providing a strong blue color and a prominent absorption peak at 650 nm. Furthermore, we optimized the impact of various factors, such as pH, molarity, nanozyme concentration, TMB concentration, temperature, and incubation time to enhance assay performance and achieve the ideal GSH detection parameters. The lowest detection limit attained with this method was demonstrated by the assay's linear response to GSH concentrations between 0.001 and 50 μM. The assay demonstrated a significantly good limit of detection (LOD) of 2.04 μM. The experiment was validated by employing human serum samples with relative standard deviations (RSD) ranging from 1.08% to 5.85% and recovery rates between 101.2% and 104.3%. This study highlights the remarkable potential of Cu/SiO2 nanozyme in biosensing. This sensing assay is an outstanding colorimetric sensor for early detection, due to its high sensitivity, low cost, and reproducible outcome in human serum samples.

Keywords: Glutathione Detection; Peroxidase-like Activity; Cu/SiO2 nanozyme; Human Serum; 3,3', 5,5'-tetramethylbenzidine (TMB).

NBPP05

Fungus Mediated Synthesis of Biogenic Palladium Catalyst for Degradation of Azo Dye

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ABSTRACT

Dyes are the coloured substances that are applied on different substrates such as textiles, leather and paper products, etc. Azo dyes release from the industries are toxic and recalcitrant wastewater pollutants, therefore it is necessary to degrade these pollutants from water. In this study, the palladium (0) nanoparticles (PdNPs) were generated through the biological process and exhibited for the catalytic degradation of azo dye. The palladium nanoparticles (PdNPs) were synthesized by using the cell-free approach i.e. extract of fungal strain Rhizopus sp. (SG-01), which significantly degrade the azo dye (methyl orange). The amount of catalyst was optimized by varying the concentration of PdNPs (1 mg/mL to 4 mg/mL) for 10 mL of 50 ppm methyl orange (MO) dye separately. The time dependent study demonstrates the biogenic PdNPs could effectively degrade the methyl orange dye up to 98.7% with minimum concentration (3 mg/mL) of PdNPs within 24 h of reaction. The long-term stability and effective catalytic potential up to five repeated cycles of biogenic PdNPs have good significance for acceleration the degradation of azo dyes. Thus, the use of biogenic palladium nanoparticles for dye degradation as outlined in the present study can provide an alternative and economical method for the synthesis of PdNPs as well as degradation of azo dyes present in wastewater and is helpful to efficiently remediate textile effluent.

Keywords: Biogenic; Palladium Nanoparticles; Azo Dyes; Wastewater Treatment.

ISSN: 2278-9197 © VSRD International Journals: www.vsrdjournals.com

NBPP06

Cutting-edge Techniques for Heavy Metal Remediation and their Removal Mechanisms

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ABSTRACT

Heavy metals have significantly increased in environment due to the growth of the world's population and industrialization, endangering human health and the environment by contaminating food chain. The environment and public health are seriously threatened by heavy metals such as Chromium, Arsenic, Lead, Mercury, etc. which can lead to cancer, developmental abnormalities, neurological damage, and organ damage. Due to their persistent nature and lack of biodegradability, these hazardous compounds' contamination must be removed from the environment. It is crucial to create economical, environmentally friendly, and effective techniques for treating wastewater that contains heavy metals. Common remediation technologies for heavy metal-contaminated sites include chemical methods such as chemical leaching and oxidation/reduction, bioremediation techniques like phytoremediation, and physical methods such as soil thermal desorption and replacement. Along with that, nanotechnology offers a sustainable solution for future heavy metal remediation as nanomaterials, despite their small size, can economically address some of the challenges associated with traditional site clean-up. Nano remediation, with both in-situ and ex-situ capabilities similar to conventional techniques, has proven to be an effective method for reducing heavy metal contamination in soil, water, and air due to the high specific surface area and reactivity of nanomaterials. Therefore, the present article thoroughly examines various remediation techniques i.e. bioremediation, phytoremediation, and nano remediation for effectively removing heavy metals and treating wastewater, while highlighting recent advancements in environmental research that offer significant potential for addressing pressing challenges. It also provides a comprehensive overview of advanced nanomaterials with a particular emphasis on their remediation mechanisms.

Keywords: Heavy Metals, Contamination, Remediation, Nanomaterials, Techniques.

NBPP07

Microplastic Remediation Technologies from Wastewater Treatment: Current Status and Future Perspectives

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ABSTRACT

Microplastics, (MPs') originate from bigger plastic objects, synthetic fibers, and personal care products, are developing as significant worldwide pollutants. The oceans are becoming pollution sinks, with microplastics being discharged into shorelines, sea surfaces, and deposits. These particles are harmful to both marine ecosystems and human health, producing inflammation, oxidative stress, and endocrine disruption. There is an urgent need to address this issue on a global basis since the manufacturing of plastic and its non-biodegradable, resistant, and persistent qualities are directly correlated with their build-up in the environment. Microplastics can be partly removed using traditional water and wastewater treatment technologies such as sedimentation, filtration, coagulation-flocculation, and activated sludge. These approaches have several disadvantages, including low removal efficiency, high running costs, and difficulty capturing tiny particles, while the variety in size, shape, and chemical composition of MPs further complicates their efficient removal. Therefore, present article summarises cutting-edge research and development in the field of microplastic remediation from wastewater. To enable more successful, scalable, and environmentally friendly remediation of MPs in treatment processes, this discussion addresses the current challenges and potential solutions, including the use of bioremediation and nanofiltration to efficiently remove microplastics. This article attempts to give a thorough foundation for cutting-edge approaches and environmental issues by examining recent research and trends. This will improve our comprehension microplastics accumulation and associated difficulties.

Keywords: Microplastics, Bioaccumulation, Biodegradation, Bioremediation.

ISSN: 2278-9197 © VSRD International Journals: www.vsrdjournals.com

NBPP08

Advancements in Nanobiotechnology for Targeted Drug Delivery

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ABSTRACT

An innovative field with important medical applications is nanobiotechnology, an interdisciplinary combination of nanotechnology and biotechnology. Innovative medication delivery devices can be designed and manufactured by utilizing nanoscale biological principles and engineering approaches. By increasing medication efficacy, decreasing toxicity, and improving patient outcomes, these developments are tackling important issues in traditional medicine.

The creation of nanomaterials like iron oxide nanomaterials, colloidal gold, and quantum dots, as well as nanocarriers like liposomes and polymer-based nanocapsules, are important advancements. These systems are especially useful in treating complicated diseases including cancer and inflammatory disorders because they are designed for accurate medication delivery, controlled release, and high bioavailability. Furthermore, the special qualities of nanomaterials, such as their adaptable size, shape, and surface functionality, which allow them to interact at the molecular level for therapeutic and diagnostic purposes and to pass through biological barriers.

Nanobiotechnology has the ability to completely transform pharmaceutical development, as evidenced by recent advances. Numerous targeted drug delivery technologies that present intriguing answers for gene therapy, biosensing, molecular imaging, and early diagnostics are about to go commercial. This technology, which has advanced quickly over the last ten years, is set to play a major role in medicine's future by fostering important breakthroughs in disease management and individualized healthcare.

In conclusion, nanobiotechnology represents a few frontier in biomedical research, with its applications in targeted drug delivery offering unparalleled potential for advancing human health and transforming medical practices.

Keywords: Nanomaterials; Diagnostic; Targeted Drug Delivery; Cancer.

NBPP09

Industrial Evolution through PHA Biopolyesters

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ABSTRACT

Polyhydroxyalkanoates (PHAs) are biodegradable, renewable biopolymers produced by microorganisms through the fermentation of carbon-rich resources like sugars and plant oils, including palm oil. These bioplastics offer a sustainable alternative to traditional plastics, as they replicate the physical properties of petrochemical plastics but decompose naturally in soil, water, and marine environments, helping reduce plastic pollution.

PHAs are synthesized using renewable feedstocks, such as plant oils, which enhance production efficiency and scalability. Microbial fermentation processes can be optimized to maximize PHA yield from materials like palm oil, soybean oil, and corn oil. These oils provide higher carbon content, which results in higher biomass and PHA production compared to sugars, making the production process more cost-effective.

The use of PHAs offers several environmental advantages, including a significant reduction in plastic waste and greenhouse gas emissions. As these bioplastics are produced from renewable resources, they contribute to a circular economy by being fully biodegradable and reducing the need for fossil fuels. PHA nanoparticles are used in controlled drug delivery systems to enhance bioavailability and solubility by targeting specific sites. Their biodegradable and biocompatible nature makes them ideal for medical applications. These nanoparticles improve treatment efficacy while reducing side effects.

By adopting PHA-based materials, industries can contribute to reducing plastic waste and reliance on fossil fuels. This shift not only supports the development of sustainable products but also promotes circular economy practices, where materials are reused and biodegrade after use, reducing environmental pollution and conserving valuable resources for future generations. Through the widespread adoption of PHAs, industries play a crucial role in advancing sustainable development goals, minimizing ecological footprints, and fostering a cleaner, greener future.

Keywords: Polyhydroxyalkanoates (PHAs), Biodegradable Biopolymers, Renewable Feedstocks, Microbial Fermentation, Controlled Drug Delivery, Biodegradable Nanoparticles Circular Economy.

ISSN: 2278-9197 © VSRD International Journals: www.vsrdjournals.com

NBPP10

Nanotechnology's Role in Overcoming Antimicrobial Resistance Challenges

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ABSTRACT

AMR has become a serious threat at the global level that requires urgent intervention in terms of development of point-of-care technologies. Inadequate diagnostic capacities and delayed diagnoses are attributed to inappropriate use of antibiotics leading to the problems associated with AMR. Most of these factors can be traced back to resource-constrained and overpopulated areas. MDRs, pan-resistant superbugs raise mortality, extend durations of hospital stays, and increase the complexity of treatment for these pathogens that normally tend to produce biofilm leading to decreased treatment effect. The rise of resistant strains and the slow pace of new antibiotic development highlight the urgent need for innovative, rapid point-of-care diagnostic strategies to monitor and manage AMR effectively. The classical methods to combat AMR have not been effective since owing to large turnaround time, i.e., more often, have no chance of finding resistant strains before inappropriate antibiotics are administered promptly. In addition, these techniques cannot efficiently cover limited and overpopulated conditions. The increase in the number of new superbugs MDR- and pan-resistant compounds and superbugs worsens all these challenges in the treatment scenario.

Nanotechnology has transformative potential in dealing with these challenges. Nanoscale materials such as nano-biosensors and nanoparticle-based diagnostic platforms could enable rapid, sensitive, and cost-effective detection of resistant strains even in low-resource settings. In addition, nanoparticle-based drug delivery systems could target biofilm-forming pathogens and increase the effectiveness of treatments while decreasing the use of broad-spectrum antibiotics.

Keywords: Antimicrobial Resistance (AMR); Superbugs; Nano-biosensors; Multidrug Resistant (MDR); Biofilm.

ISSN: 2278-9197 © VSRD International Journals: www.vsrdjournals.com

NBPP11

Data Mining Based miRNA Candidates as Cancer Biomarkers

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ABSTRACT

The number of cancer cases is expected to rise from 20 million in 2022 to 35 million by 2050, making it a major global health concern that will primarily impact low and medium Human Development Index (HDI) nations. Poor survival rates result from late-stage diagnosis due to asymptomatic presentation in early cancer stages and the lack of any cancer screening program. New diagnostic technologies that facilitate early identification and intervention are the need of the hour.

MicroRNAs (miRNAs), small non-coding RNA molecules (18–25 nucleotides), have emerged as promising biomarkers for cancer diagnosis owing to their stability, early expression, and detectability in various body fluids such as plasma, serum, and sputum. These characteristics make miRNAs ideal candidates for integration into nanoscale biosensors for cancer screening.

This study employed a systematic methodology, including comprehensive literature mining and in-silico analysis, to identify specific miRNAs or miRNA panels with diagnostic relevance across various cancer types. miRNAs exhibiting significant dysregulation were identified as potential biomarkers for developing nano-biosensor platform. Such biosensors hold the potential to offer non-invasive, cost-effective, and highly sensitive diagnostic solutions suitable for point-of-care applications.

With the ultimate goal of improving patient outcomes and survival rates, this research opens the door for innovative diagnostic technologies that utilise the specificity and stability of miRNAs to close the gap in early cancer detection.

Keywords: Cancer Diagnosis; MicroRNAs, Nano-biosensor, Biomarkers; Dysregulation.

NBPP12

Bacterial Nanocellulose: Sustainable Innovative Approach for Active and Intelligent Food Packaging to Enhance Shelf Life

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ABSTRACT

Bacterial nanocellulose (BNC) and nanocellulose-based materials have emerged as sustainable and versatile solutions for food packaging and preservation. They address significant challenges in food security and waste reduction. These materials, produced by bacterial species, are sourced from renewable resources and display exceptional physicochemical properties. These include high mechanical strength, biocompatibility, effective gas barrier performance, moisture retention, and antibacterial activity. BNC presents a promising alternative to conventional petroleum-based plastics, which are harmful to the environment and often difficult to recycle. This review focuses on advancements in the synthesis, bioengineering, and functionalization of BNC aimed at developing green, active, and intelligent packaging solutions, as well as coatings to extend the shelf life of perishable foods like fruits and vegetables. Recent improvements using bioactive compounds, nanoparticles, and responsive polymers have led to the creation of antioxidant-releasing films, antimicrobial membranes, and biosensors for monitoring food quality. However, challenges remain regarding scaling up production, ensuring cost-effectiveness, and meeting regulatory compliance. Despite these challenges, BNC- and nanocellulose-based packaging aligns with environmental goals and offers transformative opportunities for food preservation. Collaboration among scientists, regulatory bodies, and industry stakeholders is essential to realizing the full potential of these materials in the food sector and advancing sustainability.

Keywords: Bacterial Nanocellulose, Sustainable, Bioactive Compounds, Antimicrobial Membranes, Biomaterials.

NBPP13

Nanocarrier Systems for Targeted Delivery of Poorly Soluble Phyto-Compounds in the Treatment of Ovarian Cancer

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ABSTRACT

Globally, ovarian cancer accounts for 6.6% of incident cases and 4% of total cancer-related mortalities, according to GLOBOCAN 2022 estimates. Conventional treatment methods, such as bilateral salpingo-oophorectomy, platinum-based chemotherapy, and stereotactic body radiotherapy, have notable drawbacks, including side effects like premature menopause, profound hormonal changes, compromised bone health, and increased cardiovascular risks. Nanotechnology has emerged as a promising solution, facilitating the targeted delivery of antineoplastic agents. Anticancer phytocompounds such as curcumin, resveratrol, quercetin, thymoquinone, berberine, paclitaxel, genistein, ellagic acid, and betulinic acid are widely used in cancer treatments. However, these compounds face challenges such as poor solubility, extensive first-pass metabolism, instability under physiological conditions, low bioavailability, and limited hydrophilicity, hindering their effective delivery. Nanoformulation-based therapeutics, including liposomes, polymeric nanoparticles (such as PLGA, chitosan, and PEGylated nanoparticles), nanostructured lipid carriers, nanoemulsions, inclusion complexes, and solid lipid nanoparticles, have shown great potential in overcoming these barriers. These systems improve the solubility, stability, and targeted delivery of poorly soluble compounds. Recently, polycaprolactone (PCL)/polyethylene glycol (PEG) nanoparticles have gained attention as an innovative approach to enhance the water solubility of hydrophobic drugs. This review provides insights into the nanocarrier-based targeted delivery of these phytocompounds, offering a novel perspective on improving therapeutic outcomes in ovarian cancer treatment.

Keywords: Ovarian Cancer, Phytocompounds, Poorly Soluble, Low Bioavailability, Nanocarriers.

NBPP14

Nanotechnology in the Diagnosis and Therapy of Alzheimer's Disease

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ABSTRACT

Alzheimer's disease (AD) is a neurodegenerative disorder as evidenced by the accumulation of extracellular amyloid plaques that cause degeneration of vulnerable brain regions. To date the drugs available that are marked and approved are still symptomatic and slow down the disease progression but unfortunately do not cure it. The low drug bioavailability caused by the low ability to cross the blood-brain barrier (BBB) hinders the efficacy of the existing therapies. However, nanotechnology has gained immense scientific interest, providing alternative approaches to upgrade AD treatments such as by increasing the drug penetrating efficacy to BBB and drug bioavailability, by drug delivery nanosystems, and by minimizing the adverse effects. The recent progress in nanotechnology has the potential to offer therapeutic solutions on a mass scale. Targeted drug delivery of NPs and nanoparticles (NPs) can penetrate the BBB effectively with few adverse side effects, because of their physical, electrical magnetic, and optical properties nanoparticles possess great potential for nanotechnology in treating AD. Nanotechnology-based drug delivery systems and theragnostic possess the capability to have a highly sensitive molecular detection with effective drug targeting and also their combination. Advances include polymer-based nanostructures, dendrimers, lipid-based nanosystems, antibody-coated NPs, and theragnostics that target biomarkers and deliver anti-amyloid or anti-tau cholinesterase inhibitors Experimental procedures, including light scattering and nonlinear dynamics, help monitor amyloid formation. Nanotechnology has the potential to transform AD treatment and offers a promising approach to address the limitations of current therapies and improve disease control.

Keywords: Alzheimer's Disease, Nanotechnology, Drug Bioavailability, Theragnostics.

NBPP15

Synergistic Benefits of Combining Nanotechnology with Photomedicine in the Treatment of Rheumatoid Arthritis

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ABSTRACT

Rheumatoid arthritis is a systemic autoimmune disease characterized by synovial inflammation. Mostly caused by severe damage to the hands and foot joints which can lead to severe joint deformity and disability to walk. The combination of photomedicine and nanotechnology offers a novel approach to the treatment of rheumatoid arthritis (RA). Particularly low-level laser therapy and photo-biomodulation uses light to stimulate cellular processes, reduce inflammation, and promote tissue healing. Nanotechnology, on the other hand, provides advanced drug delivery systems that enable targeted therapies, improving the precision and efficacy of RA treatments. By integrating these two fields, new therapeutic modalities can be developed to address the complex pathophysiology of RA more effectively. Nanoparticles can be engineered to deliver anti-inflammatory agents directly to inflamed joints, improving drug bioavailability, and minimizing side effects. When coupled with phototherapy, nanocarriers can be activated by specific wavelengths of light, enhancing therapeutic outcomes by modulating inflammation at a cellular level. Moreover, nanotechnology enables the development of multifunctional platforms capable of combining drug delivery, phototherapy, and diagnostic imaging, providing a holistic approach to RA management. This synergy not only promises improved clinical outcomes by targeting multiple RA mechanisms but also holds potential for personalized treatments based on the patient's specific disease characteristics. This review provides potential insights of photomedicine in combination with nanotechnology for inflammatory rheumatoid arthritis

Keywords: Photomedicine, Nanotechnology, Rheumatoid Arthritis, Photo Biomodulation, Targeted Therapy, Therapeutic Modalities.

NBPP16

Nano Formulated Biopesticides: Advances and Future Prospectives

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ABSTRACT

The world faces significant challenges in meeting food security needs, with the global population projected to reach 8.6 billion by 2030. Traditional agriculture heavily relies on synthetic pesticides, but their overuse has led to environmental degradation, soil contamination, and negative impacts on human health. There is a pressing need for more sustainable and environmentally friendly pest management strategies. Hence, a focus on developing environmentally safe compounds and novel delivery methods to reduce pests' population by non-toxic mechanisms, providing a safer alternative and increased end-user adoption. Technological advances, particularly in nanotechnology, offer promising solutions. Nano-biopesticides combine the benefits of biopesticides with the enhanced delivery and efficacy of nanotechnology. These novel formulations demonstrate superior environmental friendliness, rapid action, biodegradability, and targeted delivery. Nano-biopesticides generally show higher pesticidal activity and more targeted or controlled release compared to traditional biopesticides. They have been reported to preserve plant products and oils against quick degradation, allowing them to have a longer-lasting effect on pests. To increase the efficacy of biopesticides, a variety of formulation methods have been proposed, including nano-emulsions, nano-fibres, nano-gels, and nano-capsulations. Thus, Nano-technology is a novel method of pesticide delivery which may strengthen agricultural yields and as a consequence will minimize environmental contamination. While still in development, nano-biopesticides show great potential for addressing the complex challenges in modern agriculture, offering a path towards more sustainable and effective pest management systems.

Keywords: Nano-Biopesticides, Synthetic Biopesticides, Modern Agriculture, Pest Management, Sustainability.

NBPP17

Isolation and Characterization of Amyloid-like Protein Aggregates from White Bread

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ABSTRACT

High temperature, acidic pH, and physical agitation are commonly observed during cooking or industrial food processing, which are favorable conditions for some proteins to misfold and form amyloid-like protein aggregates (APA). The formation of APA in food systems might negatively impact their nutritional properties. The proteins in various bakery products generally undergo high temperatures, which might lead to the formation of APA. To test this hypothesis, the presence of APA in white bread was examined in this study. The protein isolated by the physiological saline extraction method displayed typical characteristics of amyloids, like the bathochromic shift in Congo red (CR), increased fluorescence of Thioflavin T (ThT) & 8-anilino-1-naphthalene sulfonic acid (ANS), more than 200 nm fibrils in TEM analysis and negative minima at 223 nm in Circular Dichroism were observed. The SDS-PAGE and native PAGE revealed the presence of gliadin content in the aggregated protein. The presence of amyloid-like structures in one of the most typical foods, such as bread, consumed by people of all ages, escalates some health concerns and needs to be addressed in a scientific manner.

Keywords: Amyloid; Protein Aggregates; Amyloid-like Protein Aggregates; Food Processing; Physiological Saline Extraction.

ISSN: 2278-9197 © VSRD International Journals: www.vsrdjournals.com

NBPP18

Nanobots in Therapeutics: Biomolecular Machines for Targeted Medical Interventions

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ABSTRACT

Nanobots, nanoscale biomolecular machines, are a revolutionary advancement in precision medicine, of ering transformative capabilities in diagnostics and therapeutics. Engineered to traverse complex physiological environments, such as the bloodstream and cellular matrices, these devices utilize advanced propulsion mechanisms, including magnetic fields, chemical gradients, and biohybrid systems. Their precision enables targeted drug delivery, real-time diagnostics, and minimally invasive interventions, surpassing traditional medical approaches by minimizing of -target ef ects and enhancing therapeutic eficacy. Key applications include oncology, where nanobots deliver chemotherapeutics directly to tumor sites, reducing systemic toxicity, and regenerative medicine, where they promote tissue repair and enable gene therapy. Their potential in theranostics-simultaneously diagnosing and treating conditions—further underscores their versatility. Despite these advancements, significant challenges persist, such as ensuring biocompatibility, achieving sustainable power sources, scaling manufacturing processes, and addressing ethical considerations regarding their long-term implications in humans. Recent interdisciplinary advancements integrating artificial intelligence, nanomaterials, and bioengineering have augmented the functionality and adaptability of nanobots, while also paving the way for overcoming existing technical barriers. This review examines the latest progress in nanobot design, powering mechanisms, and medical applications, alongside critical evaluation of technical and ethical challenges. With continued innovation in nanotechnology, material sciences ,and biomedical engineering, nanobots are poised to redefine therapeutic paradigms,of ering precise, patient-specific solutions to complex medical challenges and establishing themselves as a cornerstone of future precision medicine.

Keywords: Nanobots, Precision Medicine, Targeted Drug Delivery, Biomolecular Machines, Regenerative Technology.

NBPP19

Expanding Horizons of Nanosensors: Innovations in Precision Diagnostics, Agriculture and Industrial Applications

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ABSTRACT

The integration of nanosensors in biotechnology has opened new frontiers in precision diagnostics, environmental monitoring, and industrial applications. These technologies leverage the unique properties of nanomaterials and biomolecules to enable highly sensitive, specific, and real-time monitoring of biological and chemical processes. While widely recognized for their role in healthcare and environmental sciences, emerging applications of nanosensors remain under-explored in the field of food, agriculture and Industrial production.

One such innovation is the oxygen nanosensor used in meat packaging to monitor oxygen levels, ensuring optimal storage conditions and extending shelf life. Similarly, glucose nanosensors are being explored to regulate fermentation processes in bioethanol production, enhancing yield and efficiency. In agriculture, biosensors employing nanomaterial-based platforms are being developed to detect plant stress caused by pathogens or environmental factors, enabling precision farming practices. In synthetic biology, nanosensors integrated with microbial systems are facilitating real-time monitoring of metabolic flux, streamlining the production of bio-based chemicals.

Furthermore, advancements in wearable biosensors are revolutionizing personalized healthcare by tracking biomarkers such as cortisol for stress management and lactate for athletic performance optimization. In marine ecosystems, nanosensors are under development to monitor nutrient levels and toxic contaminants, promoting sustainable aquaculture. These emerging technologies showcase the versatility of nanosensors in tackling global challenges and driving innovations across diverse sectors.

This review will highlight novel applications, emphasizing their transformative potential while addressing the challenges of scalability, affordability, and regulatory compliance. By exploring the untapped possibilities of nanosensors, this study aims to inspire further research and innovation in the biotechnology landscape.

Keywords: Precision Diagnostics, Environmental Monitoring, Industrial Applications, Nanosensors, Sustainable Aquaculture.

NBPP20

Technological Advancements in Detection of Antimicrobial Resistance

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ABSTRACT

Antimicrobial resistance (AMR) is a growing menace and is considered to be a global public health concern. The over exploitation of antibiotics is responsible for the emergence of "superbugs". These superbugs are resistant to a multitude of antibiotics which is an imminent threat to critically ill patients. In patients with a weakened immune system, intensive antibiotic therapy is a pre-requisite, thereby, significantly increasing the risk of AMR. It has been estimated that AMR will lead to close to 1 million deaths by 2050, necessitating the need for AMR surveillance. Conventional, culture based and biochemical tests are laborious and time consuming, and exhibit low sensitivity and specificity, especially in AMR detection. In addition, non culturable pathogens (VBNCs) and polymicrobial infections cannot be detected by these techniques, further compromising therapeutic decision making. Advances in genomics, proteomics, nanotechnology, bioinformatics tools have led to the development of techniques which can lead to AMR detection with improved sensitivity and specificity. Molecular techniques like nucleic acid amplification technology, polymerase chain reaction (PCR) and multiplex PCR, qRT-PCR, PCR-RFLP etc are known to be much more effective in comparison to phenotypic assays having much faster response times in response to new resistance factors. However, the major disadvantage being trained manpower requirement along with time and cost intensive. Techniques like rapid microbial methods, next generation sequencing, automation and high throughput technologies, biosensors, DNA microarrays, flow cytometry etc are extensively being explored for AMR detection. They allow quick prediction of AMR strains, and offer advantages like multiplexing of pathogens, rapid diagnosis, cost effectiveness, improved accuracy and sensitivity etc. This review highlights the latest technologies which are being employed for the diagnosis of AMR, along with their advantages and limitations. The effective detection of antimicrobial resistance will revolutionize the healthcare industry, significantly improving standards of living and critical care.

Keywords: Antimicrobial Resistance, Multiplex, Polymerase Chain Reaction, Nanotechnology, Biosensors.

NBPP21

Revolutionizing Ocular Drug Delivery: The Role of Lipid-Based Nanocarriers in Treating Ocular Diseases

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ABSTRACT

The intricate ocular anatomy and physiological barriers, including the cornea, conjunctiva, and retina, make it extremely difficult to deliver therapeutic substances to the eye. The efficacy of traditional drug delivery techniques, such as eye drops and ointments, in treating ocular conditions such glaucoma, dry eye syndrome, macular degeneration, and diabetic retinopathy is limited by their poor bioavailability, quick clearance, and low patient compliance. Treatment results are further complicated by elements including the blood-aqueous barrier and the tear film, which prevent drugs from penetrating target tissues. A potential remedy for these issues has been provided by the development of drug delivery systems based on nanocarriers, especially lipid-based nanocarriers. Therapeutic drugs' solubility, stability, and bioavailability can all be improved by lipid-based nanocarriers, allowing for tailored distribution with few systemic adverse effects. By enhancing drug release profiles and providing a more accurate and long-lasting therapeutic effect, these systems have demonstrated considerable promise in the treatment of a variety of ocular disorders. This review investigates the design concepts, manufacturing processes, drug release mechanisms, preclinical and clinical results, and possible applications of lipid-based nanocarriers in ocular pharmacotherapy. The goal is to present a thorough analysis of lipid-based nanocarriers, emphasising how they are transforming the distribution of drugs into the eyes and providing information on potential directions for further study to enhance patient outcomes and treatment effectiveness.

Keywords: Nanomedicine; Glaucoma; Pharmacotherapy; Nanoemulsions; Blood-Aqueous Barrier.

NBOP02

Quercetin Nanoparticles Mitigate Key Hallmarks of Lung Cancer in-vitro: A Comprehensive Evaluation of its Anti-Cancer Potential

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ABSTRACT

Lung cancer remains a leading cause of global mortality due to challenges in early detection and the limited effectiveness of current treatments, highlighting the need for novel therapeutic strategies. Quercetin, a flavonoid found widely in global flora, shows promising anti-cancer properties. However, its clinical application is hindered by poor bioavailability and stability. Nanotechnology-based formulations offer a potential solution to enhance quercetin's delivery and efficacy. This study investigates the anti-cancer effects of quercetin nanoemulsion on A549 cells. Comparisons were made between quercetin nanoemulsion and pure quercetin at various concentrations. Cell viability was assessed via MTT and crystal violet assays, and cell migration was evaluated using scratch-wound and trans-well chamber assays. A protein array and qPCR were employed to analyse the expression of cancer-related proteins and genes. The nanoemulsion significantly reduced A549 cell viability at 25 µM and lowered cell migration and colony formation. Protein analysis revealed changes in proteins like IL-6, VCAM-1, and Angiopoetin-1, linked to cancer progression. qPCR showed downregulation of BRAF and KRAS genes, key in lung cancer. Quercetin nanoemulsion demonstrates potent anti-cancer activity in A549 cells, likely due to enhanced cellular uptake and bioavailability. These findings support quercetin as a promising candidate for lung cancer treatment. Further preclinical and clinical studies are needed to evaluate its therapeutic potential and safety.

Keywords: Quercetin; Lung Cancer; COPD; Asthma; Nanoemulsion.

NBOP03

Use of Flavonoid-Encapsulated Chitosan Nanoparticles as Therapeutic Targets for Immunomodulation of Glioblastoma

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ABSTRACT

Glioblastoma (GBM) is the most common and aggressive form of central nervous system malignancy, also known as grade IV astrocytoma. Patients have a median survival of 11-15 months after surgery, radiation, and temozolomide chemotherapy. The treatment of brain tumors is particularly challenging due to their location and the constraints imposed by the blood-brain barrier (BBB). In recent years, nanoparticles (NPs) have garnered significant attention in medicine, emerging as a promising approach for drug development. Due to their controlled drug release and high tumor-targeting efficiency, nanoparticles are extensively utilized in developing drug delivery systems. Several types of NPs have emerged as promising candidates for enhancing drug penetration across the BBB. In our research, we are using polymer-based (chitosan NPs) which a naturally occurring linear polysaccharides and attracting much attention due to their diverse physicochemical properties, such as biodegradability, biocompatibility, and non-toxicity, which play a promising role in biological applications, including medicines and biomedical engineering. Our approach involves encapsulating flavonoids, the plant's secondary metabolites known for their anti-cancer, neuroprotective, anti-oxidative, and immunomodulatory properties in chitosan nanoparticles. This study presents the synthesis of chitosan-based NPs encapsulating flavonoids via the ionic gelation technique, optimized for effective drug delivery. We confirmed the antioxidant activity of the flavonoids using the DPPH (2,2-diphenyl-1-picrylhydrazyl hydrate) free radical assay and optimized the chitosan-flavonoid NPs for encapsulation efficiency and controlled drug release at various time intervals. Following encapsulation, we further confirmed the scavenging activity of the flavonoid-encapsulated chitosan NPs using the same DPPH assay. Additionally, we evaluated the cytotoxicity of flavonoid-encapsulated chitosan NPs on glioblastoma cell lines. Moving forward, we will investigate the immunomodulatory role of these flavonoid encapsulated NPs in glioblastoma and immune cells. We believe that combining nano-therapy and immunotherapy could yield a more effective therapeutic agent against deadly glioblastoma.

Keywords: Glioblastoma; Chitosan nanoparticle; Flavonoid; Antioxidant; Immunomodulation.

NBOP05

Formulation Approaches for Nose-to-Brain Drug Delivery

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ABSTRACT

Nose-to-brain (NTB) drug delivery has emerged as a promising strategy in treating central nervous system (CNS) disorders. NTB drug delivery is a novel approach that utilizes the olfactory and trigeminal nerves to transport drugs directly from the nasal cavity to the brain, bypassing the blood-brain barrier. The BBB is a highly specialized and selective structure that safeguards the CNS by controlling the movement of substances from the bloodstream into the brain and spinal cord. BBB acts as a vital defense mechanism, preventing the entry of potentially harmful molecules while permitting essential nutrients and gases to pass through, ensuring the maintenance of brain homeostasis. Nanocarriers have gained significant attention due to their ability to improve the effectiveness and precision of drug delivery. These nanocarriers are designed to cross the BBB and deliver drugs in a controlled manner, with the ability to be customized for improved penetration and targeted brain delivery. This review explores the potential of nanocarriers in enhancing drug delivery via the nasal pathway, highlighting recent advances, challenges, and future prospects in this field. By understanding current knowledge and identifying gaps, this review aims to inspire further research and development in nanocarrier-based nose-to-brain drug delivery systems, ultimately advancing therapeutic interventions for neurodegenerative diseases, brain tumors, and other CNS disorders.

Keywords: Nanocarriers, Drug Delivery, CNS, Neurodegenerative Diseases, Nose-to-brain (NTB).

NBOP06

Exploring Nanocarriers for Enhanced Wound Healing

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ABSTRACT

Wound can be defined as a damage to the skin, mucous membrane, tissue and even organs with impaired healing. Wounds can be divided into two categories acute and chronic wound depending upon the severity and healing time. Generally healing of these wounds involves phases like hemostasis, inflammation, proliferation, and tissue remodeling. In cases of acute wound, body shows normal healing while chronic wounds show delayed healing due to several factors like severe damage to tissue or organ, already existing diseases in the body which have continued to be a major problem in clinical treatment, even with advanced healing treatment options. To overcome the issue many advance research studies have surfaced recently amongst which nanotechnology has shown greater potential and innovative role in chronic wound healing. Nanocarriers like drug loaded hydrogel, electrospun nanofibers, heterojunction biofilm, polymeric nanoparticles, offer targeted and controlled drug delivery, thereby improving bioavailability and reducing the associated side effects. In order to promote tissue regeneration and healing, these nanocarriers can be designed to carry therapeutic agents such as growth factors, antibiotics, and antioxidants directly to the wound site. In recent advanced studies Electrospun nanofiber has shown the ability t deliver drugs to the the wound site via nanofiber dressings due to their high surface area-to-volume ratio and their structural resemblance to the extracellular matrix, which encourages cell adhesion, proliferation, and tissue regeneration. This allows for localized treatment that promotes healing and reduced side effects. Therefore, it can be concluded with the literature, that nanocarriers offer a revolutionary approach to wound care that holds great promise for improving patient care and therapeutic results.

Keywords: Wound Healing, Nanocarriers, Tissue Regeneration, Drug Delivery.

NBOP07

Nano formulation of Gelatin biopolymer with Anti-Cancer Drug for Treatment of Pancreatic Ductal Adenocarcinoma

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ABSTRACT

Cancer is a leading cause of mortality world-wide. Despite rapid advances in treatment modalities there has been little change in cancer death rate. Nano approaches are revolutionizing cancer drug development for better targeting and drug delivery. In the present work nano formulations (NFs) with anticancer drug were prepared by using biodegradable polymer. For the selection of polymer and drug, in-silico studies have been performed, which includes Molecular docking analysis of the different available biodegradable polymers with FDA approved anticancer drugs. The selection of polymer for experimental validation has been done by picking the best docking score between the polymer (gelatin) and drug (Gemcitabine). NFs of Gemcitabine (available first line therapy drug for pancreatic cancer) with gelatin polymer (Gem-Gel NFs) were prepared by double dissolvation method in different concentration of gelatin. These NFs were characterized by using different analytical techniques, revealing Nano-drug Formulations (NDF) formation between the wavelength range of 250-380nm showing ~300nm mean diameter with narrow poly dispersity index (0.51) and higher zeta potential values for the formulations. Fourier Transfer Infrared Spectroscopy (FTIR) and Transmission Electron Microscopy (TEM) were performed for morphological analysis. The experimental work has resulted in the Gem-Gel NFs with improved efficacy of the drug keeping the validation of synthesized NFs for in vitro as future aspects.

Keywords: Biodegradable Polymer; Anticancer Drug; Gelatin Nanoparticles; Nano Formulations; Pancreatic Cancer.

ISSN: 2278-9197 © VSRD International Journals: www.vsrdjournals.com

NBOP08

Graphene-Dielectric THz Biosensor for COVID-19 Detection

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ABSTRACT

In this paper, a dielectric-graphene based resonance mechanism is illustrated. The proposed structure constitutes a three-layered geometry with gold as a metal reflector situated at the bottom. The patterned silicon mounted on top acts as a resonator following the waveguide model. The dielectric, SiO_2 *sandwiched between gold and silicon layers acts as a cushion absorbing the Electromagnetic radiation. The resonance of graphene by virtue of generation of surface plasmons brings the tunability aspect to the proposed device. The patterned arrangement of silicon and graphene provides the* $\approx 100\%$ *at the resonant frequency characterized by the dip of reflection coefficient. The proposed biosensor has ultrathin geometry of the order of* $\lambda/40$*. The biosensor is polarization insensitive due to symmetricity in design configuration. The COVID-19 sample is placed in the simulation environment and change in the absorption spectra is recorded with high sensitivity (S), figure of merit (FOM) and ultranarrow FWHM to detect even the minute difference in refractive indices between healthy and COVID-19 affected samples. The tunability in design helps in detecting multiple diseases at different resonant frequencies.*

Keywords: Resonance; Ultrathin; Tunable; Full-Width at Half Maximum (FWHM), Figure of Merit (FOM); Ultra-Narrowband; Metasurface.

NBBS02

Sustainable Synthesis of Nanomaterial: Application for Single Pot Multicomponent Reactions

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ABSTRACT

Nanocatalysis is a promising area that has attracted the attention of chemist over the years. A functionalized material with nano- or submicro-dimension demonstrates significant and dramatic catalytic activity in comparison to their bulk counter parts, due to the increased surface area and multiple catalytic centers and in turns fulfils the mandate of green chemistry. Increasing aspects of catalytic potential of nanocatalyst in the synthesis of heterocycles, we recently reported hierarchically porous sheet-like copper aluminum mixed oxide (CuAl-MO) nanocatalyzed synthesis of substituted pyrrolidines/piperidines. In another study we, displayed the catalytic potential of amine functionalized silica coated magnetically recoverable palladium nanoparticles i.e. Pd@Co/C-SiO_2-NH_2 for the hydrogenation of nitro-arenes/alkenes/alkynes. We also developed powdered wurzite phased copper indium sulphite nanocomposites i.e PW-CIS500 for the sustainable synthesis of substituted imidazopyridines. In continuation to these exciting results, we designed a unique copper/palladium based nanomaterial for various organic transformation reactions such as hydrogenations, cycloisomerization reactions etc. providing better and greener results. Many important heterocycles are synthesized by making use of this methodology e.g. benzofuran, substituted piperidines/pyrrolidines, imidazopyridines etc. The present methodology has several advantages over the reported methods such as selectivity in product formation, high yields in short reaction time, and follows green principles.

Keywords: Nanomaterial; Hydrogenation; Imidazopyridines; Pyrrolidines; Piperidines; Recyclability.

NBBS03

Graphene-Dielectric THz Biosensor for COVID-19 Detection

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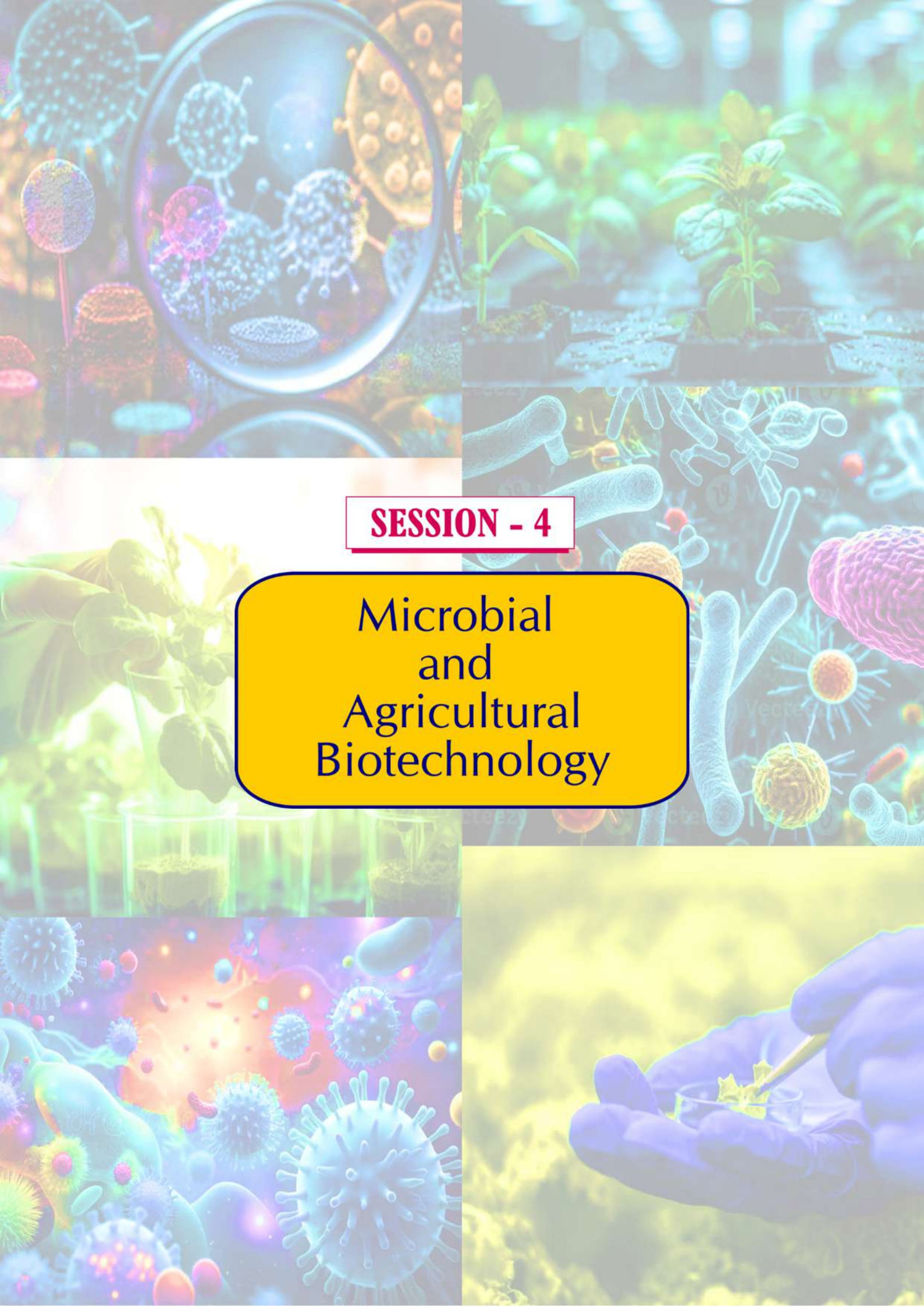
ABSTRACT

In this paper, a dielectric-graphene based resonance mechanism is illustrated. The proposed structure constitutes a three-layered geometry with gold as a metal reflector situated at the bottom. The patterned silicon mounted on top acts as a resonator following the waveguide model. The dielectric, SiO_2 sandwiched between gold and silicon layers acts as a cushion absorbing the Electromagnetic radiation. The resonance of graphene by virtue of generation of surface plasmons brings the tunability aspect to the proposed device. The patterned arrangement of silicon and graphene provides the ≈100% at the resonant frequency characterized by the dip of reflection coefficient. The proposed biosensor has ultrathin geometry of the order of λ/40. The biosensor is polarization insensitive due to symmetricity in design configuration. The COVID-19 sample is placed in the simulation environment and change in the absorption spectra is recorded with high sensitivity (S), figure of merit (FOM) and ultranarrow FWHM to detect even the minute difference in refractive indices between healthy and COVID-19 affected samples. The tunability in design helps in detecting multiple diseases at different resonant frequencies.

Keywords: Resonance; Ultrathin; Tunable; Full-Width at Half Maximum (FWHM), Figure of Merit (FOM); Ultra-Narrowband; Metasurface.



SESSION - 4

Microbial and Agricultural Biotechnology

MAPP02

Creating Broad-Spectrum Disease Resistance Against Rice Blast by The Introduction of a Non-Host Resistance Gene from Arabidopsis into Rice

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ABSTRACT

Rice is the essential cereal crop that forms a major part of the human diet and is hence popularly called "Global grain". With the increasing trend of the rising human population, it's high time to have crops with high yield potential and stability. Making the rice-based production system sustainable is crucial for the future food security of mankind. Rice blast is one of the fungal diseases that hamper the rice crop production by farmers, which could feed 6 million people a year. Rice blast is generally observed in the area where rice is cultivated. However, farmers' use of chemical pesticides to curtail the infection helps the pathogens evolve into new races with enhanced resistance, affecting the environment greatly. Non-host resistance genes from the evolved plant in nature provide broad spectrum resistance as they can resist all forms of pathovars (Heath, 2000). Arabidopsis is immune to M. oryzae and is considered a nonhost plant possibly due to functional nonhost resistance genes in it (Park et al., 2009, Nakao et al., 2011). Following forward genetics, we identified that mutation as SNP in an NHR gene, MOSA in Arabidopsis leads to a breach in nonhost resistance against rice blast. Further, from a screening of 14 mutants of Arabidopsis, we identified that SNP mutation in specific genes also breached NHR against rice blast. We aim to create transgenic rice by introducing one of the screened genes from the mutant Arabidopsis via the Agrobacterium-mediated gene transfer method in the embryogenic elite cvr rice calli. Further, evaluating the promoter activity of the identified NHR gene upon infection in this transgenic line would delineate the plausible mode of genetic control in the activation of nonhost resistance against non-adapted pathogens that can be used in generating novel germplasm.

Keywords: Non-Host Resistance; Rice Blast; Agrobacterium; Embryogenic; Transgenic.

MAPP03

Study on the Role of SlMBD15 (Methyl CpG Binding Domain Protein) in Tomato Fruit Ripening

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ABSTRACT

Methyl CpG binding domain (MBD) proteins are the readers of DNA methylation marks and help in the recruitment of chromatin-modifying enzymes which in turn affects gene expression. A total of 18 genes encoding MBD domain-containing proteins have been identified in the tomato genome. The involvement of the tomato MBDs in fruit ripening and abiotic stress responses has been reported previously.The present study focuses on deciphering the role of SlMBD15 in fruit ripening in Solanum lycopersicum. We prepared binary vectors for fruit-specific over-expression and artificial microRNA-based silencing of the SlMBD15 in tomato. To generate the overexpression and silencing construct of the SlMBD gene, binary vector pCAMBIA2301 with fruit specific promoter (RIP1) and NOS terminator was used. For Transient Expression Assay, the construct containing the MBDs and pCAMBIA (empty vector) was transformed into agrobacterium GV3101 and injected into the fruits of mature green stage to analyse the effect of SlMBD15 on ripening physiology at different stages. The fruits were observed for 10 days and the assessment of fruit firmness, lycopene content in the fruit tissues, and Real-time Q-PCR analysis of ripening associated genes was performed. To know the sub-cellular localization of SlMBD15, the gene was cloned into Binary Gateway vector pSITE-3CA. The construct was transformed into agrobacterium GV3101 and injected into 4-week-old tobacco leaves and SlMBD15 was found to be localized mainly in the nucleus. Further molecular and phenotypic analysis will reveal the role of SlMBD15 in tomato fruit ripening.

Keywords: MBD; Tomato; Ripening; Methylation; pCAMBIA2301.

MAPP04

Novel Insight of Bacterial Consortia and Its Application in Bioremediation

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ABSTRACT

Pollution is the greatest threat to humanity as well as the main factor in environmental sickness and mortality. Different wastes like agricultural, industrial, medical, electronics/e-waste etc. when discharged untreated, causes impairment to the ecosystem. Every year a massive 2.12 billion tonnes of wastes were dumped globally out of which biological waste accounts for 5.9 million tonnes. Pathological waste, infectious agent like cultures, stocks, infected animal carcasses, and biotechnological by-product effluents etc. are all included in the category of biological waste. The 3-R technology used with biological waste management is by reducing the amount of garbage produced, selling plastic, paper, glass, and metal scrap to recyclers, and increasing the potential of recyclable waste by reducing the environmental threats. Over the last few decades, microorganisms have played a significant role in breakdown of pollutants in beneficial and eco-friendly ways for a sustainable environment. In reaction to environmental stressors, it gives microbial consortia resilience to carry out intricate tasks as compared to a solitary microbe to attain. Many microbial synergic enzymes are responsible for the cessation of the majority of biologically harmful pollutants. Microbial consortia such as Bacillus sp.. Trichoderma sp., Azotobacter sp., Pseudomonas etc. are being evaluated as a whole catalyst in the breakdown of biological waste. It shortens the period of disintegration, dilapidation and yields very negligible to no secondary contaminants. Novel insights of biological waste remediation by emphasizing the crucial role of microbial consortia will help us to enhance the understanding and to acknowledge the microbial degradation of biological wastes in a more effective manner.

Keywords: 3-R; Biocatalyst; Pollution; Bioremediation; Biological Waste; Pseudomonas, Incineration; Microbial Consortia.

MAPP05

Formulation and Characterization of Biodegradable Biocomposites from Banana Peel-Derived Pectin with Plant Extract Integration for Sustainable Antimicrobial Application

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ABSTRACT

Banana peel is one of the most abundant lignocellulosic biowastes which is primarily made up of cellulose, hemicellulose, lignin, pectin, and other extractives in varying proportions worldwide. The present study described sustainable waste management by an innovative sequential biorefinery approach. The high yield with good quality commercial products pectin was found to be 11% and the structural characterization of extracted pectin using Fourier Transforms Infrared (FTIR), Scanning Electron Microscope (SEM), and X-ray diffraction (XRD) revealed the chemical and surface structure. Banana peel-derived pectin enriched with the different concentrations of Tridax procumbens leaf extract ranging from 0.1-2% and were formulated and examined for their physiochemical properties. The moisture content, thickness, water solubility, and water vapor permeability of the biocomposite increased, while the tensile strength dropped with the integration of leaf extract. The FTIR, XRD, and SEM confirm the chemical, surface morphology, and successful casting of the film, while the contact angle reveals the biocomposite has the properties of hydrophilicity in a concentration-dependent manner. The formulated biocomposite with different concentrations of plant extract formed effective UV barriers. Moreover, the bio composite not only demonstrates strong antimicrobial activity against Bacillus sp. PhNs9, Pseudomonas sp. PhNs10, Enterobacter sp. Etk3 and E. coli compared to other bacterial species but also enhances its biodegradability up to 91% during 28 days of soil degradation test. The developed films provide an eco-friendly packaging solution for the packaging industries, combining innovation with sustainability.

Keywords: Banana Peel Pectin; Biocomposite; Biodegradation; Antimicrobial Activity; Plant Extract.

MAPP06

Unravelling of the Essential Oil Biosynthesis and Underlying Molecular Regulatory Processes in the Genus Cymbopogon through Transcriptomics Approach

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ABSTRACT

The genus Cymbopogon is recognized as one of the most significant producers of essential oils from commercial perspectives. Essential oils of C. flexuosus, C. citratus and C. martinii are extensively used in fragrance, perfumery, food and pharmaceuticals. However, many aspects of essential oil biosynthesis and regulation remain poorly understood in this genus. Recently, the sequencing and analysis of transcriptomes of several species of Cymbopogon made significant advancements in understanding essential oil biosynthesis and regulation. Currently, transcriptome sequence data of C. flexuosus, C. pendulus, C. martinii, and C. winterianus are available. Their sequence data provided comprehensive insights into the genes associated with monoterpene biosynthesis and their differential expression patterns. This has enhanced our comprehension of the molecular mechanisms that control and regulate essential oil biosynthesis by identifying relevant genes and transcription factors involved in monoterpene metabolism. Furthermore, comparative analyses of transcriptomes of these species have elucidated variations in essential oil composition and content, as well as candidate genes implicated in the synthesis of monoterpene alcohols, aldehydes, and acetates. In addition, transcriptome sequencing has suggested that despite the complexities in the Cymbopogon species, significant insights into essential oil biosynthesis and regulation can be gained.

Keywords: Cymbopogon; Essential Oil; Monoterpenes; Transcriptomes; Biosynthesis; Regulation.

MAPP07

Non-Host Disease Resistance against Rice Blast by Programmed Cell Death in Arabidopsis

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ABSTRACT

A significant rice disease known as "rice blast" can reduce crop yield by up to 30%, which has an impact on world food security. Numerous investigations into finding the genes responsible for disease resistance in previously resistant cultivars failed to find a solution to eradicate the illness from the field. Nonetheless, certain plants found in nature are known to be non-hosts and are not afflicted by the rice blast pathogen. In opposition to a pathogen race, a non-host plant offers broad-spectrum disease resistance. The increasing effector repertoire actively participates in suppressing both effector- and pathogen-triggered immunity during non-host resistance (NHR). A coordinated process of communication and coordinated cell death is initiated between the infected single cell and nearby cells. The NHR pathway causes hypersensitive reactions such as oxidative bursts. Therefore, the focus of the current work is on pertinent Arabidopsis mutants that were examined and found to be homozygous using molecular markers. Thereafter, the plants were challenged with the rice blast fungus, and staining and microscopy were used to examine the infection dynamics. To assess the infection's severity, an ion leakage assay was conducted. Concurrently, by comparing the oxidative burst, ion leakage, and cell death studies, it may be possible to identify the active agents from the non-host, which will enable further research into the potential use of these agents against rice blast disease. In addition, the cell death pathway will be examined to determine whether it is relevant to the host.

Keywords: Rice Blast; Non-Host Resistance; Programmed Cell Death; Hypersensitive Response; Oxidative Burst.

MAPP08

Chromium-Reducing Bacteria Mediated Biopriming: Exploiting a Sustainable Strategy for Immunity Against Blast and Remediating Chromium Stress

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ABSTRACT

Rice production is vulnerable to a number of pressures; one of the main biotic stresses is blast disease, which is brought on by Magnaporthe oryzae and has the potential to wipe out the entire crop under extreme circumstances. Microbial-mediated seed and root prime in plants enhance defense against a broad range of pathogens by jasmonate (JA) and ethylene (ET) signaling mediated induced systemic resistance (ISR). The present work demonstrates some selected microbes like Bacillus cereus, Pseudomonas aeruginosa, Staphylococcus gallinarum, Staphylococcus hominis, and Enterobacter cloacae show an antifungal effect against the rice blast pathogen (Magnaporthe oryzae). Rice (Swarna) seed and root priming with these bacteria enhance ISR in rice against rice blast disease. The MYB transcription factor gene MYB72 together with NPR1, NPR3, and NPR4 genes function as long-distance ISR signaling molecules that are highly expressed in the rice (Swarna) root by co-cultivation with the bacteria in the rice's rhizosphere. These bacteria also resist ~1100 ppm of chromium stress and reduce around 88.94% of Cr^{6+} to Cr^{3+} within 50 days in chromium-contaminated soil. Because Cr^{3+} has a reduced ability to enter cells, it is less poisonous than Cr^{6+}, which is more toxic and soluble and can be transported to cells more easily. The carcinogenic and mutagenesis properties of hexavalent chromium Cr^{6+} make it a particularly dangerous substance. Overall, these bacteria act as a key factor against both abiotic and biotic stresses.

Keywords: Rice Blast, Microbial Priming, Antifungal Effect, Chromium, Bioremediation.

MAPP09

Probiotic Bacteria: A Multi-Ferrous Weapon to Treat Metabolic Disorders and Abnormalities

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ABSTRACT

Probiotics bacteria offer promising health benefits for human well-being and also represent a useful approach to treat several metabolic abnormalities. However, due to limits in the production and development of advanced probiotics, there is huge demand to discover new microbes that can be used as traditional probiotics. In the past, consumption of probiotics was shown to be effective in obesity, T2DD (type 2 diabetes), NAFLD (non-alcoholic fatty liver disease), acute and antibiotic-associated diarrhea, allergic disorders, etc. However, even with these successes, the mechanistic insight of strain-specific probiotic action is still unknown. Therefore, use of recent genetic engineering approaches for engineering the probiotic bacteria for various applications like food, health, and biomedical application will emerge as an advanced therapeutic tool which will also boost the economy of the country. In the present chapter, we aimed to analyze the mechanisms of probiotic action, their role in host immunity, physiological effects, and also new directions which will be certainly helpful for development of next-generation probiotics. We also tried to address biological tools in combination with clinical and preclinical studies to unravel the molecular mechanism of action and discover an ideal multifunctional probiotic bacterium.

Keywords: Amyloid Proteins; Biomedical Applications; Clinical Trials; Metabolic Abnormalities; Probiotics.

MAPP10

ACC Deaminase Producing Plant Growth Promoting Rhizobacterium Enterobacter Cloacae ZNP-2 Enhance Salinity Stress Tolerance in Wheat Plant

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ABSTRACT

Increasing soil salinity adversely affects plant growth and productivity. However, some salt-resistant rhizosphere bacteria have the potential to improve plant growth under salt stress. Among ACCD-producing bacteria isolated from the rhizosphere of plants growing in saline desert soil, ZNP-2 was selected based on its ability to produce phytohormone and ammonia, and solubilize phosphate, and further identified as Enterobacter cloacae. Furthermore, we evaluated the protective effects of the inoculation of Enterobacter cloacae ZNP-2 on morphological and physiological growth parameters, ionic balances, accumulation of osmolytes, and antioxidative defense system under both normal and salt stress conditions. The presence of AcdS, the structural gene for ACC deaminase in Enterobacter cloacae ZNP-2 was confirmed by the polymerase chain reaction. Increased salt stress resulted in the accumulation of toxic Na^+ content and a decrease in K^+ content, however, inoculation with ZNP-2 significantly decreased the level of Na^+ (25% to 55%) and improved the K^+ content (29% to 39%), thereby favoring the K^+/Na^+ ratio. Moreover, ZNP-2-inoculated plants showed improvements in biomass (13% to 31%) and chlorophyll contents (25% to 51%) as compared to the un-inoculated plants. ZNP-2 inoculation also improved the various osmolytes in wheat plants to maintain the osmotic balance. The observation implies that ZNP-2 isolate augments salt tolerance in wheat plants by modulating the intracellular level of various osmolytes. Therefore, the utilization of beneficial microbial isolate as a mechanism for inducing salt tolerance in wheat plants could be used as an effective tool to combat salt stress in plants.

Keywords: ACCD-Producing Bacteria; Ammonia Production; Phytohormone; Plant Growth; Salt-Resistant Rhizosphere Bacteria.

MAPP11

Transformative Advances in Single-Cell Genomics (SCGs): Applications in Molecular Medicine, Aquaculture, and Plant Biology

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ABSTRACT

The intersection of single-cell sequencing and genomics has opened new horizons of biological research by enabling an understanding of cellular variation and molecular complexity in different contexts like in medicine, aquaculture, or plant biology. Specifically, and thanks to advances in research scaffolds, droplet-based approaches, and new library preparation, there has been higher efficient in the performing of sequential single-cell dissections various populations and subpopulations. These approaches are crucial in dilute cellular systems such as tumours and lymphoid tissues where the diversity of cells is integral to the biology of the problem and the treatments. In the case of aquaculture, the appetites interested in the developments of single-cell genomics are associated with the species that are of global concern, such as salmon and shrimp. By allowing the conduct of cellular level molecular portraits, this technique encourages further creation of selective breeding strategies and encourages environmental conservation methods along with improving responses to diseases. Various data techniques such to as clustering grouping and comparative analysis play an important role in the processing of high dimensional data on these organisms aiding in cell type mapping as well as understanding immune reactions. In the edition of plants, scRNA-sequencing has already been implemented on useful plant species such as Arabidopsis thaliana and maize for the genetic dissection of developmental and stress adaptive processes. In spite of difficulties related to the acquisition of truly unbiased plant cell isolates, single-cell genomics is firmly increasing resilience in crops and productivity in agriculture through the discovery of new cell types or genes associated with growth or adaptations to stresses.

Keywords: Cellular Variation; Genomics; Molecular Complexity; Single-Cell Sequencing.

MAPP12

Horizontal Gene Transfer as a Driver of Antibiotic Resistance, Gene Duplication, and Expression Dynamics in Microbial and Plant Systems

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ABSTRACT

Horizontal gene transfer (HGT), widely discussed in evolutionary biology, is most useful in the fast adaptation of the organisms where microbes and even higher plants use genes to codify for antibiotic resistance and regulate expression of those genes. In the population of microbes, HGT allows the spread of drug-resistant components and even more those which are resistant to antibiotic-resistant genes in the populaces of Escherichia coli, Klebsiella pneumoniae, Enterobacter hormaechei, and other interrelated species within the guts of children and adults. Metagenomic analysis have shown that in vaccinated infants drug resistance genes and transposons are accumulated more, inferring substantial risk for horizontal gene transfer mediated drug resistance. Also, within the higher plants, HGT could be important biologically as in Rorippa indica, which encodes for genes implicated in secondary metabolite biosynthesis, reactive oxygen species production between aphid-infested plants, and this incidence may use HGT resistance mechanisms against pests. Moreover, in case of prokaryotic systems, within vertical gene transfer systemized within HGT-induced gene duplication via tandem duplication activated by HGT-TDAH (Tandem gene Duplication selected by Activation of Horizontally transferred gene in bacteria) in Bacillus subtilis, such transferred genes could integrate and be actively maintained even in the presence of antibiotics enhancing fitness of the bacteria. The brightening beam of single-cell genomics powered by high-throughput sequencing has charted plasmids and phage, plural members of mobile genetic elements MGEs families that act as vectors to facilitate the exchange of one or more genetic material between distinct bacteria.

Keywords: Antibiotic Resistance; Evolutionary Biology; Fast Adaptation; Horizontal Gene Transfer (HGT); Bacillus Subtilis.

MAPP14

Repurposing Metformin and TZDS: A New Frontier in Cancer Treatment

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ABSTRACT

Repurposing existing drugs for new therapeutic applications is gaining momentum, especially in the field of cancer therapeutics. This approach is both cost-effective and time-saving, offering a shortcut by using medications that are already proven safe for other conditions. Among these, antidiabetic medications, drugs like metformin and thiazolidinediones (TZDs) have shown potential as anticancer agents as well. Metformin's anticancer effects are achieved through dual pathways. On one hand, it directly targets cancer cells by inhibiting mitochondrial complex I, which activates AMPK and reduces activity in the mTOR pathway- key processes that slow tumor growth and promote cell death and on the other hand, it works indirectly by lowering insulin and glucose levels, creating conditions that are less supportive of cancer progression. The other drug TZDs, is primarily used to improve insulin sensitivity, have shown promise in cancer therapy by reducing inflammation, limiting tumor blood vessel growth, and altering the tumor microenvironment. While metformin has shown consistent results across different types of cancer, the success of TZDs appears to depend on the specific cancer being targeted. This emerging research highlights the exciting potential of repurposing metabolic drugs to fight cancer. While the results are encouraging, further research is essential to understand how these drugs can be most effective for cancer patients. The concept is that by rethinking the use of existing medications, we might discover breakthroughs that may have the potential to transform cancer treatment in the future. The present study describes the potential of metformin and TZDs, beyond diabetes management, offering possible promising results in cancer treatment.

Keywords: Drug Repurposing; Metformin; TZDs; Anticancer Agents; Metabolic Drugs; AMPK Activation; mTOR Inhibition; Cancer Treatments.

MAPP15

The Silent Invasion: Microplastics and the Promise of Biological Cleanup

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ABSTRACT

Plastic pollution is a critical environmental challenge worldwide that is drawing attention globally. Microplastics have infiltrated ecosystems globally, contaminating freshwater, marine environments, air, food, and drinking water. They exist in diverse forms, polymers, sizes, and concentrations. Primary microplastics are intentionally produced for industrial uses, like microbeads in exfoliating scrubs or plastic pellets in manufacturing. For example, microbeads often bypass wastewater filtration, polluting aquatic systems. Secondary microplastics form when larger plastics, such as discarded bottles, degrade due to sunlight, wind, or ocean currents, persisting in the environment for decades. Both types contribute significantly to pollution, disrupting ecosystems and entering the food chain, harming marine life, and threatening human health. Microplastics interfere with species' feeding. growth, and reproduction, while toxic substances attached to them bioaccumulate, impacting biodiversity. Humans consume these contaminants through seafood, water, or salt, risking health issues like inflammation, hormonal imbalances, and organ damage. To tackle this, physical, chemical, and biological methods are used, with biological approaches showing the most promising strategy. Microorganisms like Ideonella sakaiensis. Pseudomonas aeruginosa and fungi like Aspergillus niger can degrade plastics using specific enzymes. These methods offer an eco-friendly, sustainable solution to microplastic. pollution, breaking them into less harmful compounds. This review highlights the sources and impacts of microplastic pollution on ecosystems and human health, focusing on primary and secondary microplastics. It discusses their environmental and biological effects, and explores potential solutions, particularly biological methods using microorganisms and enzymes. These approaches are presented as sustainable, eco-friendly options to address the growing microplastic issue.

Keywords: Microplastic; Pollution; Microorganisms; Biodegradation; Ecosystem; Sustainable.

MAPP16

Utilization of Agro-Industrial Waste as a Cost-Effective Substrate for Production of Biosurfactant

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ABSTRACT

Surfactants are amphipathic molecules that play a significant role in different segments of the market including detergent and soaps industry, food and beverage industry, petroleum industry, and cosmetic industry. They are reported to exhibit significant role in the removal of environmental pollutants. Biosurfactants offer several advantages over chemical surfactants, such as low toxicity and high biodegradability, and remain active at extreme pH and salinity. Biosurfactant-producing microorganisms have been isolated from many diverse environments. A landfill leachate is thus selected as the study site, as a wide range of bacteria are present at the various ages. In our research, we successfully isolated 15 biosurfactant-producing bacteria from landfill leachate collected from waste dumping site, Lucknow.

The problem with the disposal of agro-industrial waste and the pollution caused thereof has encouraged the researchers to study bioconversion of these waste into value added products. This study explores the potential of different agro-industrial waste including Bael shell, pomegranate peels and watermelon peels as economical substrates for biosurfactant production. Strain LS8 in the presence of Bael showed the maximum reduction in surface tension of medium from 72 N/m to 31 N/m and increased the emulsification (E24) against mustard oil to 55%. The elevation in the emulsification index and a decline in surface tension were distinctively attributed to the presence of biosurfactants. However, the utilization of Bael shell for biosurfactant production is a cost-effective eco-friendly process which needs further optimization for scaling up to meet the market demand.

Keywords: Biosurfactant; Landfill Leachate; Emulsification Index; Surface Tension; Agro-Industrial Waste.

MAPP18

Future of Sustainability: Trends and Challenges in Bioplastics for Consumer Goods

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ABSTRACT

As global environmental concerns grow, the demand for sustainable alternatives to traditional plastics in consumer goods has significantly increased. Bioplastics, sourced from renewable biological materials instead of fossil fuels, present a promising solution for reducing environmental impact. The global bioplastics market, valued at $8.31 billion in 2023, is projected to reach $22.56 billion by 2032, with a compound annual growth rate (CAGR) of 11.73% from 2024 to 2032. This growth is driven by the rising adoption of bioplastics across various industries, such as automotive, textiles, and consumer goods. This review explores the expanding role of bioplastics in consumer products, focusing on key trends, innovations, and challenges in their broader adoption. It examines developments in bioplastic formulations, including bio-composites, biodegradable alternatives, and starch-based plastics, which aim to replace conventional plastics in applications like packaging. While starch-based bioplastics provide a biodegradable and renewable solution, challenges such as water resistance and mechanical strength remain. Biocomposite biofilms, which combine bioplastics with natural fibers, offer greater durability and functionality, making them suitable for flexible packaging. Despite their potential, issues related to production costs, scalability, and performance continue to hinder their widespread use. The review also discusses how bioplastics contribute to a circular economy, focusing on their recyclability, biodegradability, and capacity to reduce lifecycle emissions. By summarizing the current state of the bioplastics industry and future trends, the article highlights the essential role of bioplastics in promoting sustainability and reducing the environmental impact of conventional plastics. Ultimately, bioplastics present a critical pathway to a more sustainable, circular economy by minimizing the environmental burden of plastic use.

Keywords: Bioplastics, Sustainability, Consumer Goods, Circular Economy, Environmental Impact.

MAPP19

Recent Advancements and Cutting-edge Research for Treating Wastewater: Sources, Toxicity, and Remediation Technologies

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ABSTRACT

Water significantly influences various aspects of human life, including human health and environment. However, water sources are often contaminated by waste products from various human activities, agriculture, and industry. Therefore, there is a pressing need for cutting-edge methods to remove pollutants from wastewater. Nowadays, several modern methods for detecting and removing water pollutants have been investigated to improve wastewater treatment, with nanotechnology emerging as a revolutionary technology in this field. The goal of this cutting-edge research is to produce new devices such as nanoboots and nanosensors with improved properties by modifying matter at the molecular or atomic level. Nanotechnology makes it possible to produce products at the nanoscale that are more reactive and have a bigger surface area than their bulk equivalents in the wastewater treatment setting. Nanobiotechnology has the potential to significantly enhance the cleanup, treatment, and management of contaminated water, removing harmful pollutants, including heavy metals, organic chemicals, and microorganisms. However, difficulties such as large-scale application, cost-effectiveness, and environmental impact require further exploration in this field. This article primarily covers innovative techniques to identify and remove harmful contaminants, with a unique focus on providing an overview of contemporary uses of various types of nanomaterials and related research. In addition, this paper will address how nanotechnology can be combined with other developing technologies, such as artificial intelligence, to improve water quality monitoring and management.

Keywords: Wastewater Treatment; Heavy Metals; Hexavalent Chromium; Arsenic; Lead.

MAPP20

Unlocking Cellulolytic Microbes with High Cellulase Activity from Rumen to Boost Agricultural Waste Saccharification

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ABSTRACT

The efficient conversion of agricultural waste into fermentable sugars is a critical step for biofuel production. Rumen microbiota, known for their ability to degrade complex plant fibers, present an untapped source of cellulolytic microbes with high cellulase activity. This study aims to isolate and characterize cellulolytic microbes from the rumen of ruminants to enhance the saccharification of agricultural wastes. Rumen fluid was collected and cultured on selective media containing carboxymethyl cellulose to isolate cellulolytic strains. The isolates were screened for cellulase activity using the Congo Red assay, and quantitative cellulase assays were performed to determine enzyme activity. Agricultural residues such as wheat straw, rice husk, and corn stover were pretreated and used in saccharification assays with the most promising microbial isolates. Molecular identification of the cellulolytic strains was conducted through 16S rRNA gene sequencing to establish their taxonomic identity. Among the isolated strains, abundance of GH6, GH9, GH48, GH12, GH5, GH10, GH11, and GH43 were responsible for cellulolytic activities. These strains also showed the presence of GH5, GH7, GH8, GH10, GH11, and GH43 exhibiting xylanase activities. These results indicate that rumen-derived cellulolytic microbes could play a pivotal role in agricultural waste valorization, providing an eco-friendly and efficient solution for biofuel production. Future work will focus on optimizing the conditions for large-scale application of these microbes in biorefineries. This study highlights the potential of rumen microbiota to revolutionize second-generation biofuel production through enhanced enzymatic saccharification.

Keywords: Biofuel Production; Glycoside Hydrolases (GHs); Saccharification; Rumen Microbiota; Agricultural Waste Valorization; Cellulase Activity.

MAPP21

Microbial Approaches to Mitigate Plastic Biodegradation: Robust Methods for Addressing Plastic Waste Pollution

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ABSTRACT

Owing to the escalating challenges posed by plastic waste, there is a growing interest in the application of bioremediation techniques with microorganisms. The overview includes several currently existing methodologies for plastic decomposition by microorganisms and cites several bacteria, including Rhodococcus ruber and Ideonella sakaiensis, which are known to degrade plastics. Importantly, however, all these microorganisms must be collected from natural sources highly polluted by plastic wastes and cultured in laboratory on class-used phthalate-free plates instead of plastic wastes. Different microscopic and genetic techniques, chemical and physical methods, and microbiological experiments are suggested to evaluate microbial degradation activity. The results of such studies show that therefore several effective and reliable measures for containment such studies were not available in previous studies. Other proposals look at the use of strong experimental designs and scope expansion about biodegradation qualities and investigation of mechanisms involved. Further improvement of these techniques is important in light of the rising levels of plastic waste in the environment.

Keywords: Biodegradation; Rhodococcus Ruber; Ideonella Sakaiensis; Microorganisms; Plastic Waste.

MAPP22

Antimicrobial Anticancer & Anti-inflammatory Activity in the Extract of Cannabis Species Against Lung Cancer

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ABSTRACT

The potential therapeutic benefits of Cannabis sativa, focusing on its antimicrobial, anticancer, and anti-inflammatory properties specifically against lung cancer (cell lines A549).

As we experienced, frequently microorganisms are resisting to usual antibiotics and drugs that cause an expensive remark to treat disease. To overcome this issue plants extracts have been used to treat number of diseases, contains antimicrobial and anti-inflammatory properties. The methanolic extracts of the medicinal plant of Cannabis species has been conceal to justify its antimicrobial activity against two Gram positive organisms (Bacillus subtilis, Staphylococcus aureus), two Gram negative organisms (Escherichia coli, Salmonella typhimurium) and two fungi (Aspergillus niger and Candida albicans) by using the disc diffusion method. Cannabis is a complex medicinal plant, with numerous compounds such as delta-9-tetrahydrocannabinol and cannabidiol and more Cannabinoids have been evidently shown effectiveness to the treatment of number of infections. Additionally, it contains anticancer properties and palliative effects as well as tumour angiogenesis.

However, cannabinoids are currently used to treat the symptoms and pain which associated during chemotherapy. Since its legalization, the use of cannabinoids has been increasing worldwide due to its medicinal cancer.

This research investigates the multifaceted therapeutic properties of Cannabis sativa, focusing on its potential as a triple-threat against lung cancer through antimicrobial, anticancer, and anti-inflammatory mechanisms. Through rigorous experimentation, we explore the plant's ability to combat microbial agents, inhibit lung cancer cell proliferation (Cell lines A549).

This study contributes to the evolving landscape of medicinal Cannabis research, presenting a nuanced perspective on its potential role in addressing lung cancer through its diverse biological activities.

Keywords: Cannabinoids, Cannabidiol, Delta-9-Tetrahydrocannabinol, Anti-Inflammatory.

ISSN: 2278-9197 © VSRD International Journals: www.vsrdjournals.com

MAPP24

Synergistic Effects of Prebiotics and Probiotics on Gut Health

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ABSTRACT

The synergistic effects of prebiotics and probotics, collectively known as synbiotics, have emerged as a promising strategy to modulate the gut microbiota and promote gut health. By selectively stimulating beneficial bacteria, enhancing probiotic survival and colonization, and modulating gut microbiota composition, synbiotics can improve gut barrier function, enhance short-chain fatty acid production, and modulate immune responses. These effects have significant clinical implications for various health conditions, including inflammatory bowel disease, irritable bowel syndrome, metabolic disorders, and immune function. Prebiotics serve as specific substrates for beneficial bacteria, promoting their growth and proliferation. In turn, these beneficial bacteria can enhance the survival and colonization of probiotic strains in the gastrointestinal tract. This synergistic interaction leads to a more diverse and balanced microbial ecosystem, which can have numerous health benefits. One of the key mechanisms by which synbiotics improve gut health is through the enhanced production of short-chain fatty acids (SCFAs), such as acetate, propionate, and butyrate. These SCFAs, produced by the fermentation of prebiotics by beneficial bacteria, have been linked to various health benefits, including improved gut barrier function, reduced inflammation, and enhanced immune function. SCFAs can strengthen the tight junctions between intestinal epithelial cells, reducing intestinal permeability and preventing the translocation of harmful bacteria and toxins into the bloodstream. Additionally, SCFAs can modulate the immune response by promoting the differentiation of regulatory T cells, which play a crucial role in maintaining immune tolerance. Further research is needed to fully elucidate the mechanisms underlying these synergistic effects and to optimize the formulation of synbiotic products for maximum efficacy.

Keywords: Prebiotics, Probiotics, Synbiotics, Gut Microbiota, Gut Health.

MAPP25

Marine Potential: Parengyodontium Album as A Plastic-Degrading Agent in Ocean Environments

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ABSTRACT

Plastic pollution in marine environments is becoming a significant global challenge, with millions of tons of plastic waste accumulating in the oceans, posing severe threats to marine life and ecosystems. Recent studies have identified ***Parengyodontium album*** *(P. album), a marine-derived fungus, as a promising agent capable of breaking down plastics. This research investigates the potential of P. album to degrade commonly encountered plastics, including polyethylene and polystyrene, under oceanic conditions. Laboratory experiments revealed that P. album produces hydrolytic enzymes such as cutinases and esterases, which facilitate the breakdown of plastics into smaller, less harmful byproducts. These enzymatic activities were further supported by a significant reduction in plastic mass and the formation of microplastics over time. Additionally, genomic analysis of P. album identified key metabolic pathways that enable the fungus to adapt and thrive in plastic-laden environments, enhancing its degradation efficiency. This research underscores the potential of P. album as a bioremediation agent for mitigating plastic pollution in oceans which can be harnessed as part of a bioengineered solution to address the growing plastic crisis. By leveraging the natural plastic-degrading capabilities of P. album, this research offers a sustainable and innovative approach to combating plastic pollution and protecting marine biodiversity.*

Keywords: Plastic Pollution, Parengyodontium Album, Marine Fungi, Biodegradation, Enzymatic Degradation, Ocean Ecosystems, Plastic Waste Management.

ISSN: 2278-9197 © VSRD International Journals: www.vsrdjournals.com

MAPP26

Evolving Technology Trends in Hydroponic Systems: A Comprehensive Review of Market

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ABSTRACT

Hydroponic systems are fast emerging as popular agriculture practices, particularly to meet niche market needs and also as an independent alternative agriculture practice to meet global demand for food production. Utilizing diverse methods such as deep-water culture, ebb and flow, nutrient film technique, aeroponics, and drip irrigation, these systems offer significant advantages. The principal advantages of hydroponics are their non-requirement of huge land space, amenable for modern technology intervention focusing on resource conservation, and less dependency on chemical inputs such as fertilizers and pesticides. The accelerated growth cycle coupled with the enhanced nutritive value in hydroponically grown crops is potentially leading to improved food security; however, there is a need for optimizing energy efficiency and ensuring the long-term sustainability of this agriculture technology.

In the present times where, more and more emphasis is placed on chemical-free and organic products, the significance of hydroponic systems is unquestionable. In addition to space and resource conservation, hydroponic systems also gain on economising the "seed to product in market" time span. Thus, making it an attractive choice amongst commercial plant breeders and plantation farmers in the hospitality sector.

Keywords: Hydroponics, Sustainable Agriculture, Aeroponics, Nutrients Film Technique, Resource Management, Food Security, Global Demand, Energy Efficiency, Organic Food.

MAPP27

Exploring Synthetic Biology Approaches for the Effective Remediation of Heavy Metal Pollution

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ABSTRACT

Environmental pollution caused by heavy metals and toxic compounds has become a major global concern, particularly in agricultural ecosystems. Traditional remediation methods often fail to provide cost-effective and sustainable solutions for contaminant removal. Bioremediation, an eco-friendly approach utilizing microorganisms, has emerged as a promising alternative. Advances in synthetic biology have further enhanced the bioremediation potential of microbes by enabling precise genetic modifications to improve their efficiency, resilience, and specificity in pollutant degradation. This study explores the role of synthetic biology in developing genetically engineered microorganisms (GEMs) capable of detoxifying a wide range of heavy metals and organic pollutants. Strategies such as enhancing cellular mechanisms for metal sequestration, improving biosorption pathways, and designing biosensors for pollutant detection are key to optimizing bioremediation processes. Additionally, synthetic biology tools like CRISPR-Cas9 gene editing and metabolic pathway engineering allow microbes to adapt to harsh environmental conditions, such as contaminated soil and wastewater, increasing their effectiveness in agricultural settings. By integrating synthetic biology with bioremediation, it is possible to restore soil health, reduce toxic metal mobility in agroecosystems, and mitigate adverse effects on human and plant health. This abstract emphasizes the significance of engineered microbes as a scalable, sustainable, and efficient solution for environmental restoration, with a focus on agricultural biotechnology and the remediation of contaminated soils and water systems.

Keywords: Bioremediation; Synthetic Biology; Heavy Metals; Agricultural Ecosystems; Genetic Engineering; Environmental Restoration.

MAPP28

Micro-RNA 339 as Potential Therapeutic Target in Breast Cancer

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ABSTRACT

Breast cancer, the most common cancer among women, often involves the inactivation of tumor suppressor genes (TSGs) through mechanisms beyond genetic mutations, such as epigenetic dysregulation. Enhancers, crucial cis-regulatory elements, have emerged as significant players in TSG expression modulation. This study investigates the interplay between Nuclear Activating miRNAs and enhancers in regulating TSG activity, focusing on miR-339 and its role in activating the TSG GPER1. By analyzing 157 breast cancer tissue samples, the study reveals down regulation of both miR-339 and GPER1 in multiple subtypes, including Luminal A/B and Triple-Negative Breast Cancer. Functional assays demonstrate that miR-339 upregulates GPER1 by activating its enhancer, a process validated through CRISPR deletion and luciferase reporter assays. Furthermore, overexpression of miR-339 inhibits cancer cell proliferation without affecting migration, positioning it as a potential therapeutic target. Enhancer activation by miR-339 correlates with enriched H3K27ac histone marks, emphasizing the enhancer's integrity in this regulatory mechanism. The findings establish a novel enhancer-mediated pathway for TSG reactivation in breast cancer, where miR-339 serves as a promising agent for restoring tumor suppressor functionality. These insights underscore the therapeutic potential of targeting enhancermi RNA networks in breast cancer treatment, particularly for aggressive subtypes lacking effective therapies.

Keywords: Breast Cancer, Tumor Suppressor Genes (TSGs), miR-339, Enhancer, Regulation, Epigenetics, Therapeutics.

MAPP29

"Plant Bio-Acoustics": A Novel Strategic Approach to Explore the Association with Abiotic Cultivation Parameters and Plant Response in Ocimum Sanctum

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ABSTRACT

The novel approach of ultrasonic sounds or Plant Bio-Acoustic, is attracting scientific attention as one of the obtruding non-invasive technologies to analyse plant responses to varying abiotic environmental conditions. However, as the science of plant acoustic is at the naïve stage of intervention, research focusing on analysing the responses from different plants system are pivotal and they provide an impetus to the research in the core area of bioacoustics, which is often restricted by the tools for monitoring and analysing the responses. The current study investigates the acoustic emissions (UE) of one of the most well-known medicinal plants, Tulsi (Ocimum sanctum), in response to various physiological and environmental factors.

The 'Ultrasonic (sound-capturing) mics' were used for monitoring the acoustic signals of the plants under water stress. The findings indicate a significant correlation between soil parameters, acoustic signals, and the phytochemical profiles of Tulsi, underscoring the impact of environmental factors on the production of bioactive compounds. Therefore, the research demonstrates the efficacy of acoustic analysis as a non-invasive and cost-effective tool for assessing plant responses, and advocates for the integration of this method with traditional phytochemical analyses to enhance understanding of the biochemical adaptations in medicinal plants.

Keywords: Acoustic Emission; Tulsi (Ocimum sanctum); Ultrasonic Emissions (UE); Acoustic Analysis; Biophysical Responses; Soil Testing, Nutrient Composition; pH; Phytochemical Analysis; Environmental Factors; Medicinal Plants; Non-Invasive Assessment.

MAPP30

Synergistic Use of Plant Extracts of Achyranthes aspera and Azadirachta indica with Trichoderma spp. for Fungal Pathogen Management in Agriculture

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ABSTRACT

The management of fungal pathogens in agriculture has predominantly relied on chemical fungicides, which pose significant challenges, including environmental pollution, health hazards, and the emergence of resistant pathogen strains. In light of these concerns, integrating plant extracts from Achyranthes aspera and neem (Azadirachta indica) with Trichoderma spp., a genus of beneficial fungi with biocontrol properties, presents a promising eco-friendly alternative for disease management. Achyranthes aspera and neem, abundant in natural vegetation, are rich in bioactive compounds with potent antifungal properties. These extracts inhibit the growth of plant-pathogenic fungi through mechanisms such as disruption of fungal cell walls, inhibition of spore germination, and suppression of fungal enzymatic activity. The synergistic use of these plant extracts with Trichoderma spp. further enhances the antifungal efficacy. Trichoderma spp. suppress plant pathogens through nutrient competition, mycoparasitism, and activation of systemic resistance in plants. The integration of these agents offers a multifaceted strategy: while the bioactive compounds in the plant extracts directly inhibit pathogens, Trichoderma spp. contribute to enhanced plant health by improving nutrient availability, promoting root development, and suppressing pathogenic fungi. This approach reduces the reliance on synthetic fungicides, mitigates environmental contamination, and slows the development of resistant pathogen strains. This research delves into the antifungal mechanisms of Achyranthes aspera and neem extracts, their interaction with Trichoderma spp., and their effectiveness in integrated pest management (IPM) systems.

Keywords: Achyranthesaspera, Azadirachtaindica, Trichodermaspp., Biocontrol Agents, Antifungal Activity, Plant Extracts, Fungal Pathogens, Sustainable Agriculture, Integrated Pest Management (IPM), Ecofriendly Solutions, Mycoparasitism.

ISSN: 2278-9197 © VSRD International Journals: www.vsrdjournals.com

MAPP31

Comparative Analysis of Diverse Soil Samples for Soil Health Assessment

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ABSTRACT

Soil health is a fundamental factor influencing agricultural productivity, environmental quality, and ecosystem resilience. Understanding the variations in soil health across different land-use types is critical for implementing sustainable management practices. This study undertook a detailed comparative analysis of soil samples from diverse agricultural fields, chemical pesticide-treated soils, organic farming soils, forest soils, and other land-use systems to evaluate key soil health parameters. Physicochemical properties such as pH, electrical conductivity, organic matter content, macronutrient levels (nitrogen, phosphorus, and potassium) and micronutrients were analyzed alongside biological indicators, including microbial biomass, enzyme activities, and soil respiration. The findings emphasize the importance of integrating chemical, physical, and biological indicators for a comprehensive assessment of soil health. Agricultural soils treated with chemical pesticides often exhibited reduced organic matter and microbial activity, raising concerns about soil degradation. In contrast, soils from organic farming systems showed balanced nutrient levels and higher biological activity, reflecting sustainable practices. Forest soils displayed rich organic matter content and microbial biomass, indicative of better soil health. Other land-use systems highlighted diverse soil health attributes, depending on their specific management practices. Regular monitoring of soil health parameters can aid in identifying trends of degradation or improvement, enabling land managers and farmers to adopt evidence-based strategies to enhance soil quality. This study underscores the interconnectedness of land-use practices and soil health, advocating for sustainable approaches to mitigate soil degradation and improve agricultural productivity.

Keywords: Soil Health, Organic Farming, Chemical Pesticides, Forest Soils, Soil Degradation, Physicochemical Properties, Biological Indicators, Microbial Biomass, Enzyme Activities, Soil Respiration, Organic Matter Content, Macronutrients, Micronutrients, Soil Monitoring.

MAPP32

Bioactive Compounds in Lichens and Their Mechanisms of Neuroprotection

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ABSTRACT

Lichens are a rich source of bioactive compounds that possess remarkable neuroprotective properties. They are symbiotic organisms formed by the union of fungi and photosynthetic partners. Key compounds found in lichens, such as usnic acid, depsides, depsidones, and aliphatic acids, have been extensively studied for their potential to address neurodegenerative disorders, including Alzheimer's and Parkinson's diseases. These conditions are regularly connected to oxidative stress, neuroinflammation, and apoptotic pathways, all of which contribute to the progressive damage of neural cells. Lichen-derived metabolites possess strong antioxidant properties, which help in searching for reactive oxygen species (ROS) and reducing oxidative stress a major factor in neuronal damage. Additionally, these compounds have shown anti-inflammatory effects by inhibiting the release of pro-inflammatory cytokines and nitric oxide (NO). This action helps to alleviate neuroinflammation, an essential contributor to neurodegeneration. Recent studies indicate that lichen metabolites specifically target molecular mechanisms in the central nervous system. This includes the variation of enzymatic activities and neurotransmitter pathways. For example, usnic acid has shown potential in preventing the aggregation of amyloid-beta, which is a hallmark of Alzheimer's disease, and in enhancing mitochondrial function to support neural health. The ecological resilience of lichens to extreme environments contributes to the effectiveness of their bioactive compounds, making them a unique resource for therapeutic exploration. However, sustainable extraction methods and advanced biotechnological approaches are essential to abundantly attach their potential. Future research should focus on illustrative molecular interactions, optimizing bioavailability, and validating clinical efficacy. This would cover the technique for the development of novel neuroprotective strategies derived from lichens.

Keywords: Lichens, Bioactive Compounds, Neuroprotection Properties.

MAPP33

Bacterial Cellulose-Based Edible Films and Coatings: Enhancing Food Preservation and Sustainability

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ABSTRACT

Bacterial cellulose (BC), a biopolymer produced by various bacterial strains, has emerged as a promising material for developing edible films and coatings in the food industry. Its unique properties, including high mechanical strength, biocompatibility, biodegradability, and excellent water-holding capacity, make it an ideal candidate for enhancing food preservation while supporting sustainability initiatives. BC-based films and coatings act as protective barriers, reducing moisture loss, oxidation, and microbial contamination, thereby extending the shelf life of food products. Recent research has focused on functionalizing BC films by incorporating bioactive compounds such as antimicrobial agents, antioxidants, and essential oils. These enhancements provide additional functionalities, such as inhibiting bacterial growth and delaying spoilage, ensuring food safety. Furthermore, its adaptability allows for modifying its physical and chemical properties to get specific applications, from preserving fresh produce and meat to maintaining the quality of dehydrated foods. Efforts to improve the scalability of BC production through optimized fermentation processes and renewable carbon sources have addressed economic challenges, making BC-based films a viable alternative to synthetic packaging. Innovations in BC-based edible films also extend to smart packaging solutions, where the integration of biosensors can monitor food freshness and provide real-time spoilage indicators. BC-based edible films and coatings represent a sustainable and multifunctional approach to food preservation. Their potential to reduce food waste and reliance on plastic packaging aligns with global environmental and health objectives, making them a transformative innovation in the food industry.

Keywords: Bacterial Cellulose, Edible Films, Sustainability, Bioactive Compounds, Application.

MAPP34

Microbial Diversity in Mining-Disturbed and Undisturbed Forests: Solutions for Soil Restoration

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ABSTRACT

Microorganism play a pivotal role in maintaining forest ecosystem health by enhancing plant nutrient uptake, improving soil structure, and facilitating vegetation recovery in disturbed landscapes. Mining activities, however, severely disrupt soil ecosystems, leading to the loss of microbial diversity and functionality. This review focuses on evaluating the diversity and metabolic activities of microorganism in mining-disturbed and undisturbed forest ecosystems. Mining-disturbed sites typically exhibit reduced microbial diversity and functionality, impeding natural soil restoration processes. In contrast, undisturbed forests demonstrate robust microbial communities with enhanced metabolic activity, underscoring their ecological resilience. Advanced molecular techniques, such as DNA barcoding and metagenomics, have been studied by many researchers to characterize microbial diversity and functional potential in both ecosystems. Exploring differences in microbial diversity pattern can support bioaugmentation and soil restoration programs. Specific isolates identified by such diversities studies can be utilized to inoculate degraded soils, promoting vegetation establishment and ecological recovery. This review emphasizes the critical role of ectomycorrhizal fungi in mitigating the impacts of mining on forest ecosystems. It advocates for integrating ectomycorrhizal-based restoration strategies with broader reforestation and sustainable land-use practices to ensure the long-term recovery of degraded landscapes.

Keywords: Microbial Diversity, Forest Ecosystems, Soil Restoration, Reforestation.

MAPP35

Biotechnology of Fermented Food(s)

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ABSTRACT

Fermentation is a time-honored practice that has been in use for 8000 years with the purpose of shelf life extension and better preservation of the food, with added enhanced nutritional value and characteristic flavor. This review provides a comprehensive overview of the properties, and safety of fermented food products, and the production of bioactive compounds synthesized due to fermentation. Bioactive compounds such as omega-3, antioxidants, organic acids, carotenoids, minerals, vitamins, and peptides contribute to health benefits. The safety issues caused because of microbial contamination and foodborne pathogens present in fermented products are addressed as well as an understanding of the innovations in packaging methodologies to improve product preservation, extend the shelf life, and ensure food safety. We also focus on providing insights into the importance of fermented food products in the functional food industry.

Keywords: Fermentation, Bioactive Compounds, Fermented Products.

ISSN: 2278-9197 © VSRD International Journals: www.vsrdjournals.com

MAPP36

Effect of Cinnabar with Nanoparticles on the Dendrobine Production by Dendrobium Nobile

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ABSTRACT

This study aimed to evaluate the effects of CH-AgAuNPs (chemical synthesis silver-gold nanoparticles with cinnabar) on dendrobine production in Dendrobium nobile plants, focusing on the modulation of metabolic and transcriptomic profiles. The treatment significantly enhanced dendrobine biosynthesis, with a concentration of 1068.28 ng/mL observed in the treated plants. LC-MS analysis confirmed the identification of dendrobine, indicating that the interaction between CH-AgAuNPs and cinnabar positively influenced secondary metabolite production pathways. Transcriptomic analysis revealed substantial changes in gene expression, with 2,547 upregulated and 3,901 downregulated genes, particularly in pathways related to lipid metabolism, defense responses, and secondary metabolite biosynthesis. Metabolomic profiling using base peak chromatograms (BPC) and OPLS-DA analysis demonstrated significant metabolic differences, with specific metabolites like Ononin and 5beta-Pregnane-3,20-dione upregulated in the treated group. Pathway enrichment analysis highlighted key biological processes, including central carbon metabolism and isoflavonoid biosynthesis, potentially linked to increased dendrobine synthesis. The study concludes that PCNPCB treatment induces significant changes in the transcriptomic and metabolic landscapes of Dendrobium nobile, suggesting a potential molecular mechanism for enhanced dendrobine production. Future studies should explore the dose-dependent effects of CH-AgAuNPs and the role of varying nanoparticle concentrations and exposure times in optimizing bioactive compound production, with implications for commercial applications in plant biotechnology.

Keywords: Cinnabar; Metabolic and Transcriptomic Profiles; Dendrobine; Biosynthesis.

MAPP37

Synergistic Strategies for Sustainable Soil Remediation: Harnessing Biochar, Microbial Interactions, and Phytoremediation

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ABSTRACT

Industrialization and urbanization have led to persistent environmental contamination with heavy metals and xenobiotics, posing significant pollution challenges. Bioremediation has emerged as a crucial strategy to mitigate these pollutants, with microbial remediation standing out as an effective approach. This technique harnesses the natural metabolic pathways of soil microorganisms to produce enzymes that degrade xenobiotic compounds. Complementing microbial remediation is the use of biochar technology—a carbon-rich material derived from the pyrolysis of organic matter. Biochar enhances the growth and activity of pollutant-degrading microbes, thereby improving remediation efficiency. Genetically Engineered Microbes (GEMs) have further revolutionized bioremediation through the incorporation of superior traits via genetic engineering and recombinant DNA technology. These enhanced microbes demonstrate improved capabilities to degrade a wide range of contaminants, including oil spills, halobenzoates, naphthalenes, toluenes, trichloroethylene, octanes, and xylenes. Compared to their natural counterparts, GEMs exhibit superior adaptability and efficiency, enabling the rapid breakdown of pollutants and co-metabolism of complex compounds. The integration of biochar with GEMs holds immense potential for advancing remediation efforts by creating synergistic systems capable of addressing diverse environmental contaminants. Nevertheless, optimizing biochar properties for specific pollutants and ensuring its cost-effective production remain critical hurdles. Despite these challenges, this approach offers a safer, cost-effective, and highly efficient alternative for reducing the risks posed by organic pollutants to human and environmental health. This paper explores microbial remediation, GEMs, and biochar-microbe co-deployment as promising solutions for sustainable pollution management while discussing the limitations and future directions for their implementation.

Keywords: Genetically Engineered Microbes (GEMs), Biochar Technology, Sustainable Pollution Management, Petroleum Hydrocarbons.

MAPP38

Recent Advances in the Field of Abiotic Stress Research

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ABSTRACT

The fast-growing world population demands higher food supply which can be met through developing better yielding varieties preferably grown on less favourable arable lands. Many recent researches have focused on novel mechanisms which help plants in coping with number of abiotic stress conditions like heavy metal pollution, acidic soils, water-logging, osmotic stress, drought, heat, anaerobic conditions and salinity stress. The role of transcription factor called STOP1(sensitive to proton rhizotoxicity 1) has recently been discovered in regulating the uptake of nutrients in plants under acidic soil conditions. The application of Cenococcum geophilum, an ectomycorrhizal fungus has shown to increase the accumulation of heavy metals in pine plants. The area of plant immunity is a new addition to mechanisms of abiotic stress tolerance. The researchers have reported the identification of a gene encoding a nuclear pore complex protein, which when mutated induces osmotolerance in Arabidopsis. Similarly, treatment of Solanum Lycopersicon L with a low concentration of ethanol enhanced its vegetative growth and yield under heat stress conditions. Priming with ethanol also induced drought stress resistance and high salinity tolerance in Arabidopsis. In order to build a food secure world, it is crucial that plant research focuses on development of stress resilient varieties.

Keywords: Abiotic Stress, Rhizotoxicity, Heat Stress, Drought, Salinity, Anaerobic Stress.

MAPP39

Cutting-edge Research and Advancement in Microplastic Research: Origin, Impact and Degradation Mechanism

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ABSTRACT

Microplastics are emerging environmental pollutants which are increasingly of concern because of their detrimental effects on aquatic life and human life. Their persistence, bioaccumulation potential, and adverse effects on biodiversity and human health underscore the urgency of developing effective mitigation strategies. Since they are persistent and non-biodegradable, their build-up in the environment is directly correlated with the world's plastic output. Therefore, remediation of microplastics requires immediate attention on a global basis. There are various methods reported for degradation of microplastics but these are not very much effective and not sustainable in nature. Among these, bioremediation process that harnesses the metabolic capabilities of microorganisms and other biological entities, which offers a promising, sustainable solution for its biodegradation. This review comprehensively examines the potential of bioremediation for microplastic degradation, highlighting the roles of key microbial taxa, including bacteria (e.g., Pseudomonas, Ideonella sakaiensis), fungi (e.g., Aspergillus spp., Penicillium spp.), and algae, in breaking down various plastic polymers such as polyethylene, polystyrene, and polyethylene terephthalate. Despite its potential, bioremediation faces challenges, including the slow and incomplete degradation of plastics, the production of potentially harmful intermediates, and the need to scale up laboratory findings for real-world application. Recent technological advances that enhance bioremediation efficiency are also reviewed, including the application of genetic engineering to develop recombinant microorganisms and the use of bioreactors for controlled degradation. Present review also identifies significant research gaps, such as understanding the long-term impacts of bioremediation on ecosystems and optimizing microbial consortia for diverse environmental conditions.

Keywords: Microplastics, Biodegradation, Genetic Engineering, Metabolic Pathways, Enzymes.

MAPP40

Boosting Crop Yields with Cutting-Edge Biofertilizer Technologies

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ABSTRACT

The rising demand for biofertilizers is driven by the growth of organic agriculture for safe, healthy, and eco-friendly products. However, the biofertilizer formulations need to be optimized to extend microbial inoculant shelf life and ensure efficacy under varying field conditions. Liquid, granular, pelletized, and encapsulated biofertilizer formulations are available in the market, offering varying degrees of plant growth promotion. However, inconsistent performance remains a key barrier to their widespread adoption, limiting biofertilizers as a reliable and eco-friendly alternative to chemical fertilizers. A key challenge in microbial biofertilizer adoption is the lack of effective formulation technologies capable of maintaining inoculant viability during storage, transport, and application. Emerging formulation technologies present innovative solutions to enhance agricultural productivity and sustainability. Nanoparticle-based biofertilizers use titanium dioxide, silver, gold, nano-chitosan, and other nanoparticles along with encapsulate microbial inoculants. These formulations demonstrate superior efficiency compared to traditional carriers and offer prolonged shelf life, controlled microbial release, and improved nutrient delivery. However, issues such as nanoparticle aggregation, interactions with soil components, and potential impacts on native soil microbiomes require further investigation. Another progressive technique is Biosurfactant-based bioformulations. These are bacteria-based formulations derived to enhance plant growth and resilience. Despite their potential, high production costs and stability concerns present scalability challenges, necessitating further refinement. Other innovative approaches, such as droplet microfluidics, hydrogel-based slow-release carriers, and agro-waste based biodegradable formulations also offer promising delivery mechanisms. These emerging new technologies facilitate targeted microbial release and sustained activity. However, these are nascent and require optimization to enhance microbial survival, cost-effectiveness, and adaptability to diverse agricultural environments. If successfully implemented, these advancements can improve global food security, reduce chemical fertilizer dependency, and promote environmentally responsible farming.

Keywords: Biofertilizer, Biofertilizer Formulations, Consortia, Plant Growth Promotion, Plant Growth Promoting Bacteria.

MAPP41

Traditional Rice as a Cornerstone for Nutrition and Disease Management

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ABSTRACT

A long history of traditional rice cultivars as ingredients in various diets and traditional medicine has endowed them with multifaceted health benefits. For centuries, they have been cultivated in specific locations, and such an environment has enriched them in bioactive compounds that enhance their health applicability. Traditional rice certainly stands as one of the most potent sources of antioxidants, which help reduce the chances of developing chronic diseases such as cancers and cardiovascular problems by minimizing oxidative stress. Many traditional rice varieties, such as black rice, purple, red, brown, and medicinal types like Kattuyanam, Mapillai samba, Navara, and others, are known for their antioxidant properties. Several of the olden rice varieties have also been found to exhibit antimicrobial activities, which can be a solution to some infectious diseases. With fermentation, the traditional rice evokes therapeutic activities through bioactive extracts that have microbial diversity from beneficial genera like the Lactobacillus or Bifidobacterium for the maintenance of gut health. Other effects include stimulation of gut health, enhancement of digestion, short-chain fatty acid (butyrate) production, and health of the colon. It also enhances immune systems via T-celllevel stimulation and activation of macrophages. All these rice varieties contain complex carbohydrates, a lot of B vitamins, minerals such as magnesium and iron, and dietary fiber understood. Traditional rice varieties also emphasize culture as vital to various communities as they are rooted in their traditions of cooking and healing. The intrinsic diversity among the rice varieties provides opportunities for developing more specific nutrition and health interventions for certain regions where rice is a staple. It is the development through scientific understanding about their distinct but specific potential that will be crucial for unlocking their potential in improving health outcomes worldwide and for addressing modern challenges in nutrition and disease management.

Keywords: Traditional Rice; Fermentation; Antioxidants; Bioactive Compounds; Oxidative Stress; Beneficial Microbial Strains; Nutritional Interventions.

MAPP42

The Synergistic Role of Soil Microbiome and Endophytic Bacteria in Sustainable Agriculture: A Review

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ABSTRACT

The increasing environmental challenges posed by conventional agricultural practices, such as soil degradation and reliance on chemical inputs, necessitate innovative solutions for sustainable farming. The soil microbiome and endophytic bacteria play vital roles in enhancing plant health, improving soil fertility, and mitigating biotic and abiotic stresses. The soil microbiome, composed of diverse microorganisms including bacteria, fungi, and archaea, is instrumental in nutrient cycling, organic matter decomposition, and pathogen suppression. Endophytic bacteria, residing within plant tissues without causing harm, contribute to plant growth by mobilizing nutrients, producing phytohormones, and inducing systemic resistance against pests and diseases. This review examines the synergistic interactions between these microbial communities, focusing on their individual and collective roles in promoting sustainable agriculture. The interplay between the soil microbiome and endophytes enhances nutrient availability, stress resilience, and plant defence mechanisms, offering eco-friendly alternatives to chemical fertilizers and pesticides. Additionally, these microbial interactions facilitate soil health restoration and support crop adaptation to environmental changes. While significant advancements have been made in understanding these microbial roles, challenges remain in ensuring their stability and efficacy across diverse environments. Addressing these limitations through advanced research and targeted microbial application strategies holds promise for transforming modern agriculture.

Keywords: Endophytic Bacteria, Sustainable Agriculture, Plant Growth Promotion, Nutrient Cycling, Stresstolerance, Soil Health.

MAPP43

Phytobiological Extracts of Medicinal Plants: Sustainable Solutions for Managing Fungal Plant Diseases

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ABSTRACT

Fungal diseases are a significant, cause of crop loss worldwide, posing a serious threat to global food security and agricultural sustainability. Although chemical fungicides have been the main stay of disease control, concerns about their environmental impact, toxicity, and the emergence of resistant fungal strains have prompted the search for more sustainable and eco-friendly alternatives. Phytobiological extracts from various plants, known for their bioactive compounds, have emerged as promising solutions for managing fungal diseases in agriculture. This review examines the potential of plant-derived extracts as natural antifungal agents for controlling a variety of fungal diseases. The paper explores a range of plant species, such as Calotropis procera, Ricinus communis, Daturastramonium. Azadirachta indica, Cinnamomum verum, and Eucalyptus globulus, whose extracts have demonstrated significant antifungal activity against several common plant fungal diseases. These include Powdery Mildew, Late Blight, Leaf Spot, Root Rot, Gray Mold, and Rice Blast. The review discusses the modes of action of these extracts, including inhibition of spore germination, disruption of fungal cell walls, and interference with fungal metabolic pathways. Additionally, ithighlights the effectiveness of these plant extracts in various application methods, such as foliar sprays and soil treatments, for managing fungal diseases in crops.

Keywords: Phytobiological Extracts, Fungal Pathogens, Antifungal Activity, Biofungicides, Sustainable Agriculture.

MAPP44

Real Time Monitoring of Air Quality: Recent Advances and Future Prospects

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ABSTRACT

Air pollution is linked with severe health impacts worldwide, and the marginalized urban populace like in Delhi slums is more susceptible as they are exposed more due to higher pollutant concentration and limited access to clean energy. However, such populations are usually excluded from current air quality monitoring systems and lack evidence to support targeted interventions. Therefore, here we discuss the deployment of low-cost air quality sensors in the slums of Delhi as a community-led initiative to fill this data gap and facilitate environmental awareness. These sensors are based on affordable biosensor technology capable of measuring pollutants such as particulate matter (PM2.5, PM10), nitrogen dioxide, and carbon monoxide. The mechanisms used in the sensors include electrochemical, optical, and metal oxide semiconductor (MOS) detection. We will be discussing the mechanisms like electrochemical detection, where gas interactions generate electrical currents proportional to pollutant concentration, providing accurate and sensitive data for monitoring air quality. This shows the possibility of underprivileged communities using low-cost sensor networks in monitoring their environment and developing activism in policy changes and better public health practices.

In this review we explore the role of accessible technology in promoting environmental justice and provide a scalable model for the management of air quality in underserved urban areas around the world.

Keywords: Electrochemical Detection, Semiconductor, Biosensor, Low Cost, Particulate Matter.

MAPP45

Heavy Metal Toxicity in Plants: Tolerance Mechanism and Remediation Strategies

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ABSTRACT

Heavy metals (HMs) constitute one of the main soil contaminants which limiting crop productivity, which leads to a drop in agricultural yield also. The production of free radicals brought by HM exposure causes oxidative stress in plants, which modifies their morphophysiological and biochemical processes. To secure their survival in presence of heavy metal, plants evolved complex cellular defence mechanisms through the activation of signalling pathways that trigger the production of HM transporters. In order to cope with HM stress, plants either prevent HMs from being absorbed from the soil or initiate the detoxifying process, which includes the synthesis of both enzymatic and antioxidants for the scavenging of reactive oxygen species. In addition, phytohormones and the signalling pathways they produce aid in controlling cellular processes in order to mitigate HM stress. Several strategies to eliminate heavy metals from metal-polluted soils should be taken into consideration in order to preserve the commercial value of fruits and vegetables. The development of new crop that aid in enhancing phytoremediation will be made easier by better understanding of HM toxicity, and tolerance mechanisms. One possible method for managing HMs contamination is bioremediation, which uses tolerant bacteria and plants. Therefore, present review, examine the various cellular defence mechanisms against heavy metal toxicity and its remediation process.

Keywords: Heavy Metals, Chromium, Mercury, Bioremediation, Phytoremediation, Phytohormones, Antioxidants.

MAPP46

Cold Plasma Technology: A Sustainable Approach to Wastewater Treatment

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ABSTRACT

Ensuring access to clean water is a global challenge, with traditional water treatment methods often failing to remove pollutants like pharmaceuticals, dyes and harmful microorganisms. Cold plasma technology is emerging as a sustainable and innovative approach to wastewater treatment, offering significant advantages over traditional methods. This technology operates at ambient temperatures, making it energy-efficient and reducing operational costs. Cold plasma generates reactive species such as ozone, hydroxyl radicals, and nitrogen oxides, which are highly effective in degrading organic pollutants, inactivating pathogens, and eliminating toxic chemicals without the need for harmful additives. The versatility process allows it to treat a variety of wastewater types, including industrial effluents, municipal sewage, and agricultural runoff. Its ability to handle complex organic compounds and microbial contaminants makes it a comprehensive and reliable solution for wastewater purification. Cold plasma systems are also compact and can be easily integrated into existing treatment infrastructures or deployed in decentralized locations, facilitating on-site wastewater management and reducing transportation and associated costs. Beyond its technical benefits, cold plasma technology aligns with the goals of green chemistry and sustainable development. It minimizes secondary pollution, supports water conservation efforts by enabling water reuse, and reduces reliance on chemical-based treatments. This makes it an environmentally friendly alternative that contributes to the circular economy by transforming wastewater into a resource. Cold plasma technology represents a promising and sustainable method for wastewater treatment, offering efficiency, environmental safety, and adaptability. Its implementation can significantly enhance the sustainability of water management practices and contribute to the global efforts in preserving water resources.

Keywords: Cold Plasma Technology, Wastewater treatment, Reactive species, Toxic chemicals, Organic Pollutants.

MAPP47

Microbial Innovations in Sustainable Water Purification: Bioremediation and Pollutant Degradation

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ABSTRACT

Water contamination is one of the serious threats to ecosystems and public health; therefore, efficient and sustainable water treatment methods are under development. Microorganisms have become powerful agents in bioremediation and biofiltration due to their ability to metabolize pollutants and transform harmful substances into nontoxic byproducts. Microbial systems have been widely studied in relation to their contribution to water purification, focusing on their potential with regard to diverse contaminants such as organic pollutants, nutrients, and heavy metals.

Metabolic activities of different microorganisms are utilized in the microbial system for efficient pollutant removal. Complementary microbial synergies, including green algae and yeast, optimize nutrient uptake while generating valuable biomaterials. Other bacterial species, including Pseudomonas and Klebsiella aerogenes, have also been shown to decompose complex organic compounds and heavy metal ions. Microbial processes may be complemented by nanoparticles in the form of silver or titanium dioxide to enhance pollutant decomposition via reactive oxygen species generation or photocatalysis.

Microbial water purification probably marks one step wherein sustainable water management can be regarded as a transformational advance that really meets the basic tenets of low energy consumption and limited environmental impact. These technologies naturally use natural processes and hence can easily be described as scalable, benign, and even more environmentally friendly compared to classical chemical and physical treatment. Further integration into frameworks of global water treatment holds great potential for mitigating waterborne pollutants and responding to challenges involving water scarcity.

Keywords: Bioremediation, Microbial Water Treatment, Pollutant Degradation, Heavy Metal Removal, Sustainable Water Purification, Eco-Friendly Technologies.

MAPP48

Need for Bioherbicides and Biopesticides in Agro-Ecosystems

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ABSTRACT

To fulfil the sustainable environmental and agricultural goals the use of bioherbicides and biopesticides is essential. Bioherbicides are agents developed from natural organisms or biochemicals which target specific weeds without harming the surrounding environment. Biopesticides are composed of natural enemies, microbial agents and plant-derived chemicals, targeted at plaht pests. These eco-friendly alternatives improve soil health while maintaining crop yields by increasing biodiversity and reducing the occurrence of pest resistance. Microbial bioherbicides such as DeVine, BioAster, MycoLogic and Agralawn, BioSafe etc. as biochemicals herbicides are commercially available. Biopesticides (Neemix, Pyrethrum, B.thuringiensis, Trichoderma spp., Pheromones etc.) are also there. The integration of bioherbicides and biopesticides into agroecosystems creates a practical prospect in farming practices, especially in organic agriculture. However, challenges such as scalability, cost, and regulatory approval for widespread adoption as also complex diversity of weeds and pests across regions require intensive R&D. The critical role of bioherbicides and biopesticides can play in transforming modern agriculture into a more sustainable, resilient system; to manage the pest and weed pressures in agroecosystems.

Keywords: Bioherbicides, Biopesticides, Agroecosystem, Sustainable, Biodiversity Pheromones.

MAPP49

Modernisation of Rice Cultivars, Plant Genetic Diversity and Human Health Consequences

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ABSTRACT

Rice, a food standard for hundreds of millions of people, has been at the core of human affairs for millennia. Antiepileptic activity is retained by pharmacologic use of ancient rice genotypes in man, which is beneficial for health. It focuses on the variety of heritage rice varieties, their pharmacological effects and potential uses. It has demonstrated the antioxidant, anti-inflammatory, and antibacterial properties of rice starches and their disease-preventive effects in diabetes, cardiovascular disease, and cancer. Furthermore, the paper reports bioactive compounds which are accountable for the aforementioned medical properties, thus presenting a view on the functionalization of the food nutiraceuticals. For the sake of exploiting the therapeutic potential such ancient species of rice have, the present study also argues in favor of the possibility for preservation and enhancement of such a targeted genetic material with human health impacts. The quality of cereal products is determined by a variety of characteristics that may be assigned different significance depending on the desired and use or type of product. Rice is undoubtedly the most important cereal of the world providing 21 percent of global human per capita energy and 15 percent of per capita protein. There is a future need to expand the genetic base of the rice crop by intro grassing genes from diverse sources.

Keywords: Antiepileptic, Pharmacological, Antioxidant, Preservation, Nutiraceuticals.

MAPP50

Millets as Super Food for the Reversal of Neuro-Degenerative Diseases

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ABSTRACT

Millets, the ancient grains of wisdom, are rapidly emerging as superfoods with extraordinary benefits for human health and the planet. These nutrient-dense cereals, including pearl millet, foxtail millet, finger millet, and kodo millet, are powerhouses of polyphenols, antioxidants, dietary fibers, and essential minerals like magnesium and calcium. From boosting metabolic health to fighting chronic diseases such as cancer, neurological diseases and cardiovascular health, millets hold a unique position in the realm of nutrition. Being gluten-free and low on the glycemic index, they are perfect allies in managing diabetes, reducing obesity risks, and improving gut health. Their unparalleled resilience to droughts and low resource needs further cement their role as champions of sustainable agriculture and global food security.

But millet's benefits don't stop at the gut; they also reach deep into the brain. As neurodegenerative diseases like Alzheimer's and Parkinson's continue to rise, millets are gaining attention for their neuroprotective properties. Laden with bioactive compounds, especially polyphenols, millets combat oxidative stress and inflammation, two culprits behind neurodegeneration. Recent studies show millet polyphenols significantly reduce oxidative damage, downregulate Alzheimer's related genes such as Amyloid Precursor Protein (APP) and tau proteins, and enhance the activity of antioxidant enzymes. These grains also modulate inflammatory pathways, fortifying the brain against damage. Each millet variety brings unique benefits to the table: foxtail millet mitigates ethanol-induced oxidative stress, while finger millet, rich in calcium, strengthens synaptic connections and neuronal function.

Millets are not just food; they are a prescription for better neurological health. Incorporating these grains into daily diets offers a sustainable, functional approach to preventing and managing neurodegenerative diseases while enhancing overall well-being. With further research, the potential of millets in global healthcare could redefine dietary strategies for brain health.

Keywords: Millets; Neurodegenerative Diseases; Polyphenols; Gluten Free; Super Food.

MAPP51

Development and Assessment of Prebiotic Herbal Drink Infusion

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ABSTRACT

Prebiotic drink is a beverage made from food products containing prebiotic substances. These prebiotic substances assist the host by strengthening their gut microbial population. The effectiveness of herbal drink is boosted by adding herbal ingredients to obtain immunity enhancing benefits. In this study we prepared a drink with prebiotic and herbal properties. We used healthy ingredients with known high nutrient content, they contain prebiotic substances and have immune modulatory effects. After preparation of prebiotic herbal drink, sensory, nutritional, antioxidant test were conducted. The prebiotic herbal drink was tested to check its effect on the growth of probiotics. Physiochemical properties of the drink were also analysed. In the results, we found that out of those combinations, 182.52mg/100ml antioxidants were present in drink 1 variation 5, 143.91mg/100ml phenols were present in drink 3 variation 5, 109.96mg/100ml proteins were present in drink 2 variation 5, 164.25mg/100ml reducing sugar were present in drink 2 variation 5. Our prebiotic herbal drink increased the growth of Lactobacillus rhamnosus, where as it did not increase the growth of Lactobacillus plantarum. Consumption of prebiotic herbal drink, can notably contribute to overall health by supporting the growth of beneficial gut microbiota. The combination of immunity-boosting herbal ingredients and prebiotic substances works cooperatively to promote good microbiota to enhance digestion, strengthen the immune system. Regular intake of such drinks fosters improved well-being and long-term health benefits.

Keywords: Prebiotics; Gut Microbiota; Nutrition; Immunity; Herbal Drink.

MAPP52

Methicillin-Resistant Staphylococcus Aureus (MRSA): An Escalating Global Health Threat and Its Mechanisms of Resistance

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ABSTRACT

Staphylococcus aureus is a serious and common human pathogen, that causes multiple infectious diseases. Over a period of time, it has developed strains that are resistant to a wide range of antibiotics. Methicillin Resistance Staphylococcus Aureus (MRSA) which is resistant to methicillin and other beta-lactam antibiotic, has become an important epidemic healthcare problem, increasing rapidly across the world. It is one of the most popular commensal pathogen and a leading cause of endocarditis, bone and joint infections, bacteraemia, sepsis, toxic shock syndrome, pneumonia and number of hospital acquired infections. The mechanism of resistance can be due to any one or more than one reason (i) enzymatic drug modification and inactivation (penicillinase and aminoglycoside-modification enzymes), (ii) enzymatic modification of the drug binding site (penicillin-binding protein 2A of MRSA), (iii) efflux pumps (fluoroquinolones and tetracycline), (iv) bypass mechanisms by acquisition of a novel drug-resistant target, (v) displacement of the drug to protect the target. The selection of effective antibiotic therapy for the treatment of MRSA infection depends on a number of factors viz. the type of disease, local S. aureus resistance patterns, availability of the drug, side effect profile, and individual patient profile but the management of spread of MRSA infections in first place remain vital. Also, it is important to focus on the study of emerging resistance to the various treatments against MRSA through continuous surveillance and research.

Keywords: MRSA, Staphylococcus Aureus, Antibiotics, Resistance, Beta Lactam.

ISSN: 2278-9197 © VSRD International Journals: www.vsrdjournals.com

MAPP53

Phytochemical and Pharmacological Aspects of Datura Stramonium Leaves

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ABSTRACT

Datura stramonium is one of the best-known folkloric medicinal herb belongs to Solanaceae family. The qualitative analysis of the extract for various phytochemcals revealed the presence of Alkaloids, Glycosides, Terpenoids, Flavonoids,Tannins and Saponins in the extract of the leaves. Chemical tests and spectrophotometric methods were used for Antioxidant activity. Antioxidant activity tests like DPPH (24.30%), Ferric (Fe^{3+}) reducing power assay, Ferric Reducing Antioxidant Power Assay FRAP, Nitric oxide scavenging assay (28.42%) have been done. The antibacterial activity was detected by Disc diffusion method against Escherichia coli (E.coli). The Zone of inhibition obtained were recorded and analyzed against standard control of Ampicillin and Erythromycin. The active ingredients and possible therapeutic advantages in the creation of a herbal medication, that have sedative, analgesic, and anticholinergic properties, due to antioxidant capacity and phytochemical content, as it participates in the antioxidant defense system against free radical formation. Datura powder is a viable option for formulations that target ailments like pain, inflammation, and neurological problems. Due to their toxicity and overdose risk, Datura powder should be used with caution. Future aspects of this work is to formulate a herbal product for the betterment of Mankind.

Keywords: Datura Stramonium; Antibiotics; Formulations; Therapy; Phytochemicals.

MAOP03

Natural Anti-Diabetic Candidate(s) from Fermented Soybeans (Hawaijar) Associated Bacteria Collected from Manipur, India

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ABSTRACT

As diabetes (diabetes mellitus) is one of the burning issues in human race and discovery of the potent drug is in pipeline. For exploring a potential, microorganisms are an ultimate option due to poor success rate of synthetic drugs. Microorganisms are the valuable source of secondary products especially drugs that have been used from time immemorial in various cultures. In microorganisms, bacteria have been reported to have a variety of natural products with the evidence of diverse activities, such as anti-diabetic activity, antimicrobial, antioxidant, immunomodulatory, anti-cancer and anti-inflammatory activities. However, the bioactivity could be varying depending on the isolated genus/species of bacteria, habitats and also isolation and extraction methods. In this investigation, isolated bacteria from Hawaijar (fermented soybeans) of Manipur, North East India, and extracted potential compound that has been identified by GC-MS and reporting compound(s) that could have anti-diabetic activity. In silico investigation of selected isolates compounds are also investigated and suggested comprising of anti-diabetic activity. In the present investigation, it has been highlighted the advantages of exploring novel habitats (fermented soybeans), and also isolation of potential natural products from the promising and potential isolates that too have promising bioactive compounds. This investigation suggested the analysis of Hawaijar insights the isolation of promising and potential bacteria from Hawaijar (un-explored habitats) and also highlight the possibility of obtaining chemically diverse compounds. The present investigation revealed the isolation of bacteria that could harbor diverse bio-chemical entity, such as antidiabetic candidate that could help in the pipeline of drug discovery.

Keywords: Anti-Diabetic Candidate; Bacteria; Fermented Soybeans; Habitats; Hawaijar; Natural Products.

MAOP04

Application of Advanced Biotechnological Techniques in Poultry farm for Disease Diagnosis

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ABSTRACT

Poultry farming is a significant contributor to global food production, accounting for approximately 34.3% of chicken production worldwide, according to the Food and Agriculture Organization. However, various diseases in chickens adversely affect their immune, gut, respiratory, and reproductive systems, leading to decreased productivity and increased mortality. These challenges necessitate advanced diagnostic methods to ensure the health and productivity of poultry. This study aims to employ biotechnological techniques to diagnose diseases in poultry effectively. By analyzing blood and fecal samples from deceased chickens, we seek to identify the bacterial pathogens responsible for these diseases. Blood and fecal samples were collected from deceased chickens on a poultry farm located in Greater Noida (UP). The samples were inoculated on MacConkey agar media. DNA was extracted from the fecal samples, and PCR (Polymerase Chain Reaction) was performed using four specific primers to detect the presence of Avibacterium paragallinarum, Pasteurella multocida, Mycoplasmagallisepticum, and Mycoplasma synoviae bactria. The blood samples were spread on MacConkey agar and incubated at 37°C, where bacterial colonies were detected suggesting the presence of Escherichia coli (E. coli) as a potential cause of death. Furthermore, PCR analysis of the fecal samples targeted Pasteurella multocida, Mycoplasma gallisepticum, and Mycoplasma synoviae Avibacterium paragallinarum. However, no positive bands were detected for these bacteria, indicating their absence. The presence of E. coli in the blood samples indicates that it was the primary cause of death in the studied chickens. This study highlights the critical role of biotechnological approaches in diagnosing poultry diseases, thereby contributing to improved disease management and sustainability of poultry farming.

Keywords: Poultry; Disease; Diagnosis; Biotechnological Techniques; Avibacterium Paragallinarum.

MAOP05

Saccharomyces boulardii Mediated Inhibition of Aspergillus Flavus

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ABSTRACT

Aspergillus species (A. flavus and A. parasiticus) under optimal conditions produce carcinogenic aflatoxins contaminating food and crops. Bioactive compounds from probiotics strains such as Saccharomyces boulardii offers a promising approach as abiocontrol agent against Aspergillus flavus. In this work, Saccharomyces boulardii cocultured with Aspergillus flavus at the ratio 1:1 (Saccharomyces boulardii: Aspergillus flavus), 10:1, 15:1, 20:1, and 25:1 was assessed (1 refers to 10^6 spores). At a ratio of 20:1, the microscopic examination at 24h showed the absence of germinating conidia, thus suggesting the inhibition of conidial germination of Aspergillus flavus. To determine the gene expression, RT-PCR was carried out for selected genes such as tubulin, hsp90 and AflR. The downregulation of tubulin, hsp90 and AflR was observed in co-culture at a ratio of 20:1 (Saccharomyces boulardii: Aspergillus flavus) in comparison to A. flavus alone. Metabolomic data of co-culture using QTOF-LC/MS showed the presence of 126 intracellular and 23 extracellular bioactive compoundssuch as N6-Acetyl-L-lysine, 3,5-Dinitro-2-hydroxybenzoic acidamong the others. These belonged to flavonoids, carotenoids, polyphenols terpenoids etcexhibiting anti-microbial, anti-tumour, and anti-oxidant properties. During co-culture of Saccharomyces boulardii and Aspergillus flavus, DPPH assay showed higher anti-oxidant properties with 80.9% ROS scavenging activity of co-culture, compared to alone Saccharomyces boulardii with 22% activity. The preliminary data suggested bioactive compounds from Saccharomyces boulardii potentially inhibit the growth of Aspergillus flavus. Bioactive compounds with unknown activity and limited information could be explored further for their beneficial properties.

Keywords: Saccharomyces boulardii, Aspergillus Flavus, RT-PCR, Assays,Bioactive Compounds, QTOF-LC/MS.

MAOP06

Statistical Optimization of Fungal Chitosan Production by Trichoderma sp. in Submerged Fermentation

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ABSTRACT

Chitosan is the second most widely distributed available biopolymer in nature after cellulose. Fungal chitosan is a natural polymer derived from the cell walls of fungi. Chemically, it is deacetylated chitin, similar to crustacean-derived chitosan. However, fungal chitosan is increasingly recognized for its unique advantages, including sustainability, ethical sourcing, and consistent quality. Fungal chitosan has advantages over crustacean chitosan and is in high demand in the global market due to its vast application in different areas such as the food industry, tissue engineering, biopharma, wastewater remediation, etc. Industrial-scale fermentation systems for the synthesis of fungal chitosan have major barriers, which usually restrict their economic yield and feasibility. The extraction, production, and characterization of fungal chitosan from the less explored fungal strain Trichoderma sp., was carried out using a statistical approach. This method helped to optimize various parameters involved in the cultivation of fungi, extraction of chitin, and its subsequent conversion to chitosan, ensuring maximum efficiency with minimal resource use. The one-factor-at-a-time approach was used to assess the impact of medium constituents, such as carbon and nitrogen, on fungal chitosan production. Among all the factors tested, the sources of carbon (glucose) and nitrogen (yeast extract) provided the greatest production of fungal chitosan. A total of 10 variables affected FCH yield and the best ones were evaluated using the Plackett-Burman design. RSM was used in the optimization process, along with the Box-Behnken design (BBD).

Keywords: Fungal Chitosan, One-factor-at-a-time (OFAT), Plackett-Burman design (PDB), Box-Behnken Design (BBD).

MAOP07

Therapeutic Potential of Thuja occidentalis Against Oxidative Stress and Systemic Candidiasis in an Immunocompromised Rat Model

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ABSTRACT

*Thuja occidentalis (TO) is a well-established medicinal plant with long history in traditional medicine. This study explores its therapeutic potential for oxidative stress-related diseases and systemic candidiasis by integrating **in-vitro** assays with **in-vivo** experiments in an immunocompromised rat model. In vitro studies were performed to assess the phytochemical profile, antioxidant activity, and minimum inhibitory volume (MIV) using broth microdilution. For the **in-vivo** model, systemic candidiasis was induced in rats using **cyclophosphamide** and Candida albicans-SC5314. Evaluations included survival rate, hematological parameters, oxidative stress markers, and kidney histopathology to assess the therapeutic effects of TO. Thuja occidentalis exhibited strong antioxidant and antifungal activities. The mother tincture displayed a high total phenolic content (409.6±2.1 µg/mL, gallic acid equivalent) and potent antioxidant capacity (DPPH: 44.3±0.2 µg/mL; ABTS: 119.8±1.9 µg/mL). **In-vitro** antifungal assays demonstrated significant activity against Candida albicans, with a minimum inhibitory volume of 20 µL. In the **in-vivo** model, TO-treated immunocompromised rats showed improved survival and enhanced hematological parameters in the 6C and 30C groups. Histopathological analysis indicated protective effects in the kidneys of TO-treated animals. This study provides compelling evidence for the antioxidant, antifungal, and immunomodulatory properties of Thuja occidentalis homeopathic formulations in the treatment of systemic candidiasis. The natural compounds present in Thuja occidentalis demonstrate significant therapeutic potential, offering an alternative to conventional chemical therapies. This research highlights the promising role of natural products in combating chronic infections, underscoring their value in modern biomedicine and their potential for developing novel therapeutic strategies.*

Keywords: Antioxidant activity; Anti-candidiasis; Candida Albicans; Immunosuppression; Systemic Candidiasis; Immunomodulatory.

MAOP08

Impact of Cultivation Conditions on Yield and Thermal Properties of Bacterial Cellulose Synthesized by Gluconacetobacter kombuchae MTCC 6913

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ABSTRACT

Bacterial cellulose is a renewable biomacromolecule that offers significant environmental benefits. It is naturally found in plants and produced by specific microbes. Notably, it is synthesized by the Gram-positive bacterium Sarcina ventriculi, as well as various Gram-negative bacteria including Gluconacetobacter, Agrobacterium, and Acetobacter. Known for its excellent physicochemical properties, such as high purity & crystallinity, and improved mechanical strength, BC holds immense potential for different industrial applications. This study investigates the cellulose-producing potential of G. kombuchae MTCC 6913 under static conditions and understanding the effects of temperature and pH variations on BC yield and its thermal behaviour. The optimal cellulose yield of 5.08 ± 0.29 g/L was achieved during static cultivation at 30°C and pH 6.0 ± 0.2, using 2% w/v glucose as the primary carbon source. BC recovered was characterized using Differential Scanning Calorimetry (DSC) to infer the thermal behaviour of the BC, which is essential for various applications. DSC analysis demonstrated the variations in heat stability of BC samples produced under different pH conditions. Low pH values resulted into BC samples having weaker network structure, resulting in weaker heat stability. This study highlights the versatility of BC and illustrates the promising prospects of producing microbial cellulose under optimized conditions, contributing to the development of sustainable and eco-friendly materials.

Keywords: Bacterial Cellulose, Biomacromolecule, Static Cultivation, Sustainable Materials, Thermal Properties.

MAOP09

Comparative Analysis of PHA Production by Hydrocarbon-Contaminated Soil Bacterias Isolate Under Static and Agitated Culture Conditions

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ABSTRACT

Polyhydroxyalkanoate (PHA) is a promising biopolymer that serves as an environmentally friendly alternative to synthetic polymers due to its biodegradable nature. PHA is naturally produced by microbes, making it easily degradable by microorganisms. This biopolymer is typically synthesized by bacteria under nutrient-limited conditions, where essential growth nutrients are scarce, but carbon sources are abundant. In bacterial cells, PHA accumulates intracellularly as water-insoluble inclusions or granules, serving as a storage material for carbon and energy. These granules not only make PHA production feasible but also contribute to its unique properties, such as biodegradability, biocompatibility, and versatility. These features enable its application across various industries, including biomedical, textile, and agriculture.

This study focuses on isolating PHA-producing bacteria from hydrocarbon-contaminated soil using the serial dilution technique. The isolated bacterial strains were subsequently screened using Sudan Black and Nile Blue staining methods to confirm their capability to synthesize PHA. This study investigates the impact of static and agitation conditions on PHA production and recovery. Bacterial cultures were grown at 37°C under static and agitation conditions at 120 rpm. Mineral Salt Media (MSM) was utilized as the growth medium for PHA synthesis. PHA was recovered from bacterial cells using the chloroform solvent extraction method. To further characterize the produced product as PHA, Fourier Transform Infrared Spectroscopy (FTIR) was employed to identify functional groups, while Differential Scanning Calorimetry (DSC) was conducted to analyze the thermal properties of the recovered PHA. The results concluded the isolated bacteria as a potential producer of PHA. Study may be scaled up for large scale production of PHA for different industrial applications.

Keywords: PHA, Synthetic Polymers, Mineral Salt Media, FTIR, DSC.

MAOP10

Metabolite Profiling and Optimization Strategies for Producing Metabolite from Endophytic Bacteria Isolated from Medicinal Plants

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ABSTRACT

The rising curiosity about undiscovered organic compounds from diverse endophytic bacterial ecosystems has attracted scientific attention, owing to their versatile aspects and applications across numerous domains. The diversity of endophytic bacterial isolates from distinct geo-climatic regions underscores the individuality of each organism and their promise as rich sources for discovering novel secondary metabolites. In a current investigation, we isolated endophyte bacteria from the medicinal plant Humulus lupulus. Endophyte bacteria are well known for their diverse pool of secondary metabolites. Isolated endophyte bacteria were further studied for their metabolites by Liquid Chromatography-Mass Spectrometry (LC-MS) and Gas Chromatography-Mass Spectrometry (GC-MS). Examination of the extract revealed various secondary metabolites holding diverse applications in the therapeutic and agriculture sectors. Furthermore, Ultra-performance Liquid Chromatography (UPLC) was employed to quantify the metabolites including Indole-3-Acetic Acid (IAA). Additionally, IAA production was also optimized by different abiotic factors.

Keywords Secondary Metabolites, Gas Chromatography-Mass Spectrometry, Liquid Chromatography-Mass Spectrometry, Environment Sustainability.

MAOP11

Nano Biochar: An Innovative Approach Towards Sustainable Agriculture and Circular Bioeconomy

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ABSTRACT

Biochar has been acknowledged as a valuable resource in the framework of sustainable agriculture and circular bioeconomy. Agro-waste such as crop residues, forest waste products, and other agricultural organic matters, offers a promising feedstock for biochar production through pyrolysis. This process not only helps in lowering the amount of agricultural waste but also creates a stable carbon-rich material that can be utilized for soil improvement, carbon sequestration, and renewable energy production. Nano biochar has numerous advantages conferred by enhanced properties, including high surface area, pore volume, and surface functionalities. These attributes offered Nano biochar, the advantages over the parent biochar material and obtrude it as an efficient material for applications in resource recovery, environmental remediation, and waste management, contributing to the goal of sustainability. The role of Biochar, in sustainable development is multi-faceted; its use in the agriculture sector provides a sustainability solution by enhancing soil fertility, better water retention, and mitigating greenhouse gas emissions by sequestering carbon over long periods. Additionally, the use of agro-waste for biochar production contributes to a circular economy by turning waste into a valuable product, diminishing dependency on synthetic fertilizers, and promoting carbon-negative goals. The importance of biochar application in combination with inhibitors of nitrification as a nutrient management strategy that can play a significant role in the circular bioeconomy. Such enhancements lead to increased contaminant sorption in both soil and aqueous environments. In addition, Nano biochar demonstrates catalytic characteristics to its use in numerous applications, including targeted drug delivery, enzyme immobilization, sensors, additives, and polymer synthesis. The recent advances in the use of Biochar for diverse sectors will be reviewed.

Keywords: Biochar; Agro-waste; Pyrolysis; Sustainable Development; Soil Fertility; Carbon Sequestration; Circular Economy; Climate Change Mitigation.

MAOP12

Tapping the Role of Microbial Inoculants in Environmental Management and Agricultural Sustainability

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ABSTRACT

To feed the growing population across the world which is projected to reach 9.7 billion in 2050 according to United Nations, the green revolution made use of the chemical fertilizers and pesticides to enhance agriculture productivity and save the crops from pests. But the indiscriminate application of these has unknowingly posed a serious threat to the ecosystem such as soil fertility loss, acidification of soil, nitrate leaching, resistance of species toward pesticides and loss of biological diversity. Pesticides being recalcitrant in nature persists in soil for longer periods and make their way in food chain and water cycle resulting in an increased bioaccumulation and biomagnification in each successive trophic level. Physical and chemicals methods of pesticide detoxification prove to be very expensive owing to the use of costly membranes or solvents. Microbial remediation on the other hand is cheap and effective in degrading hydrophobic toxic pollutants. Use of microbial consortia than single bacteria proves to be more effective as microbes in consortium work synergistically by releasing multiple oxidoreductive enzymes capable of cleaving bonds in various recalcitrant structures. Consortium comprising of multi-traits as pesticide tolerance and potential to produce plant growth promoting (PGP) factors provide a sustainable solution for reclamation of pesticide contaminated soils. Consortia of such microbial inoculants colonize near plant roots and improve plant growth and health by various indirect and direct mechanisms such as IAA production, N_2 fixation, increased biotic and abiotic stress tolerance, nutrient acquisition and induced systemic resistance along with degradation of toxic chemicals such pesticides.

Keywords: Microbial Inoculants; Pesticides; Bioremediation; Environmental Restoration; Plant Growth Promotion.

MAOP14

Waste Valorisation and Health Benefits of Jackfruit Waste

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ABSTRACT

Jackfruit (Artocarpus heterophyllus Lam.), is utilized for its nutritional richness and culinary versatility, produces substantial by-products during its consumption. Jackfruit contains both edible and inedible waste parts. All parts of jackfruit have therapeutic qualities therefore they are used in many traditional medical systems to treat a variety of illness. Most of the jackfruit parts are thrown away and often overlooked including seeds, rinds, rags and core. These waste materials comprise higher-value pharmaceutical ingredients like secondary metabolites, alkaloids, flavonoids as well as phenolic molecules. Due to presence of significant quantity of proteins and bioactive phytoconstituents, these are currently used to cure a number of severe ailments like inflammation, diarrhoea, and diabetes mellitus. These bioactive compounds are being used for the treatment of various biological conditions as these are antiviral, antioxidant, antiplatelet, anthelmintic, anticancer, anti-melanin, antiatherosclerosis, immunomodulatory. Jackfruit leftovers are high in phytochemicals as well proteins, fats, and carbohydrates. By integrating jackfruit waste into value-added products, this research emphasizes the dual benefits of environmental sustainability and innovative health solutions, paving the way for future advancements in waste management and bioproduct development.

Keywords: Pharmaceutical Ingredients; Anticancer; Phytochemicals; Antiatherosclerosis; Immunomodulatory.

MABS01

Dendrobine: The Hidden Gem of Trichoderma longibrachiatum

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ABSTRACT

Dendrobine, a bioactive alkaloid, has emerged as a pivotal compound within Trichoderma longibrachiatum, a fungus celebrated for its diverse biotechnological applications. This presentation delves into dendrobine unique chemical profile, biosynthetic pathways, and precursors compounds & nanoparticle roles. It highlights the potential of dendrobine biosynthesis from Trichoderma longibrachiatum, including its extraction, detection and transcriptomics analysis. Additionally, the study explores the symbiotic relationship between Trichoderma longibrachiatum and Dendrobium nobile plant systems, emphasizing dendrobine yield. The study also explores the concentration-dependent effects of CH-Ag/Au-NPs on dendrobine production in Trichoderma longibrachiatum. By uncovering dendrobine multifaceted research, this work underscores the importance of Trichoderma longibrachiatum as a treasure trove of Dendrobine and its promising future in sustainable agriculture and medicine.

Keywords: Trichoderma longibrachiatum; Dendrobine; Biosynthetic Pathways; Dendrobium Nobile.

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ISSN 2413-3973

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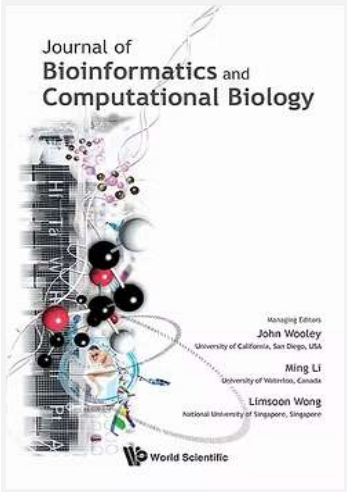

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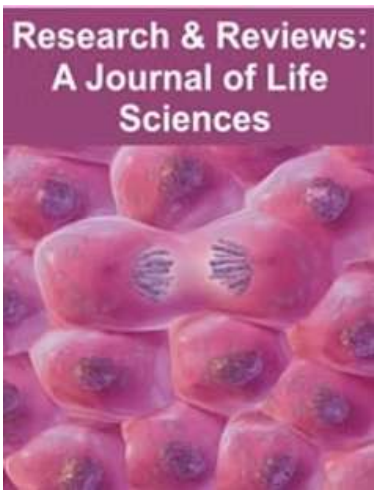

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EDITORIAL PROFILE

Prof. Pammi Gauba is the Head of the Department of Biotechnology and also the Dean (A&R, International Affairs, and Sponsored Projects. She has a vast experience of 36 years in teaching and research at different institutes in India and abroad. Her current research work focuses on Inorganic and organic pollutants and their remediation. She has published more than 65 research articles in reputed international journals and several book chapters, edited 5 books and 4 patents filed. She is supervising close to 10 PhD scholars in JIIT. She holds several sponsored R&D research projects from ICMR, MOEF, DRDO, BIRAC and AYUSH.

Dr. Shalini Mani, Associate Professor in the Department of Biotechnology at Jaypee Institute of Information Technology, Noida, India, brings 21 years of research and 14 years of teaching experience. She earned her PhD from the Centre for Cellular and Molecular Biology, Hyderabad, where she investigated genotype-phenotype correlations in Leigh syndrome patients, and completed a post-doctorate at Murdoch Children's Research Institute, Australia, as an Endeavor Research Fellowship awardee. Her research spans mitochondrial roles in chronic diseases, the impact of environmental factors on mitochondrial metabolism, and exploring the therapeutic potential of herbs in diabetes, cancer, and neurological disorders, resulting in several high-impact publications. She has an extensive publication record, with over 65 research and review articles in prestigious international journals. Additionally, she is the author of one book, editor of two books, and holds one published patent.

Dr. Nidhi Batra, has been serving as an Assistant Professor in the Department of Biotechnology at Jaypee Institute of Information Technology (JIIT) since July 2023. Before joining JIIT, she worked as a Scientist at the Indian Biological Data Centre, Regional Centre for Biotechnology, Faridabad. She completed her Ph.D. from Dept. of Biochemistry, University of Delhi, and joined CSIR-Institute of Genomics and Integrative Biology (IGIB) for her post-doctoral research. he was awarded the DBT-Research Associateship and SERB N-PDF fellowships during her 6 years tenure at IGIB. At IGIB, she expanded her expertise in molecular simulations to investigate the mechanisms and biology of critical autophagy proteins, RNA-protein interactions, and various GPCRs. She is a computational biologist with 10 years of research experience in bioinformatics, including computational structural biology, molecular biophysics, structural bioinformatics, and computer-aided drug design.

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