BioSangam 2024 6th International Conference on Bio-Technological Intervention for Health, Agriculture and Circular Economy

BioSangam 2024

6th International Conference on

Bio-Technological Intervention for Health, Agriculture and Circular Economy

February 23-25, 2024

Conference abstract proceeding

Organized by

Department of Biotechnology
Motilal Nehru National Institute of Technology Allahabad, Prayagraj-211004, India

Sponsored by :

SERB INDIA

CSIR-INDIA
सीएसआईआर
CSIR
भारत का नवाचार इंजन
The Innovation Engine of India

INNOVATION & INCUBATION HUB MNNIT FOUNDATION
MNNIT ALLAHABAD

BioSangam 2024

6th INTERNATIONAL CONFERENCE

on

Biotechnological Intervention for Health Agriculture and Circular Economy

February 23-25, 2024

Editor-in-chief

Dr. Sangeeta Negi

Organized by

Motilal Nehru National Institute ofTechnology Allahabad

Prayagraj – 211004, U.P., India

First Impression 2024

© Motilal Nehru National Institute of Technology Allahabad
Prayagraj – 211004, India

No part of this publication may be reproduced or transmitted in any form by any means, electronic or mechanical, including photocopy, recording, or any information storage and retrieval system, without permission in writing from the copyright owners.

DISCLAIMER
The authors are solely responsible for the contents of the papers compiled in the any manner. Errors, if any, are purely unintentional and readers are requested to communicate such errors to the editors or publishers to avoid discrepancies in future.

ISBN: 978-81-963268-9-0

Published by:
Mohan Enterprises
55/14, Motilal Nehru Road
Prayagraj - 211002
Mobile No. 9935048482

Printed by:
Belvedere Press
55/14, Motilal Nehru Road
Prayagraj - 211002
Mobile No. 9935048482

Our Sponsors

SERB
INDIA

वैज्ञानिक तथा औद्योगिक अनुसंधान परिषद-भारत
CSIR-INDIA
सीएसआईआर
CSIR
भारत का नवाचार इंजन
The Innovation Engine of India

INNOVATION & INCUBATION HUB MNNIT FOUNDATION
MNNIT ALLAHABAD

• • •

मोतीलाल नेहरू राष्ट्रीय प्रौद्योगिकी संस्थान इलाहाबाद
प्रयागराज-211004 [भारत]
Motilal Nehru National Institute of Technology Allahabad
Prayagraj-211004 [India]

Professor Rama Shanker Verma
Director
Ph.D., FNASc, FBRSI, FAMI

प्रो. रमाशंकरवर्मा
निदेशक
Ph.D., FNASc, FBRSI, FAMI

Message

It is great pleasure to extend a warm welcome to all participants to the 6th edition of International Conference “Biosangam 2024”, organized by the Department of Biotechnology under the theme "Bio-Technological Intervention for Health, Agriculture, and Circular Economy", scheduled for February 23-25, 2024.

I take this opportunity to congratulate the Department of Biotechnology, MNNIT for taking the initiative to conduct the conference, which promises to explore innovative biotechnological solutions, aiming to enhance human health, agricultural productivity, and sustainability within the circular economy framework. Ultimately, these advancements hold the potential to revolutionize various sectors, offering promising solutions to pressing global challenges and paving the way for a healthier, more resilient future. I am delighted by the participation of esteemed speakers and delegates, both national and international, whose contributions will undoubtedly enrich our deliberations.

I am confident that this conference will provide interactive deliberations, paving the way for the emergence of innovative ideas and fostering effective collaborative research efforts. Once again, I extend a heartfelt welcome to all delegates and participants, and look forward to fruitful deliberations.

I wish “Biosangam 2024” a grand success.

(Prof. R.S Verma)

Director

मोतीलाल नेहरू राष्ट्रीय प्रौद्योगिकी संस्थान इलाहाबाद
प्रयागराज-211004 [भारत]
Motilal Nehru National Institute of Technology Allahabad
Prayagraj-211004 [India]

Dr Sangeeta Negi
(Head and Chairman
Biosangam 2024)

Message

I am delighted to extend a warm welcome to all participants of Bio Sangam 2024: "Bio-Technological Intervention for Health, Agriculture, and Circular Economy". This conference serves as a unique platform for faculty, scientists, researchers, students, and learners to explore new frontiers and emerging trends in Biotechnology. Now in its 6th edition since its inception in November 2013 this conference has gradually gained its fame, and it is the most awaited conference in the region.

Biosangam has garnered renown and anticipation within the region, akin to the convergence of the holy rivers Ganga and Yamuna at Prayagraj, creating 'Sangam'.

Through interactive sessions, keynote addresses, plenary talks, and invited lectures, participants will gain valuable insights. The presence of students from across India offers them the opportunity to engage with esteemed scientists and researchers from around the globe. To recognize exemplary contributions, awards in categories such as poster presentations, oral presentations, and the Young Scientist Award (YSA) will be presented, acknowledging their dedication and hard work.

The success of this event is a testament to the tireless efforts of those working diligently behind the scenes, and I express my heartfelt gratitude to my colleagues and the entire team for their unwavering support.

Once again, I extend a warm welcome to all delegates and participants, and I am confident that this conference will be a resounding success.

Sangeeta
(Dr. Sangeeta Negi)

Head Of
Department

Organizing Committee

Patron	Prof. R.S. Verma, Director, MNNIT Allahabad, Prayagraj, U.P. India
General Chair	Head, BTD, MNNIT Allahabad, Prayagraj
Chairperson and Convener	Dr. Sangeeta Negi, BTD, MNNIT Allahabad, Prayagraj
Treasurer	Dr. Ashutosh Mani, MNNIT Allahabad
Organizing Secretaries	Dr. Sameer Srivastava Dr.Joyabrata Mal Dr. Rupika Sinha
Coordinators	Prof. Shivesh Sharma, BTD MNNIT Allahabad Prof. Anjana Pandey, BTD MNNIT Allahabad Dr. N.K. Singh, BTD, MNNIT Allahabad Dr. Vishnu Agarwal, BTD, MNNIT Allahabad Dr. Manisha Sachan, BTD, MNNIT Allahabad Dr. Seema Nara, BTD, MNNIT Allahabad Dr. Ashutosh Mani, BTD, MNNIT Allahabad Dr. Sameer Srivastava, BTD, MNNIT Allahabad Dr. Ambak Kumar Rai, BTD, MNNIT Allahabad Dr. Radha R. Mewaram, BTD, MNNIT Allahabad Dr. Monika P Rai, BTD, MNNIT Allahabad Dr.Joyabrata Mal, BTD, MNNIT Allahabad Dr.Girijesh K. Patel, BTD, MNNIT Allahabad Dr.RupikaSinhaa, BTD MNNIT Allahabad

Editorial Board

Editor-in-Chief Dr. Sangeeta Negi

Editors Prof. Shivesh Sharma, BTD MNNIT Allahabad

Prof. Anjana Pandey, BTD MNNIT Allahabad

Dr. N.K. Singh, BTD, MNNIT Allahabad

Dr. Vishnu Agarwal, BTD, MNNIT Allahabad

Dr. Manisha Sachan, BTD, MNNIT Allahabad

Dr. Seema Nara, BTD, MNNIT Allahabad

Dr. Ashutosh Mani, BTD, MNNIT Allahabad

Dr. Sameer Srivastava, BTD, MNNIT Allahabad

Dr. Ambak Kumar Rai, BTD, MNNIT Allahabad

Dr. Radha R. Mewaram, BTD, MNNIT Allahabad

Dr. Monika P Rai, BTD, MNNIT Allahabad

Dr.Joyabrata Mal, BTD, MNNIT Allahabad

Dr.Girijesh K. Patel, BTD, MNNIT Allahabad

Dr. Rupika Sinha, BTD, MNNIT Allahabad

Content

Speakers

Session 1:Biotechnological Intervention in Complementary, Herbal and Transitional science

Session 2: Biotechnological Intervention in Integrative and Computational research

S3: Biotechnological Intervention in Process Development and Manufacturing

Session 4: Biotechnological Intervention in Agriculture and Food sector

Session 5: Biotechnological Intervention in Interdisciplinary Approach in Design and Innovation

Session 6: Environmental issues and Sustainability

Session 7 : Biotechnological Intervention in Biomedical and Health

Session 8 : Biotechnological Intervention in Resource recovery and circular economy

Session- 9: Young Scientist Award

SPEAKERS

Plenary lecture

Health care through Sangam of Cells, Engineering and Medicine

Dr. Amulya K Panda, Ph. D., FRSC
One Stream Research Centre
Panacea Biotec Ltd, New Delhi-110044

Medicine in the form of small molecules either from plants or through chemical synthesis and from biological origin has been the main treatment option for many diseases. Particularly in last century modern medicine based on small molecules and biologics has improved the life expectance of humans considerably. However, the effectiveness of small molecules and biologics to heal the human suffering is limiting either due to development of drug resistance or evolution of new pathogens. With many more pandemics in comparison to that experienced in 20th century has diverted the attention of medical treatment to kill the pathogen concept to heal the body. More and more attention being paid to make the whole human body more robust to fight the pathogens than destroying the pathogens using different mode of treatments. The concept of prevention is better than cure is becoming more prevalent option for medical treatment. Vaccine and immunity are the best weapon for protection against pathogens. As the whole body is composed of cells in particular pattern, the research on how cell function leading to different organs provide a viable mode of understanding its function and generating solutions to correct it in case of abnormality. Cells in body act as therapeutic intervention in many cases. Living Cells are architect of themself and can be used to develop engineering discipline if used properly. The living cells because they sense, move and act can be a combination of drug, device and diagnostic tool. The current trend is to use the power of living cells and use them as drug for treatment. This concept of treatment is called advance therapeutic medicinal products (ATMP) and essentially involves treatment of the body at the level of gene, cell and tissue. These are essentially the gene therapy, cell therapy and tissue engineering currently used as treatment option. Even if the field is new, US FDA has approved more than 30 products as ATMP in the recent years. Immunotherapy using engineered T cells is becoming the best treatment modality for cancer patients. Tissue engineering help in regenerating the damage tissue rather than using prosthetic or replacement. The details of gene therapy, cell therapy and tissue engineering as mode of treatment will be discussed during the presentation.

"Self-Nano Emulsifying Curcumin-30 (SNEC-30): Unleashing theTherapeutic Potential of Curcumin"

Dr. Ganesh Ramamurthi* and Dr. Saurabh Arora
*ganesh@aurigaresearch.com

Abstract

The invited lecture on "Self-Nano Emulsifying Curcumin-30 (SNEC-30): Unleashing the TherapeuticPotential" will delve into the innovative realm of drug delivery systems, specifically focusing on thetransformative technology of self-nano emulsifying formulations for curcumin. Curcumin, a potentnatural polyphenol found in turmeric, is renowned for its diverse therapeutic properties, includinganti-inflammatory, antioxidant, and anticancer effects. However, its limited bioavailability has been alongstandingchallengeinmaximizingits clinical efficacy.

The presentation will comprehensively explore the formulation and characterization of Self NanoEmulsifyingCurcumin-30(SNEC-30), a ground breaking approach designed to overcome the bioavailability constraints associated with conventional curcumin delivery. The lecture will elucidatethe principles behind SNEC-30, detailing its ability to spontaneously form nano-sized emulsions upon contact with gastro intestinal fluids, there by enhancing curcumin solubility and absorption.

Moreover, the discussion will encompass the pharmaco kinetic advantages of SNEC-30, emphasizing its potential to enhance cellular uptake and improve therapeutic outcomes. It will also touch upon thepromising preclinical and clinical studies that underscore the efficacy and safety profile of SNEC-30, positioning it as a promising candidate forarangeoftherapeuticapplications.

In conclusion, the presentation on Self-Nano Emulsifying Curcumin-30 aims to provide a comprehensive understanding of this innovative drug delivery system, shedding light on its formulation, mechanisms of action, and its potential impact on advancing the therapeutic utility ofcurcuminin various medical contexts.

Session-1

Moringa leaves and its fruits

Dr. Sweta Singh, AYUSH

Moringa leaves and it's fruits were administered according to their PRAKRITITarget group: Low immunity patients and patients suffering from nutritional deficiency disorders. In this comprehensive study, our primary objective was to meticulously investigate the impacts of moringa leaves and it's fruits on immunity malnutrition nutritional deficiency related disorders and overall holistic well-being among a diverse cohort of individuals diagnosed with low immunity and malnutrition The study engaged 200 participants, selected through a meticulous screening process, ensuring representation across various demographics and encompassing a range of ages, medical histories, and dietary preferences.Participant Selection: The recruitment process involved identifying individuals aged between 20 and 80 years with either low immunity or suffering from nutritional related disorders. The selection aimed to capture the intricacies of responses across different age groups and disease stages. Participants were recruited from diverse backgrounds, reflecting the broader population with metabolic health concerns.

Dietary Intervention: Each participant received individualized dietary advice, incorporating moringa into their daily meals. The types and quantities of moringa were determined based on participants' dietary preferences, ensuring realistic and sustainable integration into their existing eating patterns. Clear instructions were provided regarding the preparation and incorporation of moringa leaves or fruits considering taste preferences and culinary habits. Participants were encouraged to maintain their usual physical activity levels and were advised to report any noticeable changes in lifestyle factors during the intervention period.Regular Follow-up: The study incorporated regular follow-up sessions to monitor participants' progress and assess adherence to the moringa intervention. During these sessions, participants were interviewed to gather qualitative insights into their experiences. Detailed dietary logs were maintained to track moringa consumption, and any modifications to participants' overall dietary habits were documented. Adherence was reinforced through personalized counselling, addressing individual challenges and concerns related to the inclusion of moringa in their diets. Primary outcome measures included changes in biochemical levels, monitored at regular intervals throughout the intervention period. subjective experiences were documented, encompassing perceived improvements in overall well-being, energy levels, and any observed changes in weight. This holistic approach aimed to capture the broader impacts of moringa consumption beyond traditional markers.

Bio-computational tools for cyanobacterial metabolites production: emerging technologies and challenges

Pratyoosh Shukla*

Enzyme Technology and Protein Bioinformatics Laboratory, School of Biotechnology, Institute of Science, Banaras Hindu University, Varanasi-221005, India

The cyanobacteria are source of various biologically important metabolites which are useful in many applications. These metabolites are non-toxic and safe to the environment. Due to the rising interest of scientific fraternity towards using bio-computational tools viz. Artificial intelligence- Machine Learning (AI-ML) for production optimization, it is becoming little convenient to enhance the yield of the cyanobacterial metabolite. However, the large-scale production of such metabolites is a challenging task and there are few limitations. Here, in this study, we have explored the Machine Learning and Artificial intelligence (AI-ML) based tools for the production optimization cyanobacterial metabolite i.e. phycobiliproteins (PBPs) from *Nostoc* sp. CCC-403 and *Anabaena variabilis* CCC421. Our studies have recommended significant improvement in the production yield by the integrative use of combinatory evolutionary algorithm (CNN and MOGA) and ANN based tools. Our study also elucidated that the production and optimization of phycobiliproteins (PBPs) from *Nostoc* sp. CCC-403 and *Anabaena variabilis* CCC421 can be made more effectual by using such tools. Furthermore, we are also working on cyanobacterial transcriptional engineering for constructing competent cyanobacterial strains.

Session- 2

Biomedical Text Mining and Genomics

Prof. N. Jeyakumar,
Dept. of Bioinformatics, School of Life Sciences, Bharathiar University
*n.jeyakumar@yahoo.co.in

Abstract

Besides experimental data, there is a substantial amount of biomedical knowledge recorded only in the form of free-text in abstracts, full-text articles and clinical records etc. For example, the biomedical literature database PubMed currently contains about 30 million abstracts and an average about 50,000 new abstracts are added every month. Storage of articles in PubMed has tremendously increasing every year, biomedical literature data mining is one of the recent challenges in Big Data Analysis. The discipline text mining is evolved for automatic extraction new knowledge from published literature. Text mining is defined as the utilization of automated methods for the enormous amount of knowledge available in text documents. The application of biomedical text mining includes biomedical named entity tagging (e.g. genes, proteins, enzymes, drugs etc.), entity concept relation extraction (e.g. protein-protein interactions, drug-disease relations etc.) and mining new knowledge (e.g. biomarker discovery, biomedical pathways, functions etc.). This presentation serves as an introduction to the applications of various text mining approaches in genomics. It is divided into two parts with the first half as an overview of text mining in the biosciences with some of the tools developed by my group. The second part reviews strategies and methods for few case studies of biomedical text mining in genomics and biomarker discovery.

Session-2

Validating Fractalkine receptor as a target and identifying candidates for drug discovery against type 2 diabetes

Madhu Yadav* and Yusuf Akhter

Department of Biotechnology, Babasaheb Bhimrao Ambedkar University, Vidya Vihar, Rae-bareli Road, Lucknow 226025, Uttar Pradesh, India.

* madhuyadav2003@gmail.com

Abstract

Type 2 diabetes mellitus (T2DM) is widely acknowledged as a prevalent chronic condition globally, characterized by a complex pathogenesis closely associated with metabolic disorders manifesting in elevated blood sugar levels. The regulatory processes governing the Fractalkine/CX3CR1 system in islet β-cell function play a pivotal role in boosting insulin secretion and facilitating glucose uptake in human islets. The expression of CX3CR1 in islets is negatively influenced by several factors, including a high-fat diet, obesity, and aging, implying that reduced levels of CX3CL1/CX3CR1 may contribute to β-cell dysfunction in T2DM. This establishes it as a promising therapeutic target for the condition of T2D. Despite the efficacy of lifestyle modifications, such as weight loss and exercise, in treating T2D, a substantial portion of patients faces challenges in implementing these changes. Therefore, this study employs *in-silico* analysis to pinpoint the Fractalkine receptor protein CX3CR1 as an innovative drug target for type 2 diabetes. The genome-wide analysis of Fractalkine receptor CX3CR1 in β-cells identifies novel drug targets and informs the development of new therapeutic interventions. Single differential gene expression evaluations of CX3CR1 in pancreatic beta-cells from individuals with type 2 diabetes are conducted using samples from the GEO database. In this investigation, sequence, structure, and functional analysis are carried out through homology modeling, revealing that the CX3CR1 protein consists of seven transmembrane helical structures and a central transport channel spanning the protein. Structural alignment with homologous protein structures identifies a single binding pocket. Subsequently, an optimized CX3CR1 structure is screened against the ZINC15 database library of drug-like molecules, resulting in the identification of three notable compounds with high binding affinity at the CX3CR1 active site region. Three potent virtual hits are identified based on different cut-off values, including binding energy, hydrogen bonding, and ADMET properties. The stability of the protein-ligand complex is explored through an MD simulation study spanning a 50 ns time scale. Results indicate that ZINC000032506419 emerges as the most suitable lead molecule, displaying a high binding affinity for the catalytic region of CX3CR1 and forming robust hydrophobic and polar interactions with the amino acid side chains involved in the binding site.

Investigating diverse roles of nuclear factor-y transcription factor in finger millet: a genomics and bioinformatics approach

Prof. Dinesh Yadav* and Varsha Rani
Department of Biotechnology
D.D.U. Gorakhpur University, Gorakhpur (U.P.) 273009, INDIA
dinesh_yad@rediffmail.com

The Nuclear Factor Y (*NF-Y*) transcription factor (TF) family is ubiquitously present in most eukaryotes in the form of heterotrimeric complex protein and play diverse regulatory functions in plants, particularly related to stresses and developmental processes. Finger millet (*Eleusine coracana* (L.) Gaertn) is one of the significant nutraceutical grains, well known for its ability to thrive well in harsh environmental conditions of drylands. The availability of its genome sequence in public domain made to characterize a few transcription factors, but still, the *NF-Y* gene family is not well taken. *In-silico* characterization of *NF-Y* genes of Finger millet led to identification of a total of 59 *NF-Y* genes, among which 18 encode for *EcNF-YA*, 23 for *EcNF-YB* and 18 for the *EcNF-YC* subunits. The *In-silico* characterization of these genes in term of genomic and chromosomal organization, gene duplication, subcellular localizations, conserved motifs, miRNAs and evolutionary analysis result into that most of the *EcNF-Ys* genes are harbour at chromosome 5 followed by Chromosome 3. The conserved domain of *EcNF-YAs* gene, involved in DNA interaction and *NF-YB/C* interaction. Phylogenetic relationships displayed that finger millet *NF-YC* genes shows evolutionary similarity with *EcNF-YB* genes. And members of the *EcNF-Y* family evolved through synonymous substitution and through strong stabilizing selection during the process of evolution. In the analysis of promoters, it was found *EcNF-Y* genes harbour with *ABRE, DRE* and *MYB* cis-elements, associated with drought tolerance. Whereas, interaction of *EcNF-YA* and *miRNA169*, indicating its diverse role against devasting pathogen (*Magnaporthe oryzae*) causing blast disease in finger millet. The expression profiling of *EcNF-Y* genes under 20%PEG treatment result in induction of *EcNF-YA5, EcNF-YA16, EcNF-YB10, EcNF-YB14* and *EcNF-YC2* genes indicating its ability for drought adaptation. Likewise, under 250mM NaCl treatments, the induction of *EcNF-YA16, EcNF-YB10, EcNF-YB14, EcNF-YC1* and *EcNF-YC2* genes indicating their putative role in salinity tolerance. Interestingly, expression of seven members of *EcNF-Y* family (*EcNFYA1, EcNFYA5, EcNFYA16, EcNFYB3, EcNFYB6, EcNFYB14* and *EcNFYC2)* under both drought and salt stress suggesting a cross talk among them. As far as we are aware, this is the first report describing functional characterization and extensive evaluation of the *NF-Y* gene in finger millet, which may be useful in improving crop tolerance to abiotic and biotic stresses.

Keywords: Abiotic stress, Biotic stress, Finger millet, nuclear factor Y, Transcription Factor

Biogas to bio-methanol: A biotransformation for applications in jet fuel

Prof. Rintu Banerjee
Professor and Dean R&D
IIT Kharagpur- 721 302
rb@iitkgp.ac.in

Abstract

The usage of energy has steadily increased since the industrial revolution resulting in a severe alteration of the global ecosystem. The synthesis of bio-methanol from agricultural waste is a viable option for sustainable energy generation, while also solving waste management issues and lowering dependency on fossil fuels. Renewably produced methanol entirely eliminates emissions of sulfur-oxide and particulate matter, reduces emissions of nitrogen oxide by up to 80%, and reduce emissions of carbon-dioxide by up to 95% when compared to traditional fuels. Agro waste, which is abundant from agricultural operations, poses an environmental threat if not adequately managed. Conventional disposal methods frequently include ineffective disposal, which contributes to pollution and greenhouse gas emissions. This presentation focuses on the comprehensive approach for the synthesis of bio-methanol from agro waste, integrating various stages, including enzymatic pretreatment to enhance reducing sugar content, biogas formation, and syngas generation from biogas. However, with anaerobic digestion, agricultural waste is turned into biogas, which is mostly constituted of methane and CO2 but there is no efficient management system of CO2 which is released from bio-gas production operation. So, this biogas is a potential precursor for bio-methanol production. Syngas, a combination of carbon monoxide and hydrogen, can be produced by steam and dry reforming of carbon dioxide and methane. This flexible intermediate can be converted into methanol using catalytic methods. Production of syngas from biogas production diversifies the feedstock sources for methanol synthesis, improving process robustness and resource use. Enzymatic processing of agricultural waste prior to biogas generation is a critical step toward increasing bio-methanol output, by reducing recalcitrant lignin. Enzymes are used to hydrolyse complex carbohydrates into fermentable sugars, increasing the efficiency of anaerobic digestion. This enzymatic improvement considerably enhances the availability of substrates for microbial conversion to methane, boosting biogas output and, eventually, bio-methanol synthesis.

Keywords: Bio-methanol, Bio-gas, Enzymatic pretreatment, Reform reaction, Syngas

Ectomycorrhizae: Their role in environmental management using biotechnological approaches

Prof. Veena Pande
Department of Biotechnology, Kumaun University, Sir J.C. Bose Technical Campus, Bhimtal
Nainital-263136

Ectomycorrhizal fungi also known as ectomycorrhizae (ECM) are symbiotic association of fungi with the feeder roots of higher plants in which both the partners are mutually benefited and indeed the association appears to be significant for the existence of both the partners. The mycorrhizae, due to their key position in the soil-plant interface, are important to consider in the study of the ecosystem. It is known that mycorrhizae affect plant performance through the benefits they confer on their hosts. It is likely that mycorrhiza-mediated processes influence plant nutrition, plant competition and the nutrient cycle in the soil. ECM can alter the chemistry of mycorrhizosphere by increasing the rate of weathering of soil minerals and supply the released nutrients to the plant. It also benefits the host indirectly by influencing important ecosystem properties such as soil structure. The diversity of ECM fungi is likely to contribute to the resilience of forest ecosystems to changing environmental factors, such as pollution and global climate change. In addition, N fixing bacteria appear too associated with specific types of ECM.Some plant growth promoting rhizobacteria stimulate tree growth only in the presence of mycorrhiza. Hence, an urgent consideration forharnessing this natural source of biofertilizer for growth, improvement of natural tree species is requisite. Most previous mycorrhizal research is focused on interactions between plant fungi; its role in the development of the community ecosystem, although important, remains poorly understood. Uttarakhand state is very rich in tree biodiversity however Ectomycorrhizal fungal diversity and its possible impact on tree diversity in the Himalayan region have not been well studied. As these fungi are very important for the growth and development of higher tree species, it is essential to document the outcome of the tree species of kumaun Himalayan occurring together in forests with the change in associated ectomycorrhizal fungal species. The study of diversity of ectomycorrhizal fungi at community or local level to develop management plans and to understand the pattern of diversity in relation to environmental changes are also important for finding ways to conserve it. With this broad prospective this work had been designed to study the improvement in the growth, performance and fitness of important himalayan tree species in presence of specific ectomycorrhizal species. Oak and pine seedlings were artificially inoculated with selected ectomycorrhizal fungal species and improvement in growth and fitness was assessed after six months growth of seedlings under glass house conditions using standard protocol and very fruitful results were obtained.

As the fungal diversity of local region is poorly known in India as well as in the Himalayan region, it is essential to document this important wealth of our state and also to find out the ways to conserve and strengthen our important tree species by utilizing this important component of the nature. Uttarakhand state is very rich in biodiversity but a very little work has been done in the area of ectomycorrhizal fungi. These fungi are very important for the growth and development of higher tree species. Ectomycorrhizal diversity through effective plant growth would affect tree species composition, ecosystem functioning and ultimately the whole environment. In Uttarakhand, Oak forests are very important as they retain water and are essential for conservation of natural water resources. The major problem these days in the state is replacement of oak forests with pine forests which is very alarming for natural water resources. This study on the comparative symbiotic efficiencies of two ectomycorrhizal fungi viz., *Amanita hemibapha* and *Russulavesca* assessed in association with oak (*Q. leucotrichophora*) and pine (*P. roxburghii*) seedlings indicated that the fungal species seem to have a marked influence on competitive outcome of the seedlings, their growth and health status. This work will help us to trace out the new ectomycorrhizal species which will be more beneficial to a particular tree species and will help in conservation of important forest types of Central Himalayas as well as natural resources. It will also provide a platform in development of a technology package which is relevant for nursery rising of these important tree species.

Keywords: **Ectomycorrhizae; Oak (QuercusSp.); Pine(Pinussp.); Amanita; Russulla**

Genetically modified cyanobacteria applications for biofuel and value-added products generation

Dr. Sanjay Kumar
Biofuel Research Laboratory, School of Biochemical Engineering, IIT(BHU) Varanasi, Varanasi, U.P. 221005 INDIA
*sanjaykr.bce@iitbhu.ac.in

Abstract

The advent of genetic engineering and the latest accomplishments in synthetic biology and metabolic engineering allow microbial synthesis of terpenoids. Photosynthetic microorganisms like cyanobacteria have emerged as ideal cellular factories for the sustainable production of terpenoids for carbon-neutral biofuels and other value-added products. Additionally, these organisms use environmental CO_2, light energy, and low-cost minerals for their growth and can be cultivated on nonarable land. Cyanobacteria are preferred phototrophic microorganisms due to rapid growth and low nutritional requirement than other phototrophic microalgae/algae for such kinds of metabolites production. Nowadays, fourth-generation advanced biofuel molecules of high energy density and low viscosity are produced by metabolically engineered cyanobacteria strains like *Synechocystissp.* and *Synechococcuselongatus*. Cyanobacteria are endowed with methyl erythritol 4-phosphate pathway (MEP) for the synthesis of terpenoid molecules. Various terpenoid molecules having the ideal fuel properties like isoprene, α-farnesene, limonene, n-alkanes, and bisabolene have been produced by engineering the MEP pathway of cyanobacteria.

In this aspect our research group has engineered a fast-growing and CO_2 tolerant cyanobacteria *Synechococcus elongatus* UTEX 2973 using key and bottle neck genes overexpression at neutral sites of genome for isoprene / farnesene production. The overall increase of isoprene production in UTEX modified is found to be 29.52-fold using an integrated approach of inhibition and ANN-GA optimization in comparison to unoptimized cultures without inhibition strategy. Whereas, farnesene production in UTEX *AFS::dxs::idispA* is 31 times higher than the UTEX *AFS* strain, with a productivity of 2574 µg/L/day, which is the highest amongst engineered cyanobacterial studies so far. This productivity could be improvised by adaptive evolutionary engineering, process parameters optimization and different modes of reactor operation/ scale up studies.

References:

1. I. Yadav, A. Rautela, A. Gangwar, S. Rawat and Sanjay Kumar* (2023) Enhancement of isoprene production in engineered *Synechococcus elongatus* UTEX 2973 by metabolic pathway inhibition and machine learning-based optimization strategy. Bioresource Technology, 387, 129677.
2. I. Yadav, A. Rautela, A. Gangwar, V. Kesari, A. K. Padhi, and Sanjay Kumar* (2023) Geranyl Diphosphate Synthase (CrtE) Inhibition using Alendronate Enhances Isoprene Production in Recombinant *Synechococcus elongatus* UTEX 2973: A Step towards Isoprene Biorefinery. Fermentation 9 (3), 217.
3. A. Rautela & Sanjay Kumar* (2022) Engineering Plant Family TPS into Cyanobacterial Host for Terpenoids Production. Plant cell reports. 41:1791–1803.
4. I. Yadav, Akhil Rautela, Sanjay Kumar* (2021) Approaches in the Photosynthetic Production of Sustainable Fuels by Cyanobacteria using Tools of Synthetic Biology. World Journal of Microbiology and Biotechnology 37, 2

Non-transformative gene silencing for crop improvement: The promise of exogenous dsRNA

Professor Jennifer Ann Harikrishna Ph.D.
Faculty of Science,
Director, Centre for Research in Biotechnology for Agriculture (CEBAR), Universiti Malaya,
50603 Kuala Lumpur, Malaysia
jennihari@um.edu.my

Abstract:

Gene silencing is a down-regulation of specific gene targets that has promising benefits for application to crop protection, particularly against plant viruses. This field of research has grown together with improved understanding of the mechanisms of RNA-mediated gene silencing. After initial applications via trangenesis, RNA silencing though the direct application of double stranded RNA (dsRNA), a non-transgenic approach using ectopically applied dsRNA, or RNA sprays, has been demonstrated to provide effective crop protection, as well as being a useful reverse genetics research tool. Working with non-transformative dsRNAs targeting plant virus sequences, our team has demonstrated protection of orchids against Cymbidium mosaic virus (CymMV), a major pathogen affecting commercial orchid production operations and hobbyists. More recently, we have shown similar result for local isolates of Cucumber Mosaic Virus (CMV) a pathogen we found to be affecting muskmelon farms in Malaysia. Happily, our work has led to development of intellectual property and industry linkages, however the translation of this technology to the field in order to have a tangible impact, is faced with various challenges. This presentation will cover our recent experimental studies and discuss the potential and challenges for translational research for non-transformative gene silencing technology.

Session - 5

The Nano - Bio - Info - Cogno convergence for a sustainable society and its implications for Bio, Health and Agro.

Prof. Lars Montelius
Lund University

Abstracts

For the years to come, reaching climate neutrality, circularity, healthy food-systems and sustainability in agriculture, transportation, construction, packaging, electronic appliances, as well as completing the transition to renewable energy sources are among the greatest challenges humanity is facing. The major scientific advances of the 20th century introduced the ability to manipulate substances (inorganic and organic) at an atomic level that made it possible to realize new, purpose-built materials that massively outperform naturally occurring materials. The last decades have enabled the convergence of Nano, Bio, Info and Cogno that has allowed the introduction of new concepts for applications in a diverse range of fields. These advancements are revolutionising devices, systems, and infrastructures which improves our quality of life, saving labour, enhancing recreation as well as our workplaces. The present challenges and bottlenecks call for the need to accelerate and shorten Advanced Materials development cycles, invent game changers, implement circular symbiotic value chains, cut costs, reduce risks, align stakeholders, secure coordinated investments and policy frameworks. These developments will profoundly transform society bringing immense opportunities for a multitude of various sustainability initiatives and possibilities for disruptive green and digital innovations based on breakthrough technologies and game changing discoveries that can both scale up the world´s start-ups and SMEs into a new generation of world leading companies as well as transforming established industry for a greener future, paving the way for a major change for people, planet and prosperity.

Unravelling protein signatures for early diagnosis in leprosy and screening of aminoglycosides resistant tuberculosis

Dr. Deepa Bisht, Devesh Sharma, Sakshi Gautam, Sakshi Singh, Mamta Arora and A M Khan
ICMR-National JALMA Institute for Leprosy and Other Mycobacterial Diseases, Dr M. Miyazaki Marg, Tajganj, Agra 282001, Uttar Pradesh, India
*abd1109@rediffmail.com

Abstract

Mycobacterial pathogens are responsible for the severe infectious diseases such as leprosy and tuberculosis. Early identification of cases remains one of the primary objectives of leprosy research. Our comprehension of the proteome of contacts of person affected with leprosy, which accounts for the highest risk category for leprosy infection, is inadequate. It is crucial to develop extremely sensitive diagnostic approaches for screening this population. Biomarkers play a major role in early diagnosis and proteins being the functional moiety could be attractive biomarkers. The current study uses proteomics approaches to investigate the differences in the expression of novel proteins in the sera of contacts of person affected with leprosy and person affected with leprosy, compared to healthy controls. Two-dimensional gel electrophoresis, liquid chromatography-mass spectrometry and bioinformatics tools were employed for protein identification. Comparison and analysis of the two-dimensional patterns of proteins uncovered five differentially expressed proteins. Alpha 1B glycoprotein (A1BG) and haptoglobin 1 (Hp 1) were considered as potential biomarkers for early diagnosis of leprosy. These proteins might serve as potential biomarkers for diagnosis of early leprosy and would allow interventions before the onset of clinical symptoms. Further, we employed two-dimensional gel electrophoresis and mass spectrometry techniques to juxtapose the cell wall proteomes of clinical isolates that are resistant to aminoglycosides with those that are susceptible. This analysis revealed distinct protein expression patterns and profiles. Subsequently, we excised the overexpressed protein spots and employed Liquid Chromatography Mass Spectrometry (LCMS) for their identification. As a result, we pinpointed nine proteins that exhibited significant upregulation in aminoglycoside-resistant isolates. Rv2501c, Rv2247, and Rv0295c to lipid metabolism; Rv2115c to cell wall and cell processes; Protein Rv3841, Rv1308 intermediary metabolism and respiration; and Rv2416c belonged to virulence, detoxification/adaptation. The knowledge gathered can direct the creation of better tuberculosis diagnostic instruments and treatment strategies.

Field Deployable Opto-Electronic Sensing Devices in Healthcare Industries

Prof. Pranjal Chandra, PhD., FICS, MRSC, MNASc, M-INYAS
Associate Professor and Ramanujan Fellow
Laboratory of Bio-Physio Sensors and Nanobioengineering
School of Biochemical Engineering
Indian Institute of Technology (BHU), Varanasi
Varanasi - Uttar Pradesh 221005, India
Web: www.chandraslab.com

Abstract

Robust, reliable and quantitative detection of biomarkers at ultra-low concentration is of great importance in clinical settings. Sensor, an analytical device used for sensitive and selective detection of biomarkers offers various advantages over the conventional clinical diagnosis, which is both time consuming and not suitable for point of care/onsite diagnosis. The bioreceptors embedded in sensing chip include antibodies, aptamers, enzymes, bio bodies etc. for detection as well as providing the analytical signals. A revolution in the understanding and synthesis of nanomaterials in the last couple of decades has also contributed significantly to the development of the biosensors in terms of sensitivity, catalytic activity, biocompatibility, and robustness. Additionally, nanomaterial engineering helped in miniaturization of the sensing platform eventually helping in the commercial success of portable biosensing devices. Such platforms have tremendous promise in detecting various analytes including disease biomarkers, microbes, chemical compounds. This presentation is focused on the engineering design of sensor systems using bioreceptors and nanocatalytic systems etc. Recently developed nanoscale materials-based transduction system will be discussed with standard biomarkers that can be further directed towards the detection of various biomarkers in clinical research. Recently reported signal transductions strategies, promising personalized smart phone assisted electrochemical sensing platform for disease diagnosis will also be discussed.

Keywords: Nanobioengineering; Disease; Biosensors; Human Heath, Material Engineering

Session - 6

Gene, Genome and Microbiome for ecological sustainabilitYoundy of contaminated sites

Dr. Natesan Manickam
Environmental Biotechnology Laboratory, Environmental Toxicology Group,
FEST Division, CSIR-Indian Institute of Toxicology Research, Vishvigyan Bhawan,
31 Mahatma Gandhi Marg, Lucknow-226001, India.

Owing to the extensive use of pesticides, polyaromatic hydrocarbons (PAHs) and plastics over several decades, bacteria have evolved catabolic pathways to metabolize these compounds. In our laboratory, a large number of bacteria capable of biodegrading the above compounds belonging to diverse genus have been isolated and characterized. To give few examples, *lin* genes for lindane degradation, *nid* genes responsible PAHs pyrene biodegradation including the metabolic pathways were elucidated. The genetic details provided the functions of key enzymatic process of the metabolism of specific pollutants. More recently, for the biodegradation of plastics and plasticisers, several bacterial species were isolated and studied for biodegradation and biochemical investigations in our laboratory. Additionally, when these robust biodegradative bacteria were subjected to whole genome sequencing, it has provided details about degradative machinery, size, genetic arrangements, their spread in the genome and plasmids. Besides, novel insights on polyethylene terephthalate (PET) and plasticizers biodegradation genes, the genomic analysis provided presence of lower pathway genes such as benzoic acid and catechol metabolic gene clusters. Metagenomic studies of the river water microbiome recently begun to explore the differences in taxonomic composition between different ecosystems of the rivers. Here, we compared microbiome of four major Indian rivers namely Ganga, Narmada, Cauvery, and Gomti originating from geographically diverse locations. The taxonomic profiles allowed us to understand the core-microbiome of each rivers. Results also indicated the prevalence of Acidobacteria, Actinobacteria, Verrucomicrobia, Firmicutes, and Nitrospirae phyla, and a decline in Proteobacteria and Bacteroides where anthropogenic activities were high. A marked difference in microbial communities were observed at the locations of urbanization and industrialization. These insights provide new perspectives to understand anthropogenic influence on river microbial dynamics of polluted ecosystems.

Session - 6

Innovations in Biotechnological Solutions for Waste Management and Circular Economy

Rahul Rautela and Sunil Kumar
CSIR-National Environmental Engineering Research Institute (CSIR-NEERI)
Nehru Marg, Nagpur-440 020

With the pressing global challenges of waste management and the imperative to transition towards a circular economy, biotechnology has emerged as a pivotal tool driving innovation in sustainable practices. The management of solid waste presents a pressing challenge amidst the global pursuit of sustainability and circular economy principles. Biotechnological solutions offer promising avenues for addressing this challenge, harnessing the power of biological processes to transform waste into valuable resources. This abstract explores recent innovations in biotechnological applications for solid waste management and circular economy initiatives, focusing on biodegradation, bioconversion, and biovalorization processes. Microorganisms such as bacteria, fungi, and algae are engineered or naturally occurring agents utilized to break down complex organic compounds present in solid waste streams. These microorganisms play pivotal roles in composting, anaerobic digestion, and fermentation processes, transforming organic waste into compost, biogas, and bio-based products. Furthermore, biochar production through pyrolysis of organic waste offers a sustainable approach for carbon sequestration and soil amendment, enhancing agricultural productivity and mitigating greenhouse gas emissions. These biotechnological innovations synergistically complement traditional waste management practices, promoting the transition towards a circular economy paradigm. Furthermore, the integration of biotechnological approaches with digital technologies enhances process monitoring, optimization, and automation, thereby improving the efficiency and scalability of waste-to-resource conversion processes. These advancements hold promise for revolutionizing waste management practices, mitigating environmental pollution, and fostering a more resource-efficient society. Continued research and development in this field are essential for unlocking the full potential of biotechnological solutions in solid waste management and circular economy initiatives.

Compact trickling bed bioreactors to treat odours and VOCs – Case studies

Damian Kasperczyk[a,*], Krzysztof Urbaniec[b], Krzysztof Barbusiński[c], Ramon F. Colmenares Quintero[d] and Eldon R. Rene[e,*]

[a]Ekoinwentyka Ltd, Ruda Śląska, Poland

[b]Warsaw University of Technology, Plock, Poland

[c]Silesian University of Technology, Gliwice, Poland

[d]UniversidadCooperativa de Colombia, Medellín, Colombia

[e]Department of Water Supply, Sanitation and Environmental Engineering, IHE Delft Institute for Water Education, Westvest 7, 2611AX, Delft, the Netherlands

biuro@ekoinwentyka.pl; e.raj@un-ihe.org

Environmental pollution results from the discharged ventilation air containing Volatile Organic Compounds (VOCs) from the automotive painting industry. In order to aid in the reduction of VOCs, Ekoinwentyka Ltd. (Poland) designed, constructed, and field-tested the Compact Trickle Bed Bioreactor (CTBB) technology. This system operates by co-currently passing contaminated air (gas phase) and a solution of mineral salts (liquid phase) through a packed bed. The active microorganisms are immobilized in the biofilm that grows on the packing materials surface. The pilot-scale bioreactor 0.32 m in diameter and 1.50 m total height had its packed bed inoculated with a consortium of microorganisms dominated by *Pseudomonas fluorescens*. During the experimental phase that lasted several months, the flow rate of air drawn from the ventilation system of the painting shop was changing between 1.0 and 10.0 m^3/h and the inlet concentration of VOCs ranged from 10 to 200 ppm. By measuring VOC concentration in the purified air, the factor of VOC biodegradation/removal was found to range between 85 and 99%. Based on pilot-scale experiments, full-scale CTBB has been developed 2.8 m in diameter and 10 m total height and installed as an add-on component of the ventilation system of the painting shop. The test operation at gas flow rates up to 6000 m^3/h confirmed VOC biodegradation factor at the level of 85–99% thus proving a positive result of CTBB technology adaptation to the conditions of the automotive painting industry.

Mindfulness and scientific research A summary developmend

Dr. Sanjay K. Kapoor
A Coach and Founder and CEO
Connected Mindful Living
*http://connectedmindfulliving.com

Abstract

Enhanced Focus and Concentration: Mindfulness practices help in improving concentration and the ability to maintain focus over extended periods. This is particularly useful in research where tasks often require deep concentration, such as data analysis, writing, and experimental design.

Improved Creativity: Mindfulness can foster an environment where creativity flourishes. By being present and open, researchers may find novel solutions to problems or innovative approaches to their studies that they might not have considered otherwise.

Enhanced Problem-Solving Skills: The non-judgmental aspect of mindfulness encourages researchers to view challenges and setbacks as opportunities for learning and growth, rather than failures. This perspective can enhance problem-solving skills and resilience in the face of obstacles.

Better Collaboration and Communication: Mindfulness promotes empathy and active listening, which can improve communication and collaboration within research teams. Understanding and respecting different viewpoints can lead to more effective teamwork and innovative research outcomes. Furthermore, it opens the possibilities of wider collaborations.

Rigor and Resilience: To work at a rigorous level needed for research, one requires to build resiliency furthermore, the ups and downs of research require a resilient mindset. Mindfulness practices can help build resilience, enabling researchers to recover more quickly from setbacks such as failed experiments or rejected papers.

Reduced Cognitive Bias: Most applied research in essence are human centric, they in some way aims to help humankind directly or indirectly. Our environment, fauna, flora, and human race are extremely diverse so are our researchers. What is said is that if you are a human you have bias, that exists as our primitive protective mechanism. However, having unmitigated biases in research can not only hinder but has a grave potential to harm what we are bias towards. Mindfulness encourages an awareness of one's thoughts and feelings without being overly reactive or overwhelmed by them. This can help researchers recognize and mitigate cognitive biases that may affect their work, leading to more objective and reliable results.

Balance and Stress Reduction: Scientific research can be a source of significant stress due to tight deadlines, the pressure to publish, and the uncertainty of research outcomes. Mindfulness techniques can mitigate stress and anxiety, promoting a healthier work environment and mental well-being.

Conclusion

Integrating mindfulness into scientific research can have a profound impact on both the process and the outcomes of research. By fostering focus, resilience, creativity, and collaboration, mindfulness can contribute to more effective, sustainable, and enjoyable research practices. Furthermore, Peer-to-peer mindfulness programs can significantly improve employee wellbeing by creating a supportive community where employees share techniques and experiences related to mindfulness. This shared learning environment fosters a sense of belonging, reduces stress, and enhances emotional resilience. Through regular practice and peer encouragement, employees can develop better coping mechanisms for stress, leading to increased job satisfaction, reduced burnout rates, and overall improved mental health. Such programs promote a culture of mindfulness that contributes to a healthier, more engaged, and productive workforce.

Initiator tRNA-centric mechanisms of faithful translation initiation and ribosome maturation in bacteria

Prof. Umesh Varshney
Department of Microbiology and Cell Biology, Indian Institute of Science, Bengaluru 560012

Abstract:

Translation of messenger RNA (mRNA) in bacteria occurs in the steps of initiation, elongation, termination and ribosome recycling. The initiation step comprises multiple stages and uses a special transfer RNA (tRNA) called initiator tRNA ($tRNA^{fMet}$ or i-tRNA), which is aminoacylated with methionine and then formylated with N^{10}-formyl-tetrahydrofolate (N^{10}-fTHF). Both methionine and N^{10}-fTHF are produced via one-carbon metabolism, which makes the process of translation initiation dependent on energy sufficiency in cell. The fidelity of i-tRNA binding to the ribosomal peptidyl-site (P-site) is attributed to the structural features in its acceptor stem, and the highly conserved three consecutive G-C base pairs (3GC pairs) in the anticodon stem. While the acceptor stem region is important in formylation of the amino acid attached to i-tRNA and its initial binding to the P-site, the 3GC pairs are crucial in transiting i-tRNA through various stages of initiation. Further, the use of the same $tRNA^{f-Met}$ in initiation and elongation steps (for example in mammalian mitochondria) is regulated by the extent of its formylation. Our studies also provide renewed ways of effective use of trimethoprim and sulfa drugs to control bacterial growth. Towards our studies on ribosome maturation, we show that initiation complex formation, in the pioneering round of initiation, triggers the final stages of ribosome maturation. Interestingly, use of an anticonvulsant drug, lamotrigine, has provided important insights into the mechanism of the role of IF2 in the process of ribosome maturation.

Extending human life: Are anti-aging interventions a reality?

Syed Ibrahim Rizvi
Department of Biochemistry, University of Allahabad, Allahabad 211002, India,
*sirizvi@gmail.com

Abstract

Aging is a universal phenomenon of accumulation of diverse deleterious changes in cell and tissues with time that disrupt the cellular homeostasis and increase the onset of age-related disease and death. The human history is replete with mention of anti-aging interventions. In the last few decades several interventions have been extensively investigated however no intervention has been able to validate scientific scrutiny. In the quest for a viable anti aging strategy, scientists stumbled upon caloric restriction (CR) as a potent tool for life extension effect. CR refers to the reduction in caloric intake without occurrence of malnutrition. When applied to experimental models, caloric restriction involves a reduction in caloric intake by 40% of the ad libitum diet throughout the lifespan of the animal. CR has been reported to extend life span in organisms, including yeast, rotifers, spiders, worms, fish, mice, rats and primates, however, currently there are no well-controlled long term studies showing the effects of CR in humans. Although limited data concerning the short-term effects in humans have shown health benefits. CR is difficult in humans for lifelong implementation due to the degree of food restriction and the attention given to food selection to assure adequate nutrition. For these reasons, there has been great interest in the development of drugs (CR mimetics) that can serve as alternatives to classical CR. Possible CR mimetics must target any of the possible metabolic pathways including adenosine monophosphate (AMP)-activated protein kinase (AMPK), the Insulin/insulin-like growth factor signaling (IIS) and mTOR pathways, as well as sirtuins. Among the candidate CRMs metformin has emerged as the most promising candidate. Studies from our group in the last couple of years have shown anti-aging role of metformin on rats (naturally aged and accelerated senescence model). Other promising CRMs tested in our laboratory include glycolytic inhibitor 2 deoxy D glucose and fisetin. With new scientific data adding to the already existing literature in leaps and bound, one is forced to debate the question whether it is actually possible to extend human lifespan. An analysis of approximately ten billion individuals reveal that no one has been able to live for more than 122 years.

Session - 7

Interdisciplinary research in medical science: conceptual scenario

Dr. Sunil chauhan

Around the world, so many organizations are working for social uplifting either independently or in accordance to the concerned authorities in innumerous perspectives and platforms related to science, arts and commerce where regular efforts are being sacrificed for sustained improvement of social and personal standards of life.

Our concern is the health and health-related issues where Medical Science, Ayurveda, Homeopathy, Unani, Yoga, Naturopathy and their ancillaries are dedicating their synchronized services for the same noble cause i.e. long and healthy life. Every disciplines have its own prime thinkers, researchers, journals, publications, seminars, conferences and mass media communication to put forward their efforts regarding diagnostic and remedial development of several chronic, rare & terminal diseases but as an output, cost of the treatment is increasing day by day while confidence of the patients is decreasing because status of ailment is unaltered.

Now the question arises **"where is the gap?"** Just to observe, look at the scenario that most of the scientists are working to find out or to modify any drug or modality to fulfill the remedial requirement of the patients but to understand the causes of the disease, no one or least are there because nothing is here to do except thinking, …, thinking & thinking. For any financial support or monetary benefits, you forget then who will exhaust his life with esteem enthusiasm for this field where dense darkness is pervaded everywhere. So this field is absolutely deficient of prime thinkers. In this situation whatever the cause is mentioned once, it is mentioned forever and taken as truth. No matters whether it is actual, factual or virtual but it has been established on the basis of contemporary social structure and it is never analyzed and not even questioned. Although, absolute truth can never be known and there is nothing like a "last word" so sincere efforts should be given to the "Problem" until it is shorted out and resolved.

As a mission we should focus on the problem to observe the facts, justified on the basis of chemistry, biochemistry and physics, and try to bring them to light through their aware society and concerned authorities. For us the disease of any living system is a discomfort (dis-ease) either in resting or mobile phase that reflects as an incident, demanding an explanation on molecular basis if it persists for long to fabricate pathophysiological variations.

At last, we hope to get an esteem social support on every path and direction to achieve and to put forward the truth lying with the **"re-main" part of the "main"**, known to every one

Antimicrobial Resistance: Exploring Marine Actinobacteria as source of Antibiotics and Biofilm Inhibitors

Prof. Sunil Khare
Institute Chair Professor of Biochemistry
Enzyme and Microbial Biochemistry Research Group
Dept of Chemistry
Indian Institute of Technology Delhi, New Delhi, INDIA

Antimicrobial resistance (AMR) remains a significant global health concern, exacerbated by the formation of bacterial biofilms. Biofilms, complex communities of bacteria encased within an extracellular matrix, pose challenges to antibiotic treatment efficacy. Biofilm formation progresses through distinct stages, offering targets for intervention to prevent or disrupt biofilms and enhance antimicrobial effectiveness. Biofilms contribute to AMR by impeding antibiotic penetration, reducing bacterial growth, and facilitating horizontal gene transfer. Novel strategies are needed to combat biofilms and address AMR.

Natural compounds from various sources, including plants, microorganisms, and marine environments, show promise as biofilm inhibitors. Specifically, plant-derived compounds, polymers, enzymes, polysaccharides, and biosurfactants exhibit the potential in disrupting biofilm formation.

Interestingly, Actinobacteria, particularly Streptomyces species, have been a source of most of the antibiotics in the world. They produce bioactive compounds with antimicrobial properties, offering opportunities for developing novel antimicrobial agents targeting biofilms. In this context, marine actinobacteria, are largely unexplored, offer a vast reservoir of potential biofilm inhibitors due to their ability to thrive in extreme environments. Advancements in genomic and metagenomic technologies enable the exploration of marine actinobacteria, potentially uncovering valuable antimicrobial compounds.

In summary, understanding biofilm formation and developing innovative strategies to target biofilms are essential for addressing AMR. Leveraging natural compounds and exploring microbial sources, especially marine actinobacteria, hold promise for combating biofilm-related infections and mitigating AMR proliferation. The talk will encompass above aspects with current work of our lab in this area.

Unveiling the Molecular Toolbox: Transcriptomics Insights into Secretory Lipases and β-Oxidation in Thraustochytrids for the Transformation of Hydrophobic Substrates into Nutraceutical Fatty Acids

Alok Kumar Patel*, Iqra Mariam, Eleni Krikigianni, Paul Christakopoulos, Ulrika Rova, Leonidas Matsakas
Biochemical Process Engineering, Division of Chemical Engineering, Department of Civil, Environmental, and Natural Resources Engineering, Luleå University of Technology, SE-971 87 Luleå, Sweden
*alok.kumar.patel@ltu.se

Uncontrolled disposal of hydrophobic waste, such as used cooking oil or other industrial waste, upsets the balance of the ecosystem and can be harmful to human health. These wastes require efficient treatment techniques because of their resilient nature. This makes microbial bioconversion an attractive option since it can convert these low-quality oils into valuable chemicals that are safe for human consumption. In this investigation, we focused on the marine thraustochytrid *Schizochytriumlimacinum* SR21, renowned for its ability to thrive in highly saline and oily environments. Our findings demonstrate SR21's capability to utilize a remarkable 120 g/L of waste cooking oil (WCO) under saline conditions (18 g/L), showcasing its adaptability. In addition to its remarkable ability to utilize high concentrations of oil, a key discovery of our study was the conversion of low-quality oil into high-quality DHA and squalene-rich microbial lipids. By co-utilizing hydrophilic and hydrophobic substrates, we observed a significant increase in DHA and squalene levels in this microorganism. Specifically, we found that the synthesis of lipids from waste cooking oil (WCO) was enhanced by volatile fatty acids produced through acidogenic fermentation, resulting in a remarkable DHA content of up to 40% of total lipids and 40.47 mg/L of squalene. This surpassed the yields obtained from simultaneous de novo and ex novo fermentation experiments using glucose and WCO, which yielded 23.96% DHA and 30.21 mg/L of squalene. Traditionally, fish oils and deep-sea shark liver are common sources of such nutraceutical compounds, particularly PUFAs and squalene. Our study presents an alternative and sustainable approach for nutraceutical compound production, offering dual benefits by bioremediating hydrophobic wastes from the marine environment and reducing the pressure on fish stocks and marine ecosystems, aligning with the United Nations Sustainable Development Goal 14. To further understand the metabolic processes involved in lipid-to-lipid conversion, we employed omics platforms, which allowed us to identify the interactions between several metabolic pathways. In-depth research is done using systems biology techniques to clarify hitherto unknown pathways and identify possible targets such as acylcarnitine transferase and lipases that might improve the assimilation of hydrophobic waste.

The β7–β8 loop of the p51 subunit of Human Immunodeficiency Virus type-1 reverse transcriptase (HIV-1RT) is crucial to support the Enzyme’s Molecular Structure and Function

Prof. Bechan Sharma
Department of Biochemistry, Faculty of Science, University of Allahabad, Prayagraj 211002;
sharmabi@yahoo.com

Background:

The Human Immunodeficiency Virus type-1 reverse transcriptase (HIV-1RT) is a heterodimeric enzyme, consisting of two subunits p66 and p51. Earlier reports from our group have shown that the β7-β8 loop of p51subuint is crucial in enabling the enzyme to undergo dimerization (Pandey et al., Biochemistry 40: 9505, 2001). It was observed that the deletion of 4 amino acid residues or their substitution by Alanine in the loop may adversely influence the enzyme’s catalytic function and DNA binding affinity. In this study, the impact of increase in the size of the loop by repeating in tandem its six amino acids sequences on the catalytic activity and the dimerization process of HIV-1 RT.

Results:

The data displayed severe impairment in the polymerase and the RNase activities with significant loss of DNA binding affinity of HIV-1 RT containing insertion in the β7-β8 loop of both the subunits (p66INS/p51INS). Importantly, the activities of the enzyme were restored when wild type p51 subunit was dimerized with p66INS subunit. The results from the glycerol gradient sedimentation analysis indicated the inability of mutant p51INS subunit to constitute a stable dimer either with the mutant p66INS or wild type p66. Also, the p66INS/p66INS mutants sedimented as a monomeric subunit species, suggesting their inability to form a stable homodimeric complex.

Conclusion:

The results indicated that the β7-β8 loop of the p51 subunit of HIV-1 RT is assigned the job to sustain the molecular organisation, catalytic function, and DNA binding affinity of HIV-1RT as any alteration in the loop causes severe loss in these properties of the enzyme.

Session-1

Biotechnological Intervention in Complementary, Herbal and Transitional Science

Green synthesized nanoparticles and nanofibers for potential use in wound healing

Soumi Sadhu[a,*], Shuaib Burgee[a], BarghaviVaraprasad[a], S. Shankara Narayanan[b]
[a*]Department of Life Sciences, Sharda University, Greater Noida, U.P., India,
[b]Nanomaterials Laboratory, Department of Physics, Sharda University, Greater Noida, U.P., India

*soumi.sadhu@sharda.ac.in

Background

Skin injuries trigger a chain of events that includes tissue fluid secretion, inflammation, and tissue remodelling. Besides, chronic wounds show a disorganized repair process, causing wounds to take longer time to heal. Features of chronic wounds include persistent inflammation, biofilm formation and decreased angiogenesis. Further, biofilm impart anti-microbial resistance. Nanoplatforms penetrate skin without causing too much discomfort or irritability while transporting different antibacterial agents to the lower layers of the skinand address the problem of antibiotic resistance as well.

Review

AgNPs containing active ingredients of *Azadirachta indica* embedded in a cotton fabric has found to be a potential nano-bandage as they tend to show zone of inhibition against the fungi Candida albicans, gram-negative bacteria *Escherichia coli*, and gram-positive bacteria *Staphylococcus aureus* (Pawar et al., 2022). Local application of *Shorea robusta* (SR) ethanolic extracts to the wound led to a dose-dependent acceleration of wound contraction. (Wani et al., 2012).

Major findings

In the current study, we have employed green synthesis method to synthesize *Shorea robusta* resin-based and *Azadiracta indica* leaves-based carbon dots (CDs) and investigated their anti-microbial properties. Carbon nanofibers from banana pseudostem have been synthesized using acid-alkali extraction method. The physical, chemical, and optical properties of resulting green-synthesized CDs were studied, followed by their application. The Zone of Inhibition assay findings demonstrated existence of anti-microbial activity of these carbon dots against both gram-positive and gram-negative bacteria (*Streptococcus aureus* and *Pseudomonas stutzeri* respectively). The results of biofilm inhibition assay showed that carbon dots inhibited production of biofilms in microorganisms. After in vitro evaluation for cell migration, in vivo studies for wound healing can be performed with final wound healing patch made from synthesized carbon nanofibers incorporated with the green-synthesized carbon dots. Our future endeavour is the development of a biocompatible, environmentally friendly, and cost-effective nanofiber-based wound healing patch for patients with chronic wounds.

Keywords: Wound healing, Carbon dots, Carbon nano fibres, Anti-microbial, Biocompatible

References:

1. Pawar, A.A., Sahoo, J., Verma, A., Alswieleh, A.M., Lodh, A., Raut, R., Lakkakula, J., Jeon, B.H. and Islam, M.R., 2022. *Azadirachta indica*-derived silver nanoparticle synthesis and its antimicrobial applications. Journal of Nanomaterials.

PI: 47

Study of Nutritional value enrichment in hybrid of black wheat and common wheat varieties

Nidhi Shukla, Nand kumar Singh*
Department of Biotechnology, Motilal Nehru National Institute of Technology
Prayagraj U.P 211004, India
*nksingh@mnnit.ac.in

Background

Wheat is one of the important cultivatedcropon a global scale. Major wheat breeding programmes are starting to focus more on quality than quantity.Coloured wheat offers a unique approach to addressing malnutrition by increasing antioxidants like anthocyanin, carotenoids, flavonoids, polyphenols, and other nutritional levels. The pigments carotenoids and anthocyanin are what give kernels their distinctive blue, purple, black, and red hues. Purple and blue wheat were crossed to create black wheat which is a coloured form of wheat. The outer layer of wheat grains contains anthocyanin, which is ultimately gives them their black colour. The primary limitation in black wheat production lies in its comparatively lower productivity when compared to conventional wheat varieties. Furthermore, the adaptability to diverse climatic regions is a crucial factor for gaining popularity in India, that offer different climatic zones.

Review

According to Monasterio et al., (2017) the goal of biofortification is to create crop varieties enriched with micronutrients using traditional plant breeding methods. It is crucial to identify genetic resources containing elevated levels of the desired micronutrients and to assess the heritability of the specific traits being targeted. Sharma et al.,2020, assess the anthocyanin biofortification of black, purple, and blue wheat flour, examining their antioxidant potential and antimicrobial activity against prevalent human pathogens. Dhua et al., 2021, elevated grain protein content, increased carotenoid content, and disease resistance in a superior bread wheat variety through molecular breeding. The PsyE1 gene (Y gene) and the GpcB1 gene were employed as innovative sources to augment both grain carotenoid and protein content in the commercially elite bread wheat cultivar HD2967.

Major findings

Hybrids were created by breeding technique to improve production and nutrition value of wheat. Crossing had donebetween less yielding black wheat varietyand different common Indian wheat variety. After analysis of morphological parameter, confirmed hybrid grain and their flour were analyzed for different biochemical test to determine and compare the nutrition profile in hybrids and their parents. The result showing that hybrid perform better in term of Anthocyanin content, Total phenolic content (TPC), Antioxidant capacity and reduced gluten protein content in hybrid than parent cultivars. The ultimate result offer high yield and nutrition enriched genotype.

Keywords: Wheat, Breeding, Biofortification, malnutrition, Anthocyanin

References

[1] Dhua, et al 2021 Composition, characteristics and health promising prospects of black wheat: A review. Trends in Food Science & Technology.

Strategies to enhance the production of Polyunsaturated fatty acid in microalgae for human health

Nidhi Chaudhary [a] and Nand K. Singh*
[a]Department of Biotechnology, Motilal Nehru National Institute of Technology
Allahabad, Prayagraj,211004India
*nksingh@mnnit.ac.in;

Background

Microalgae have emerged as a potential source of omega-3 polyunsaturated fattyacids, crucial nutrientsthat offer healthbenefits when usedas functional foodsforhumans.

Review

Various economical and effective methods are now being investigated to enhance theproduction of these fatty acids in algae. Additionally, the production of these metabolites in algaecanbestimulated by several environmental stresses.

Major findings

The current research explored the impact of four abiotic factors, namely indole-3-acetic acid (IAA), abscisic acid (ABA), salinity, and pH, on the growth and production ofomega-3 polyunsaturated fatty acids in freshwater microalgae species, including *Chlorococcumoleofaciens*, *Leptolyngbya* sp., *Chlorellavariabilis*, and *Monoraphidium contortum*. Underoptimal cultivation conditions, microalgae have the capacity for rapid growth and the productionof substantial amounts of oil rich in omega-3 polyunsaturated fatty acids. Following treatmentswith plant hormones and changes in salinity, the cells exhibited an increase in both biomass andlipid content, with the most pronounced stimulatory effect observed in cells treated with indole-3-acetic acid (IAA). pH variations did not influence the algal cells. Conversely, abscisic acid(ABA) demonstrated the most significant enhancement in the content of omega-3 fatty acids, specifically eicosapentaenoic acid (EPA) ranging from 2.15% to 5.82% and docosahexaenoicacid (DHA) from 1.95% to 3.1%. By investigating these abiotic factors, it becomes feasible todevise strategies that optimize cultivation conditions to promote the production of omega-3 fattyacids.

Keywords: **Microalgae, Abiotic factor, omega-3 polyunsaturated fatty acids, Eicosapentaenoicacid, Docosahexaenoic acid**

References

[1] Perdana, B.A., Chaidir, Z., Kusnanda, A.J., Dharma, A., Zakaria, I.J., Bayu, A. and Putra, M.Y., 2021. Omega-3 fatty acids of microalgae as a food supplement: A review of exogenousfactorsfor production enhancement. *Algal Research*, *60*, p.102542.
[2] Kumar, B.R., Deviram, G., Mathimani, T., Duc, P.A. and Pugazhendhi, A., 2019. Microalgaeas rich source of polyunsaturated fatty acids. *Biocatalysis and agricultural biotechnology*, *17*, pp.583-588.
[3] Salama, E.S., Jeon, B.H., Chang, S.W., Lee, S.H., Roh, H.S., Yang, I.S., Kurade, M.B., El-Dalatony, M.M., Kim, D.H., Kim, K.H. and Kim, S., 2017. Interactive effect of indole-3-aceticacid and diethyl aminoethyl hexanoate on the growth and fatty acid content of some microalgaeforbiodiesel production. *Journal of CleanerProduction*, *168*, pp.1017-1024.

PI: 60

A synergistic boost in the rice productivity by combined supplementation of zinc and selenium nanoparticles.

Monalisha Mishra and NandK. Singh*
Department of Biotechnology, Motilal Nehru National Institute of Technology Allahabad,
Prayagraj 211004, India

*nksingh@mnnit.ac.in

Background

The need to boost crop production through the application of newfangled technologies like nanotechnology has arisen from the rapid growth of the global population. Enhancing production and reducing biotic stress require better uptake of active agricultural ingredients such as fertilisers and pesticides (Karny et al., 2018). As a matter of fact, the bulk of sprayed crop-protection-agents are thought to be lost to the environment, with only 0.1% believed to achieve their biological target.

Review

According to recent studies, treating plants with low concentrations of Zn and Se nanoparticles improves their growth and productivity (Chauhan et al., 2019; Al-Khayri et al., 2023). Selenium (Se) andzinc (Zn)may function as cofactors andessential elements fora variety ofenzymes, impacting anumber of physiological processes. According to a research by Dimpka et al. (2020), using ZnONPs significantly improved the growth, yield, and absorption of macro- and micronutrients in abiotically stressed soybean plants.

Major Findings

This study aims to explore the potential benefits of combinatorial use of zinc (Zn) and selenium (Se) nanoparticles on rice plants in the vegetative growth phase, with a focus on sustainable farming practices. We investigated the possible advantages of these nanoparticles on plant development and subsequent productivity using controlled application techniques. In this experiment, rice plants at the critical stage of their vegetative growth were given targeted delivery of zinc and selenium nanoparticles in the optimal proportion. Our results reveal a notable improvement in anumber of growth metrics, such as better nutrient uptake, more biomass in the roots and shoots, and higher chlorophyll content. Interestingly, the beneficial effect goes beyond vegetative growth and eventually results in higher yield during the reproductive stage. According to our findings, strategically applying Se and Zn nanoparticles in a 1:1 ratio during the vegetative growth phase can serve as a potential method to bolstering rice plant performance as well as promote resilient and sustainable agricultural practices.

Keywords: Nanotechnology; Zinc; Selenium; Rice; Productivity

References

[1] Al Khayri,J.M.,Rashmi,R.,SuryaUlhas,R.,Sudheer,W.N.,Banadka,A.,Nagella,P.,Aldaej,M.I.,Rezk,A.A.S., Shehata, W.F. and Almaghasla, M.I., 2023. The role of nanoparticles in response of plants to abiotic stress at physiological, biochemical, and molecular levels. Plants, 12(2), p.292.
[2] Chauhan, R.,Awasthi, S., Srivastava, S., Dwivedi, S., Pilon-Smits, E.A., Dhankher, O.P. andTripathi, R.D., 2019. Understanding selenium metabolism in plants and its role as a beneficial element. *Critical Reviews in Environmental Science and Technology*, *49*(21), pp.1937-1958.
[3] Dimkpa, C.O.; Andrews, J. ; Sanabria,J.;Bindraban,P.S.;Singh,U.;Elmer,W.H.;Gardea-Torresdey,J.L.; White, J.C. Interactive effects of drought, organic fertilizer, and zinc oxide nanoscale and bulk particles on wheat performance and grain nutrient accumulation. *Sci Total Environ.* 2020, *722*,

Essential Oils vs. *S. aureus*: Unveiling Potent Antimicrobial Effects

Anmol Srivastava[a], Nidhi Verma[a], Vishnu Agarwal[a*]
[a]Department of Biotechnology, Motilal Nehru National Institute of Technology, Allahabad (Prayagraj) 211004, Uttar Pradesh, India.

* vishnua@mnnit.ac.in

Background

This study delves into multifaceted realm of essential oils, to comprehensively elucidate the therapeutic potential of these concentrated hydrophobic volatile liquids derived from plants. In the present study we have screened some essential oils (*Salvia sclarea*, *Pelargonium graveolens*, *Rosmarinus officinalis*, *Melaleuca alternifolia*) for their antimicrobial activity against a gram-positive bacteria *Staphylococcus aureus*.

Review

This notorious pathogen is known to cause severe infections ranging from nosocomial respiratory tract infections to skin and cardiovascular infections. Infections resulting from antibiotic resistant strain methicillin-resistant *S. aureus* (MRSA) are more serious and hence have increased mortality. So, researchers are exploring newer alternatives to combat such infections and essential oils can help in our fight against such pathogens.

Major findings

All the essential oils used in this study were found to be effective against *S. aureus* however, *Pelargonium graveolens* oil was most active and has the lowest minimum inhibitory concentration (MIC) of 1ul/ml and a larger zone of inhibition in comparison to other oils (at 2% v/v concentration). On the other hand*Rosmarinus officinalis* oil was least active and has a MIC of 4ul/ml. However*Salvia sclarea* and *Melaleuca alternifolia* oil showed moderate activity against *S. aureus* with a MIC of 2ul/ml. This data may assist in development of an active formulation against infections caused by *S. aureus*.

Keywords: Essential oils, *S. aureus*, antimicrobial activity, MIC

References

1. Man, A., Santacroce, L., Iacob, R., Mare, A., & Man, L. (2019). Antimicrobial activity of six essential oils against a group of human pathogens: A comparative study. Pathogens, 8(1), 15.
2. Cheung, G. Y., Bae, J. S., & Otto, M. (2021). Pathogenicity and virulence of Staphylococcus aureus. Virulence, 12(1), 547-569.
3. Edwards-Jones, V., Buck, R., Shawcross, S. G., Dawson, M. M., & Dunn, K. (2004). The effect of essential oils on methicillin-resistant Staphylococcus aureus using a dressing model. Burns, 30(8), 772-777.

PI: 163

Ameliorative effects of Baicalin on streptotozotocin-induced oxidative stress and hepatotoxicity

Aditya Kumar Yadav, Pratibha Mishra, Abhay Kumar Pandey*
Department of Biochemistry, University of Allahabad, Prayagraj-211002

* akpandey23@rediffmail.com

Streptozotocin (STZ) is a chemical compound that causes pancreatic islet β-cell destruction and is widely used experimentally to produce a model of type 1 diabetes mellitus. Further, introduction of STZ in living system might result in adverse effects on hepatic, renal, neuronal, and reproductive functions because of oxidative damage. The present study was planned to assess the oxidative stress and hepatotoxiceffects of STZ on male albino Wistar rats and the protective efficacy of baicalin, a natural flavone glycoside against these adverse effects. The effect of the compound was studied on several serum enzymatic and biochemical markers. Administration of STZ at dose of 35mg/kg body weight caused elevation in levels of AST, ALT, total bilirubin, ALP, creatinine, uric acid, and some other parameters in serum while levels of total protein and albumin decreased. In hepatic tissue glutathione peroxidase and glutathione transferase activities declined with reduction in glutathione content signifying oxidative stress. Co-administration of baicalin showed partial restoration of serum and tissue markers suggesting the protective potential of baicalin against STZ-induced hepatotoxicity and oxidative stress.

Keywords: **Streptozotocin, Oxidative stress, Hepatotoxicity, Baicalin, Serum markers**

PI: 180

Inhibitory potentials of phytocompounds from *Callistemon lanceolatus* leaf extracts against MDA-MB-231 Breast cancer cell: an invitro and computational study

Ramesh Kumar[a], Shashank Kumar[b], Abhay Kumar Pandey[a*]
[a]Department of Biochemistry, University of Allahabad, Prayagraj, India 211002
[b]Department of Biochemistry, Central University of Punjab, Bathinda, Punjab 151401

*akpandey23@rediffmail.com

Background

Cancer is one of the leading causes of death and significantly burdens the healthcare system. Due to its prevalence, there is undoubtedly an unmet need to discover novel anticancer drugs. The natural products have been an incomparable source of anticancer drugs in the modern era of drug discovery

Review

The present study reports anticancer and antioxidant activities of *Callistemon lanceolatus* leaf extracts. Anticancer activity was studied against MDA-MB-231 cells. Antioxidant assessment of the chloroform and methanol extracts showed considerable free radical scavenging, metal ion chelating, and reducing power potential.

Major Findings

Chloroform extract exhibited potent inhibition of cancer cell proliferation in MTT assay and promoted programmed cell death. Reactive oxygen species (ROS) generation, mitochondria membrane potential (MMP) disruption ability, and nuclear morphology changes were studied using H2-DCFDA, JC-1, and Hoechst dyes, respectively, using confocal microscopy. Apoptotic cells exhibited fragmented nuclei, increased ROS generation, and altered MMP in dose- and time-dependent manner. Chloroform extract upregulated the BAX-1 and CASP3 mRNA expression coupled with downregulation of BCL-2 gene. Further, in silico docking of phytochemicals present in *C. lanceolatus* with anti-apoptotic protein MDM-2 endorsed apoptosis by its downregulation and thus corroborated the experimental findings.

Keywords: *Callistemon lanceolattus*, Phytochemical, Anticancer, molecular docking

PI: 181

Study of ROS induced stress on antibiotic production during co-culture: a short review

Hanshita Yadav, Rupika Sinha*
Department of Biotechnology
Motilal Nehru National Institute of Technology, Allahabad (Prayagraj)
* rupika@mnnit.ac.in

Background

Understanding the complex relationship between microbial communities and their environment, particularly during co-culture, is crucial in various scientific fields due to its significant impact. This review explores the intriguing connection between Reactive Oxygen Species (ROS) and antibiotic production in microorganism co-cultures. ROS are crucial signaling molecules within biological functions, but their role in microbial community dynamics during co-culture remains unexplored.

Review

Numerous works have been done on the ROS generation, effect on different antibiotic production, application. This study focuses at how stress from reactive oxygen species (ROS) affects the synthesis of antibiotics in co-cultures. It finds that excess of oxygen, a byproduct of photosynthetic cyanobacteria, drives biological evolution. It will explain the mechanisms of interaction between two microbes during co-culture in order to provide a spotlight on the ecological significance of antibiotic biosynthesis. Transcriptome analysis, physiological measurements, and gene functional analysis will be used to study co-culture scenario in detail and will also explain the role of ROS in production of antimicrobial compounds.

Major findings

The function of ROS at the physiological levels during co-culture of antibiotic producing organism with other microbial species will be the main focus of this review. This would open-up new avenues for co culture-based production of secondary metabolites and their application at industrial scale.

Keywords: ROS, Streptomyces, co-culture, Antibiotic production

References

1.Checa J, Aran JM. Reactive Oxygen Species: Drivers of Physiological and Pathological Processes. J Inflamm Res. 2020 Dec 2; 13: 1057-1073. doi: 10.2147/JIR.S275595. PMID: 33293849; PMCID: PMC7719303.
2. Snezhkina AV, Kudryavtseva AV, Kardymon OL, Savvateeva MV, Melnikova NV, Krasnov GS, Dmitriev AA. ROS Generation and Antioxidant Defense Systems in Normal and Malignant Cells. Oxid Med Cell Longev. 2019 Aug 5; 2019: 6175804. doi: 10.1155/2019/6175804. PMID: 31467634; PMCID: PMC6701375.

PI:193

Investigation into the long and short-term effect of Hridaya Mudra (Apaan Vayu Mudra) on different HRV indices & Blood Pressure

Shruti Kumari[a*], Dr. Anjana Dwivedi[a]
[a]Department of Bioengineering and Biotechnology
Birla Institute of Technology, Mesra Ranchi
*shrutikmr87@gmail.com

Background

Apaan Vayu Mudra is a therapeutic yoga hand mudra that is mostly concerned with healing heart-related diseases. Heart rate variability (HRV) reflects beat-to-beat changes in RR intervals, which are related to the ongoing interplay between the two arms of the autonomic nervous system. Higher Heart rate variability (HRV) is an indicator of good physical and emotional health and fitness Electrocardiogram (ECG)-based evaluation of HRV may be performed by several methods, including time- and frequency-domain analyses as well as nonlinear techniques. Different indices used are PNN50, rMMSSD, SDNN and HF power.

Review

A few scientific studies have been conducted to assess the effectiveness of different mudras, viz. the effect of apaanvayu mudra on blood pressure in hypertensive patients (Sunita and Sharma, 2020); and the effect of Jñāna mudra on anxiety level among young adults (Saraswat and Kumar, 2021).

Material & Methods

A group of (N=60) healthy young adults with no cardiovascular complain divided into control and experimental arms. ECG recording of 6 minutes using BIOPAC, MP45 setup followed by 15 to 45 mins of Hridaya Mudra in calm environment followed by second reading. Control reading would be taken at same interval as experimental, without any intervention. HRV feature would be extracted using Kubios Software.

Expected outcome

We hypothesize that regular Hridaya mudra practice will improve HRV and vagal tone and lower heart rate all indicating increase in parasympathetic dominance. It is a no cost, easy and non-invasive strategy and can be used as a preventive measure for anxiety, palpitations and heart related disorders

Keywords: Vagal tone, Parasympathetic dominance, Apaan Vayu Mudra, HRV, RMSSD, pNN50

References

Cygankiewicz, I., & Zareba, W. (2013). Heart rate variability. *Handbook of clinical neurology*, *117*, 379-393.

Tyagi, A., & Cohen, M. (2016). Yoga and heart rate variability: A comprehensive review of the literature. *International journal of yoga*, *9*(2), 97.

Francesco, B., Maria Grazia, B., Emanuele, G., Valentina, F., Sara, C., Chiara, F., ... & Francesco, F. (2012). Linear and nonlinear heart rate variability indexes in clinical practice. *Computational and mathematical methods in medicine*, *2012*.

Saraswat NK, Kumar S. Effect of Jñāna mudra on anxiety level among young adults. International Journal of Physical Education, Sports and Health [Internet]. 2021;8(3):31-4.

Sunitha S, Sharma CP. The Effect of mudra therapy (Apan Vayu Mudra) on level of blood pressure among hyper tension clients. International J of Health Sciences and Research. 2020;10(6):321-7

Session-2

Biotechnological Intervention in Integrative and Computational research

PI: 11

Di-cyclohexyl phthalate (DCHP) alters the activity of rat liver catalase: an *in vitro* and *in silico* study

Lalit Kumar Singh[a, *], BechanSharma[a]

[a]Department of Biochemistry, University of Allahabad, Allahabad 211002, India,

*mylalitkumar@gmail.com

Many endocrine-disrupting chemicals produced each year are known to cause potential harm to living systems. The ubiquitous presence of phthalates can pose risks to humans and wildlife. Phthalates such as DCHP, and di(2-ethylhexyl) phthalate (DEHP) are lipophilic diesters, which can be easily metabolized to their corresponding monoesters and cause toxicity in living organisms. The main objective of this study was to determine the impact of DCHP on rat liver catalase (CAT) activity in vitro. Wistar rat liver was excised and liver homogenate (10% w/v) was prepared in 0.25M sucrose solution under ice-cold conditions (4^0C). The homogenate was centrifuged at 9000 rpm for 30 min at 4^0C. The post-nuclear supernatants were stored in aliquots at -20^0C and used for further experiments. Protein content was determined using the Lowry method. CAT displayed optimum activity at pH 7.4 and temperature 37^0C. Using Lineweaver-Burke double reciprocal plots, the K_m, K_{cat}, and V_{max} values for CAT were found to be 43.26 mM, 19.75 sec^{-1}, and 0.079 U/mg, respectively. This in-vitro study indicated significant changes in CAT activity due to DCHP. The results showed a negative regulatory effect of DCHP on CAT activity. IC_{50} and K_i values for DCHP were found to be 359µM and 0.937mM, 0.612mM respectively. The *in-silico* study shows that DCHP has the maximum docking score. The inhibitory pattern of DCHP with CAT was found mix-type inhibition. This *in-vitro* and *in-silico* study reveals the negative regulatory effects of DCHP on rat liver CAT.

Keywords: Catalase, Di-cyclohexyl phthalate, in-vitro, auto dock analysis, docking score

Whole genome re-sequencing and genome wide polymorphism in Indian Arboviral mosquitoes: A vector control perspective

Preeti Acharya[1], Upasana Shyamsunder Singh[2], Mayilsamy Muniaraj[3], Binata Nayak[1*], Aparup Das[4*]

[a]Sambalpur University, Jyoti vihar-768019, Jyoti vihar-768019, Odisha, India
[b]Department of Biological Sciences, Vanderbilt University, Nashville, TN, USA
[c]ICMR-Vector Control Research Centre field Station, Madurai, Tamil Nadu, India
[d]ICMR-National Institute of Research in Tribal Health, Madhya Pradesh, India

*binatanayak@suniv.ac.in; aparupdas@nirth.res.in

Background

In this study, we investigated the genomic diversity of two significant hematophagous arboviral vectors native to India, namely *Aedes aegypti* and *Aedes albopictus*. Our focus centered on the examination of endo-peptidases, particularly serine proteases, recognized for their pivotal roles in both digestion and immunity processes within these vectors.

Review

We employed Illumina DNA sequencing to conduct whole genome sequencing on field strains of *Ae. aegypti* and *Ae. albopictus*. Comparative analysis involved evaluating predicted DNA polymorphisms, encompassing single nucleotide polymorphisms (SNPs) and insertions/deletions (InDels). This analysis considered the frequency and distribution of these polymorphisms across the genome, drawing comparisons with reference genomes.

Major Findings

A notable revelation emerged as *Ae. albopictus* exhibited nearly double the level of DNA polymorphism in comparison to *Ae. aegypti*. Within the identified high-impact polymorphisms, a substantial proportion comprised stop-gain and frame-shift mutations, particularly within serine proteases. These findings provide crucial insights into the distinctions between field isolates and reference genomes. Importantly, this information forms a promising foundation for the development of innovative vector control strategies. Future investigations are warranted to delve into the expression patterns of the identified target genes, further advancing our understanding of these arboviral vectors and enhancing the efficacy of vector control measures.

Keywords: genome; *Aedes*; serine protease; serpin; DNA polymorphism; dengue

PI: 36

Ecological assessment of Sharda River by application of diatom indices

Saleha Naz[a*], Prateek Srivastava[a]
[a]Department of Botany, University of Allahabad, Prayagraj, India

*saleha_phd2020@allduniv.ac.in

Background

Rivers are among the most diverse and threatened ecosystems on Earth (Sabater *et al*., 2013). Biological communities of rivers reflect the overall ecological integrity by unifying various stressors, thus providing a broad measure of their synergistic impacts. Diatoms have been extensively used in rivers for bioassessment purposes throughout the world (Hughes *et al*., 2012). The Sharda River is a tributary of the river Ghaghara which originates from Kalapani in the Lesser Himalayas and flows along the international boundary of India and Nepal. The Sharda River is proposed to be linked to Yamuna in the National River Interlinking Project.

Review

The European Commission had passed a legislation mandating the use of different organism groups to monitor the integrity of inland waters and coastal regions (The Water Framework Directive 2000/60/EC (WFD). Many diatom indices were developed in the last decade of twentieth century, which were based on multiple taxa (genus or species). They are determined either in terms of presence/absence of key indicator species (e.g. Palmer's index) or are based on the weighted average equation of Zelinka and Marvan (1961). Although the taxonomy of diatom flora has been well documented (Sarode & Kamat, 1984; Gandhi, 1957 – 1998; Nautiyal & Nautiyal, 1999; Karthick & Kociolek, 2011;) studies of the ecology and application of diatom assemblages in assessment of water quality have been dismally neglected.

Major findings

In the present study, water and diatom samples were collected from 17 sites in November 2022. PCA revealed three groups of sites, exhibiting moderate pollution (MP), Low pollution (LP) and Pristine conditions (PR). A high diversity of diatoms belonging to 40 genera were identified. CCA was employed to investigate the correlation between the composition of diatom assemblies and environmental factors. Using data from the diatom assembly, seventeen distinct diatom indices were computed in OMNIDIA software. Studies were also conducted into the association between index scores and measured water quality metrics which exhibited strong correlations with water quality variables. SPI and TDI were found to be most efficient and ascertaining in water quality assessment. Water quality maps for the Sharda River were hence prepared in accordance with these two indices. The results showed that Sharda River is a slight to medium polluted, oligotrophic-mesotrophic; quality ranging from moderate to good.

Keywords: Biomonitoring, Water quality, OMNIDIA, Diatom indices, Sharda River

References:

[1] Gandhi, H. P., 1998. Freshwater Diatoms of Central Gujarat. Bishen Singh Mahendra Pal Singh. Dehra Dun.
[2] Hering, D., Johnson & R. K., Kramm, S. (2006). Assessment of European streams with diatoms, macrophytes, macroinvertebrates and fish: a comparative metric-based analysis of organism response due to stress. Freshwater Biology, 51, 1757–85.

PI: 37

Bioinformatics intervention for the identification of novel therapeutic candidates for type ii diabetes in finger millet

Varsha Rani[a, *], Mukesh Kumar Singh[a], Dinesh Yadav[a*]
[a]Department of Biotechnology, D.D.U. Gorakhpur University Gorakhpur (U.P.) 273009, INDIA

*rani.varsha007@gmail.com

Background

According to the latest reports by the World Health Organization (WHO, 2022), approximately 77 million people over 18 years of age suffer from type II diabetes. Thus, diabetes mellitus has become one of the greatest health concerns in India as well as many other countries. This condition is characterized by hyperglycemia- a chronic metabolic disorder. Generally, prandial hyperglycemia is managed clinically by chemically synthetic inhibitors of α-glucosidase and α-amylase. The potential safety of natural inhibitors is evident from the many studies that reported that phenolic extracts from seed coats can inhibit these enzymes effectively. Finger millet seed coat is a treasure trove of such polyphenols with potentially incredible but under-explored nutraceutical properties. A critical obstacle to the development of nutraceutical products is poorly understood functional mechanisms and molecular interactions of the potential polyphenols in finger millet. In this study, we explored the inhibitory role of polyphenols of finger millet on human alpha-glucosidase and pancreatic amylase through a molecular docking approach and performed a comparative study between 16 different types of finger millet polyphenols with regularly used synthetic drugs like voglibose, miglitol and insulin secretagogues for controlling type II diabetes.

Review

Polyphenols possess anti-diabetic properties by reducing insulin resistance or secretion through various signaling pathways. Several polyphenols found in whole-finger millet fractions have been shown to decrease starch digestibility and absorption, lowering the glycemic response. In alloxan-induced hyperglycemic rats, meals based on finger millet whole grain were shown to have positive effects on glycemic status due to their antioxidant properties (6). Furthermore, diabetics are at risk for wound healing delays and cataracts. According to independent research on rat models, finger millet diet significantly increased the healing time of dermal wounds and delayed cataract formation. A comparison of (3mg) methanolic extracts of finger millet with a chemical antiglycation agent (125 mg) demonstrated significant inhibition of collagen glycation in vitro, demonstrating health benefits in diabetes mellitus complications.

Major findings

Using a molecular docking approach, sixteen-finger millet phenolic compounds' binding affinity and interaction patterns were evaluated against two human pancreatic enzymes, α-glucosidase and α-amylase. Out of thirty-two docked complexes against both targets, the top three docked complexes were shortlisted based on their binding affinities and good ADMET (absorption, distribution, metabolism, excretion, and toxicity) profile. Among the top three selected docked complex taxifolin (ΔG = -8.7 kcal mol-1), catechin (ΔG =-8.6 kcal mol-1) and acarbose (ΔG =-8 kcal mol-1), taxifolin shows the best target for hyperglycemia followed by catechin and acarbose. The comparative docking analysis of taxifolin (ΔG = -8.7 kcal mol-1) for hyperglycemia with commonly used drugs voglibose (-5.9 kcal mol-1), miglitol (-5.6 kcal mol-1) and insulin secretagogues (Gliclazide (-7.9 kcal mol-1)) indicates that finger millet taxifolin has a greater affinity for reducing hyperglycemia. We further evaluated the stability of taxifolin with both targets using molecular dynamics simulations at 50ns and binding energy tests with MM-GBSA (Molecular-Mechanism-Generalized Born and surface area), which concluded that both taxifolin- α-glucosidase and taxifolin- α-amylase docked complexes are highly stable, and possess van der Waals and electrostatic interactions. Based on this evaluation, the selected ligands met the drug-like criterion and demonstrated good anti-diabetic activity. To the best of our knowledge, this is the first report that revealed taxifolin is a functional inhibitor of glycosidase and amylase activities, suggesting that it could be used as an alternative treatment for post-prandial hyperglycemia.

Keywords: - Diabetes, Finger millet, Polyphenols, Molecular Docking, MD Simulation

Insilico characterization of a cadmium tolerant micro-eukaryotic gene screened from meta transcriptomic library of contaminated soil

Shristy Maurya[a], Bhupendra N.S. Yadav[a], Priyanka Shrama[a], Rajiv K. Yadav*

[a]Molecular Biology & Genetic Engineering Laboratory, Department of Botany, University of Allahabad, Prayagraj-211002, UP, India

* rky@allduniv.ac.in

Background

Ecosystem contamination byheavy metal poses a significant hazard to soil, water, and theatmospheric environment. Heavy metals not only contribute to soil pollution by altering itsphysical and biochemical characteristics, but they also pose significant environmental threats and are recognized as potential health hazards. Soil microbes play key role in the organic mineralization process and the capability to transform heavy metal contaminants into more stable and less toxicforms.

Review

Metagenomic and meta transcriptomic methodologies have been pivotal in unraveling the structural and functional diversity within organisms present in polluted soil environments. The present study aimed to utilize *in silico* approach for the structural characterization and functional annotation ofgene deposited in the NCBI database (Accession Number: OR882125). The gene was screenedfromamicro-eukaryoticmeta transcriptomiclibrarybyyeastfunctionalcomplementationassay.

Keyfindings

To predict gene function, ORF search was performed. The nucleotide sequence was translated to668 amino acid sequence. The ExPASy-ProtParam tools were then employed to analyze the physicochemical properties. The sequence was scanned for conserved functional domain at default E-value and identified the presence of the DJ1/pfp1 domain. This domain was found to contain acatalytic triad or dyad in its active site and involved in oxidative stress responses. It has also beenreported to possess chaperone and protease activity. Thus, in silico approach play key role in thefunctionalpredictionofgenesdiscoveredfromenvironmentalsampleandtheinformationobtainedcanbefurtherused for experimentalvalidation.

Keywords: **Heavy-metal, microbes, meta transcriptomics, functional complementation**

References:

[1] Sourav Bandyopadhyay; MarkR Cookson (2004). Evolutionary and functional relationships within the DJ1 superfamily.,4(1),6–0.doi:10.1186/1471-2148-4-6

[2] Ariga, Hiroyoshi; Iguchi-Ariga, Sanae M. M. (2017). [Advances in Experimental Medicine and Biology] DJ-1/PARK7Protein Volume 1037 || Structural Biology of the DJ-1 Superfamily, 10.1007/978-981-10-6583-5(Chapter 2), 5–24.doi:10.1007/978-981-10-6583-5_2 https://web.expasy.org/protparam/

From Cells to Systems: Navigating the Complexity of Brain Organoids for DiseaseModelingandInterdisciplinaryAdvancements

Ishita Bhardwaj[a]*, Dr. Sippy Singh[b], Dr. Durgesh Singh[b]

[a]P.G Scholar Department of Zoology S.S Khanna Girls' Degree College (A Constituent College of University of Allahabad) Prayagraj 211003

[b]Assistant Professor Department of Zoology S.S Khanna Girls' Degree College (A Constituent College of University of Allahabad) Prayagraj 211003

*ishitabhardwaj28@gmail.com

Background

Brain organoids are three-dimensional structures created from pluripotent stem cells, resembling the embryonic humanbrain. These organoids serve as valuable models for studying human brain development and disorders. They replicatemany aspects of early brain development in termsof molecular, cellular, structural, and functional characteristics. Inrecent advancements, brain organoidmethodologies haveprogressed, offeringinsights into disease modeling. Despite their ability to mimic key features of the embryonic human brain, there are limitations in fully reproducing certaincomplexities. An attempt has been made to review and cover the latest developments in brain organoid technologies, emphasizing their applications in modeling diseases. It also involves a comparison between current organoid systems and the embryonic human brain, highlighting both achieved and yet-to-be-achieved features and outlines the existing capabilities of brain organoids. It also addresses the potential for advancing the technologies to broaden their applications in the future.

Review

Organoid research, focusing on three-dimensional cultures, has emerged as a promising approach using ESCs or iPSCs.Organoids replicate living tissue cell types and functions, providing advanced in vitro models. However, their complexitychallenges traditional stem cell analyses, necessitating interdisciplinary approaches, brain organoids also highlight theexamples of interdisciplinary research incorporating machine learning, genetic engineering, and optical imaging. Suchapproaches offer insights into complex biological phenomena, unraveling the potential applications and future prospects, emphasizing the role of interdisciplinary researchin advancingorganoidforclinicalpurposes.

Major findings

Organoid research has unveiled key insights into disease modeling, developmental biology, and personalized medicine. These miniature organ-like structures have advanced neurodegenerative diseases research by providing more representative models compared to animal model and hold promising option for regenerative medicine. Interdisciplinaryapproaches, including machine learning and genetic engineering, have enhanced the understanding of organoid. Ongoingeffortsaimto refine organoid technologies for broader application in science and medicine.

Keywords: Stem cell, brain organoids, interdisciplinary research, regenerative medicine, disease modeling.

References:

[1] Qian, X., Song, H., & Ming, G. L. (2019). Brain organoids: advances, applications and challenges. *Development(Cambridge,England),146*(8), dev166074.https://doi.org/10.1242/dev.166074

[2] Kodera,T.,&Osakada,F.(2023).*Nihonyakurigakuzasshi.FoliapharmacologicaJaponica,158*(1),64–70.https://doi.org/10.1254/fpj.22097

[3] Lancaster, M. A., Renner, M., Martin, C. A., Wenzel, D., Bicknell, L. S., Hurles, M. E., Homfray, T., Penninger, J. M.,Jackson,A.P.,&Knoblich,J.A.(2013).Cerebralorganoidsmodelhumanbrain development andmicrocephaly.*Nature,501*(7467),373–379.https://doi.org/10.1038/nature12517

PI: 61

Genetic and omics techniques as holistic approaches for the nutritional improvement in rice (*Oryza sativa L.*).

Archana Patel[a], Monalisha Mishra[a], Nidhi Shukla[a], Kaamini Bisht[a] and Nand K. Singh[a, *]
[a]Department of Biotechnology, Motilal Nehru National Institute of Technology
Allahabad, Prayagraj 211004, India

*nksingh@mnnit.ac

Background

Rice stands as a fundamental cereal crop prevalent in tropical Asian regions, boasting both palatability and nutritional value. It thrives in tropical and subtropical regions characterized by diverse thermal conditions, encompassing an atmospheric temperature span of 25 to35 degreesCelsius. Rice is cultivated on more than 162 million hectares of land, according to various researchers (Mishraet al.,2018). The predominant focus of studies on rice has revolved around characteristics associated with the improvement of its productivity. There is a requirement to create novel rice varieties and enhance their nutritional content.

Review

In the cultivation of rice (*Oryza sativa L.*), the primary objectives involve augmenting both yield and nutritional excellence (Ku et al.,2020). Conventional methods of rice farming frequently depend on the indiscriminate application of fertilizers to fulfill nutritional needs. Several Genome-Wide Association Studies (GWAS) and mappings of Quantitative Trait Loci (QTL) have been carried out recently, focusing on traits associated with commercial quality, such as elongation ratio, Grain dimensions and aromatic output are often targeted, yet these endeavors seldom attain the optimal nutritional excellence in rice.

Major Findings

The assets generated for Genome-Wide Association Studies (GWAS) and Quantitative Trait Loci (QTL) analysis can be efficiently utilized to develop genetic selection and prediction models (Yoshidaet al.,2022). The consecutive application of various methods that make use of similar resources will prove to be an effective strategy for crop improvement endeavors.This article promotes nutritional approaches employing omics methodologies to enhance the nutritional composition of rice. Recent progress in genetic reservoirs provides diverse strategies to grasp the molecular mechanisms influencing specific characteristics, facilitating the accurate up- or down- regulation of traits in marker-assisted breeding for the development of novel rice varieties. Genome- wide association studies, genome selection(GS), and QTL mappingare geneticanalysesthatcontribute to the targeted enhancement of specific nutritional attributes in rice grain. These comprehensive strategies not only illuminate the intricate genomics of rice but also show potential for sustainable and high-yield cultivation.

Keywords: Rice; GWAS; QTL; Nutritional quality; Genomeselection

References:

[1] Mishra, R., Joshi, R.K. and Zhao, K., 2018. Genome editing in rice: recent advances, challenges, and future implications. *Frontiers in Plant Science*, *9*, p.1361.
[2] Ku, H.K. and Ha, S.H., 2020. Improving nutritional and functional quality by genome editing of crops: status and perspectives. *Frontiers in plant science*, *11*, p.577313.
[3] Yoshida, H., Hirano, K., Yano, K., Wang, F., Mori, M., Kawamura, M., Koketsu, E., Hattori, M., Ordonio, R.L., Huang, P.andYamamoto, E., 2022. Genome-wide

PI: 63

Molecular docking studies of cell wall degrading enzymes of *fusarium graminearum*and bioactive compounds of *trichoderma* species

Kanchan Yadav[a] and Dinesh Yadav[a*]
[a]Department of Biotechnology, Deen Dayal Upadhyaya Gorakhpur University, Gorakhpur (U.P.) 273009, INDIA

* dinesh_yad@rediffmail.com

Background

Cell wall-degrading enzymes (CWDE) are a class of extracellular hydrolytic enzymes secreted by plant-pathogenic fungi that allow them to enter and infect host tissue. They may promote tissue invasion and the transmission of pathogens by the breakdown of cuticle, cell walls, and wax, resulting in illness of plants. Among the various types of identified CWDEs, the enzymes Polygalacturonase, Pectin esterase, Xylanase, and Cutinase play a significant role in promoting the pathogenesis (1).*Fusarium graminearum* is a prominent pathogen that cause Fusarium head blight (FHB), seedling blight, and brown foot rot in several crops such as wheat, barley, and other small grains.Additionally, it causes the collar and root rot of soybean seedlings(2).*Trichoderma sp* is a biocontrol agent (BCA) that is well known to maintain crop health and disease prevention. In addition to secreting secondary metabolites and enzymes, these BCAs also stimulate the immune system, prevent pathogen mycelium coiling, promote plant development, possess mycoparasitic activity, and synthesise antifungal compounds (3). Since dealing with problems in the farming sector has become more challenging, employing biological approaches, such as the use of *Trichoderma sp*., seems to be a great way to find sustainable solutions. However, it is time-consuming and expensive to compare bio active compounds against the enzymes synthesised by various fungal pathogens.

Review

Generally, plant cell walls serve as major barriers against pathogen invasion. They are composed primarily of cellulose, matrix materials (pectic substances, hemicelluloses, structural proteins) and water. To get through the plant cell wall barrier, phytopathogenic fungi produce enzymes known as cell wall–degrading enzymes (CWDEs), which are primarily focused on the breakdown of cellulose, xylan, and pectin. Polygalacturonase degrade pectate during the hydrolysis process. Pectin esterases are involved in the de-esterification of pectin (4). Cutinases degrade cutin by the hydrolytic mechanism(5). Xylanases degrade β-1,4-bonds in the polyxylose backbone producing oligosaccharides with different chain lengths. Typically, F. graminearum infects plants by secreting a variety of enzymes (CWDEs) that break down cell walls. These enzymes aid in the pathogen's sporulation by allowing it to enter the tissues of plants and thrive on the nutritional substances that the plant polysaccharides release.

Major findings

In order to evaluate the potential role of bioactive compounds produced by Trichoderma species in inhibiting the four enzymes namely, polygalacturonase, pectin esterase, cutinase and xylanse secreted by *F. graminearum* that degrade the cell wall, in-silico methods involving homology modelling, molecular docking and simulations were employed. Based on the results of the studies, Trichodermamide B, a compound produced by *Trichoderma harzianum*, was identified as a potential inhibitor of all four CWDEs. According to the docking analysis, complex xylanase+Trichodemamide B possessed most stable energy (-11 kcal/mol) followed by Polygalacturonase+Trichodermamide B (-9.3 kcalmol^{-1}), cutinase + Trichodermamide B (-8.1 kcalmol^{-1}) and Pectin esterase+ Trichodermamide B (-8.1 kcalmol^{-1}). The proposed research could potentially be used to produce bioformulations that function as biopesticides, offering a viable alternative to synthetic chemicals.

Keywords: Bioinformatics, Docking, Enzymes, *Fusarium graminearum*

PI: 79

Molecular Phylogeny of Light signal transduction component

Akanksha Maurya[a], Aparna Singh[b,*]
[a]Department of Bioinformatics, MMV, Banaras Hindu university
[b]Department of Botany, MMV, Banaras Hindu university

*aparnasingh@bhu.ac.in

Background

Spontaneous change incorporated during replication of genetic material is recognized in biological system as mutation. If these mutations occur in coding region of a protein molecule it may or may not change the amino acid in peptide chain depending upon the position of the change nucleotide in the codon. Point mutation which account for the change in amino acid are called non-synonymous mutations and those which do not change the amino acid are called synonymous mutation.

Review

Ratio of the rate of non-synonymous substitution to that of synonymous substitution (□) is considered as parameter measure to constrain on a protein. More than one □ ratio shows that the changes in amino acid accumulating during time are positively selected and changes are retained. This information may provide with the idea about evolution of signal transduction network and their crosstalk.

Major findings

Basic leucine zipper (bZIP) transcription factors have been reported to be involved in a variety of biological activities, including the response to biotic and abiotic stressors. In this study, we investigate and analyze whether natural selection pressure is exerted on bZIP transcription factor GBF1 in Arabidopsis thaliana and other species followed by gene duplication events and outburst of mutations. We compared the rates of silent and replacement substitution among related species and assessed the selection pressure using Phylogenetic Analysis by Maximum Likelihood (PAML). In translated Open Reading Frames coding a polypeptide, amino acid substitutions on a given lineage can be identified using maximum-likelihood (ML) analysis of codon substitution models. We found the positive selection pressure upon the lineage consisting GBF1 of Arabidopsis thaliana, Camelina sativa and Capsella rubella in comparison to the paralogue bZIP68.

Keywords: Phylogenetic Analysis by Maximum Likelihood, Light Signal Transduction, G box BindingFactor1

References

[1] Yang, Z. (1997). PAML: a program package for phylogenetic analysis by maximum likelihood. *Computerapplicationsin the biosciences,13*(5), 555-556.

[2] Mallappa, C., Singh, A., Ram, H., and Chattopadhyay, S. (2008). GBF1, a Transcription Factor of BlueLight Signaling in Arabidopsis, is degraded in the Dark by a Proteasome-mediated Pathway IndependentofCOP1 andSPA1. JBiol. Chem.283, 35772-35782.

PI:91

Degradation of fungicide Carbendazim using isolated soil bacteria in monoculture and co-culture: A sustainable approach

Moumita Das[a], Sumer Singh Meena[a], Anee Mohanty[a*]
[a]Department of Biotechnology (Dr B R Ambedkar National institute of technology Jalandhar-144008)

* mohantya@nitj.ac.in

Background

Excessive use of Carbendazim for extended periods leads to their accumulation in the agricultural soil, which is further taken by the plants and transfer along the food chain causing serious environmental and health concerns followed by neurotoxicity (Ma et al., 2023), carcinogenicity (Fan et al., 2021), toxicity to aquatic animals (Andrade et al., 2015). Certain soil bacteria have the ability to use these compounds as a carbon source and turn them into non-toxic or less toxic compounds.

Review

Treating Carbendazim contaminated agricultural soil with soil bacteria is a sustainable and eco-friendly approach. In this study isolation of plant growth promoting soil bacteria was done from a field that had received carbendazim treatment. After serial dilution of collected samples in Minimal Salt Media (MSM) with increasing concentration of carbendazim, couple of colonies were isolated. Spectrophotometric analysis and HPLC were done for both of the strains in mono culture and co-culture. Further a few tests were done to check plant growth promoting activity of the isolated strains.

Major findings

In this study it is observed that the degradation activity is higher in co-culture than mono culture and the isolated strains shows different plant growth promoting activity.

Keywords: Carbendazim, Neurotoxicity, Degradation, Spectrophotometric analysis, Co-culture.

References

[1] Andrade, T. S., Com, T., Henriques, J. F., Almeida, A. R., Machado, A. L., Koba, O., Giang, P. T., Soares, A. M. V. M., & Domingues, I. (2015). *Carbendazim exposure induces developmental, biochemical and behavioural disturbance in zebrafish embryos*.
[2] Fan, R., Zhang, W., Li, L., Jia, L., Zhao, J., Zhao, Z., Peng, S., Yuan, X., & Chen, Y. (2021). Individual and synergistic toxic effects of carbendazim and chlorpyrifos on zebrafish embryonic development. *Chemosphere*, *280*. https://doi.org/10.1016/j.chemosphere.2021.130769
[3] Ma, X., Chen, X., Hou, H., Liu, D., Liu, X., Wang, P., & Zhou, Z. (2023). Low Dose of Carbendazim and Tebuconazole: Accumulation in Tissues and Effects on Hepatic Oxidative Stress in Mice. *Toxics*, *11*(4). https://doi.org/10.3390/toxics11040326

PI: 92

Computational assessment of mango-derived compounds as dUTPase inhibitors for anti-leishmanial drug development

Ankita Mallick[1], Nisha Kumari Pandit[1], Shivani Chauhan[1], Anee Mohanty[1], Sumer Singh Meena[1*]

Department of Biotechnology, Dr. B. R. Ambedkar National Institute of Technology
Jalandhar, Punjab-144008, India[1]

*meenass@nitj.ac.in

Background

Leishmaniasis, endemic to 99 countries, impacts over 12 million people globally, with 1 million new cases of Cutaneous Leishmaniasis caused by *Leishmania major* each year [1]. This primarily affects populations with limited access to healthcare in both developed and developing nations [2]. The treatment using synthetic chemical drugs often leads to adverse side effects. Mango fruit being rich in phenolic, anthocyanin, antioxidant, flavonoid and carotenoid compounds, can be an effective alternative candidate for drug screening to inhibit dUTPase enzyme in *Leishmania major*, thereby disrupting nucleotide metabolism [4].

Review

A total of 37 phytochemicals from mango fruit (pulp, peel and seed kernel) were initially filtered by Veber's and Lipinski rule, and 18 filtered compounds were virtually screened against dUTPase. The 8 docked ligands underwent further studies like C-Docking to assess binding energies and analyzing molecular properties to check ADMET and toxicity profile. The best two docked bioactive compounds with acceptable toxicity profile used for molecular dynamic study.

Major findings

This study marks the first of its kind to investigate the specific natural compounds and their potential in combating Cutaneous Leishmaniasis. The phytochemicals that can eliminate complications within the body offer promising prospects for drug development, potentially mitigating the prevalent issues associated with conventional treatments.

Keywords: **Cutaneous leishmaniasis, dUTPase, Mango Fruit, Molecular Docking**

References

[1]. S. Mann *et al.*, "A Review of Leishmaniasis: Current Knowledge and Future Directions," *Curr Trop Med Rep*, vol. 8, no. 2, pp. 121–132, Jun. 2021, doi: 10.1007/s40475-021-00232-7.

[2]. A. C. Pinheiro and M. V. N. De Souza, "Current leishmaniasis drug discovery," *RSC Med. Chem.*, vol. 13, no. 9, pp. 1029–1043, 2022, doi: 10.1039/D1MD00362C.

PI:119

In silico screening of Potential Natural Compounds against Rheumatoid Arthritis

Samriddhi Singh[a], Pramod Katara[a]*
[a]Centre of Bioinformatics, IIDS, University of Allahabad, Prayagraj, U.P., India

*pmkatara@gmail.com

Background

Rheumatoid Arthritis (RA) is an autoimmune disease condition affecting mainly bones and joints or the synovium, where the immunity of the person starts attacking itself too; causing distortion that cannot be reversed. In the long run, other systems of the body are also getting affected. As of 2021, 1.3 million people in India are suffering from RA. There is no clinical cure for RA but its effect could be minimized to a great extent using appropriate drugs. RA is a chronic disease and the drug intake for prolonged period produces side effects. It is hypothesized that use of natural compounds may reduce the chance of side effects.

Review

As per literature, Matrix Metalloproteinase-13(MMP-13) enzyme has been found to play major role in collagen degradation, especially type II collagen as it is upregulated by the inflammatory cytokines. The other proteins interacting with MMP-13 such as TIMP (1, 2), ADAMTS (4, 5), ACAN, PLG, COL10A and COL2A1 are also playing central role, chosen as potential targets. The researches on autoimmunity are still under trial. Meanwhile, the symptoms could be managed by preventing collagen degradation. Published literatures show that natural compounds from various sources like honey, olive oil, spices, few terpenes, is oflavones, *Boswelia* and *T.cordifolia* etc. have potential to act against MMP-13 proteins. 26 of such most effective compounds were chosen as the ligand candidates.

Major findings

In current study, molecular docking approach has been used to screen out the most compatible natural compound against proteins involved in RA. These predicted compounds may control RA without producing side effects. The screened compounds have been tested for their ADME properties using bioinformatics tools. Screening results indicate that two natural compounds, i.e., Fisetin($C_{15}H_{10}O_6$) and Chrysin($C_{27}H_{30}O_{13}$) have potential to be considered as probable drug. Fisetin($C_{15}H_{10}O_6$) shows binding affinity with ADAMTS4 (-9.2 kcal/mol) and with MMP-13 (-8.4 kcal/mol), and Chrysin($C_{27}H_{30}O_{13}$) shows binding affinity with MMP-13 (-8.6 kcal/mol). Both compounds display considerable drug-likeness properties. We further recommended experimental testing of Fisetin and Chrysin against MMP-13.

Keywords: Rheumatoid Arthritis; Matrix Metalloproteinase-13; docking; Fisetin; Chrysin

References:

[1] Ashruf OS, Ansari MY. Natural Compounds: Potential Therapeutics for the Inhibition of Cartilage Matrix Degradation in Osteoarthritis. *Life (Basel)*. 2022 13(1):102. doi: 10.3390/life13010102.
[2] Hu Q, Ecker M. Overview of MMP-13 as a Promising Target for the Treatment of Osteoarthritis. *Int J Mol Sci.* 2021 22(4):1742. doi: 10.3390/ijms22041742.
[3] Katara P, Computational Approaches for Drug Target Identification. In: Singh, D.B. (eds) Computer-Aided Drug Design. Springer, Singapore (2020). https://doi.org/10.1007/978-981-15-6815-2_8
[4] Singh B, Nathawat S, Sharma A. Ram, Ethnopharmacological and phytochemical attributes of Indian Tinospora species: A comprehensive review. *Arabian Journal of Chemistry*, 2021, 14(10) 103381

PI: 132

Computational Modeling for Mycoremediation of Toxic Pollutants using *Pleurotus* species

Saba Ehsan[a], M P Singh[a, *]
[a]Center of Biotechnology, University of Allahabad, Prayagraj, Uttar Pradesh 211002, India

*mpsingh16@allduniv.ac.in

ABSTRACT:

Rampant anthropogenic activities and industrialization have given rise to a global environmental crisis, marked by the proliferation of toxic pollutants. The diverse array of toxic pollutants, including pharmaceutical residues such as antibiotics, steroids, antidepressants, analgesics, anti-inflammatories, antipyretics, beta-blockers, lipid regulators, and diuretics, not only contaminates the environment but also has far-reaching implications for human health.

Mycoremediation is a type of bioremediation in which toxins are removed or mitigated from the environment by fungi. Numerous mycological products play an essential role in the removal of the extensive variety of toxins from environmental pollutants. Mycoremediation is based on the action of extracellular enzymes which degrade the various types of recalcitrant and resistant contaminants. Mycological products are very helpful to clean up the contaminant's sites of the environment. It has the multiple modes that implement to detoxify different types of toxins or recalcitrant compounds through several types of prominent fungal enzymes i.e. laccase, peroxidase, catalase etc. Pleurotus ostreatus is a white-rot fungus that produces a lignolytic enzyme complex rich in several laccase iso-enzymes. Laccase are copper-containing oxidases biocatalyst, responsible for oxidation of electron rich natural and synthetic organic substrates in a nonspecific manner. It degrades them into nontoxic molecular species without forming any recalcitrant metabolites so only laccase is been used for bioremediation process due to their ability to degrade Azo, heterocyclic, reactive and polymeric dyes. On the basis of protein sequence availability of purifying laccase enzyme, we modelled the 3-D structures of laccase through homology modeling for the study of interaction between laccase and dyes. After that we go through in-silico studies of the interactive molecules on the structure based molecular docking method.

Keywords: Macro-fungi, Pollutants, Molecular Docking

References:

[1] Kulshreshtha, S., Mathur, N., & Bhatnagar, P. (2014). Mushroom as a product and their role in mycoremediation, 1–7. https://doi.org/10.1186/s13568-014-0029-8

[2] Singh, D., Sharma, K. K., & Jacob, S. (2014). Molecular Docking of Laccase Protein from Bacillus Safensis DSKK5 Isolated from Earthworm gut : A Novel Method to Study dye Decolorization Potential Molecular Docking of Laccase Protein from Bacillus Safensis DSKK5 Isolated from Earthworm gut : A Novel Method to Study dye Decolorization Potential, (October). https://doi.org/10.1007/s11270-014-2175-7

[3] Velu, C., Veeramani, E., Suntharam, S., & Kalimuthu, K. (2011). Insilico Screening and Comparative Study on the Effectiveness of Textile Dye Decolourization by Crude Laccase Immobilised Alginate Encapsulated Beads from Pleurotus Ostreatus, 1(4), 1–6. https://doi.org/10.4172/2155-9821.1000109

PI: 139

Effect of quercetin on diabetes mellitus: A bioinformatic approach

Shree Agarwal, Yogender Aggarwal, Koel Mukherjee
Department of Bioengineering and Biotechnology
Birla Institute of Technology Mesra, Ranchi

Diabetes mellitus is a metabolic disorder having an alarming effect all over the globe. Type 2 diabetes mellitus is mainly controlled by the changes found in dietary and lifestyle changes. It may cause severe complications to the other vital organs, one of them being cardiac complications. Diabetic cardiomyopathy is a complication that arises as a proceeding of the diabetes mellitus. This condition is a manifestation of patients with diabetes mellitus characterized by left ventricular hypertrophy and diastolic dysfunction with reduced systolic function in the advanced stages. The present work demonstrated the molecular docking of quercetin on the targeted protein (GLUT4, Kir6.2, & Troponin) through the signaling pathway of diabetes mellitus type 2 and diabetic cardiomyopathy. The quercetin showed an appreciating response with the proteins excavated from the pathways.

References:

1. Ansari P., Choudhury ST., Seidel V., Rahman AB., Aziz MA., Richi AE., Rahman A., Jafrin UH., Hannan JMA., & Abdel-Wahab Y. (2022). Therapeutic Potential of Quercetin in the Management of Type-2 Diabetes Mellitus. Life, 12(8), Article 1146.
2. Bartosova L., Horvath C., Galis P., Ferenczyova K., Kalocayova B., Szobi A., DurisAdameova A., Bartokova M., Rajtik T. (2022). Quercetin alleviates diastolic dysfunction and suppresses adverse pro-hypertrophic signaling in diabetic rats. Volume 13.

Structural analysis of Human DPP4/CD26 by Computational tools

Ashish kumar[a], Dr. Ashutosh mani[a*]
Department of Biotechnology
MNNIT-ALLAHABAD
Prayagraj, 211004 India

*amani@mnnit.ac.in

Background

The human DPP4 is a functionally multifaceted molecule present in the epithelial and endothelial membranes of the liver, lungs, intestine, and nearly all tissues. It has a variety of impacts on human metabolic illnesses such as diabetes, cancer, PCOS, and immunomodulation.

Review

DPP4 is a 766 amino acids long transmembrane protein. It has two domains: the N-terminus 8-bladed β-propeller domain from AA 61-495 and a C-terminal α/β hydrolase domain from AA 39-55 and 497-766. Structures of the DPP4 is present in the PDB databases are in conjugate form or have incomplete Starting sequences which are play a important role in the dimerization of the DPP4. Which forms the soluble DPP4 and active form of the protein.

Major findings

The Protein PDB ID 4A5S 4A5Swith 1.62 resolution was retrieved and refined by removing the conjugated ligands. It lacks the initial 38 amino acids in the sequence; however, we have obtained the whole sequence of DPP4 from the uniport database with uniprot id P42658. Then after, the 3D structures were predicted using Modeller and Alpha fold. Later the structures were analyzed. The active site is divided into two sub-regions: a catalytic triad made up of Ser630, Asp708, and His740; an oxyanion cavity including Tyr47 and Ser631; and a region having saline bridging residues including Glu205, Glu206, and Tyr662. The pockets S1 and S2 contain Arg125, Ser209, Phe357, Arg358, Tyr547, Ser631, Val656, Trp659, Tyr62, Tyr666, Asn710, and Val711, regions of importance for the action of DPP-4 inhibitors. The non-catalytic binding region that interacts with adenosine deaminase complexing protein 2 (ADA-2) consists of Asn281, Leu294, Leu340, Val341, Ala342, and Arg343 AA. Until January 18, 2024, there are 88 structures of human DPP4 in the PDB database available.

Keywords: DPP4, CD26, Diabetes type-2

References

1. Liao, P., Hemmerlin, A., Bach, T. J., and Chye, M. L. (2016). The potential of the mevalonate pathway for enhanced isoprenoid production. Biotechnol. Adv. 34, 697–713. doi: 10.1016/j.biotechadv.2016.03.005.

2. 1. Abdalla MA, Deshmukh H, Atkin S, Sathyapalan T. The potential role of incretin-based therapies for polycystic ovary syndrome: a narrative review of the current evidence. *Therapeutic Advances in Endocrinology and Metabolism*. 2021;12. doi:

12. De Meester I., Scharpé S., Vanham G., Bosmans E., Heyligen H., Vanhoof G., Corte G. Antibody binding profile of purified and cell-bound CD26.Designation of BT5/9 and TA5.9 to the CD26 cluster. *Immunology.* 1999;188:145–158

13. Weihofen W.A., Liu J., Reutter W., Saenger W., Fan H. Crystal structure of

PI: 176

Title: In-silico survey of molecular responses during plant-biotic interaction.

Meghna Agrawal[a], Dr. Ashutosh Mani[a,*]
[a]Department of Biotechnology, Motilal Nehru National Institute of Technology, Prayagraj

*amani@mnnit.ac.in

Backgroud:

Molecular interactions during host-pathogen/symbiont interaction determine the behaviour of the system. The survey on plant – biotic interaction includes the molecular responses (coding and non-coding RNA, proteins and signalling), beneficial and antagonist interactions, between crop plants, and fungi and invertebrates.

Review:

Agriculture contributes to 17% to the GDP of India, thus it is considered as 'Back Bone' of the Indian Economy. Wheat is main cereal crop and tomato is major vegetable crop in India providing food security to the growing demand of the country. There are various studies in recent years related to molecular mechanism during biotic interaction of symbionts and pathogen with these agriculture plants. The survey will reveal unique and common miRNA, genes and signalling pathways which are regulated during the interaction. In addition, the survey provides the overview of literature abundance, interacting microbes and invertebrates, interacting parts of the plants, gene abundance, etc.

Major findings:

There are 17,789 unique entries in the survey from manually curated 138 literatures, containing 10,450 unique genes in 14 different plant parts. The common genes in only pathogenic interaction in wheat plants are PR5, PR-2-2a, ZFP1 and the common genes in wheat and tomato during both pathogenic and symbiotic interaction are XTH3, XTH1, PR1, PR1B1, LePT2 and CAT, Chi, PDR1, Glc2, PER1 respectively. The deeper and synergistic understanding of the mechanistic interactions in crop might lead to novel, sustainable and better agricultural practices with higher crop yields.

Keywords: Plant-Biotic Interaction, Pathogen, Symbionts, Genes.

References:

1. Schirawski J, Perlin MH. Plant⁻Microbe Interaction 2017-The Good, the Bad and the Diverse. Int J Mol Sci. 2018 May 5;19(5):1374. doi: 10.3390/ijms19051374.

2. Utami YD, Nguyen TAN, Hiruma K. Investigating plant-microbe interactions within the root. Arch Microbiol. 2022 Sep 22;204(10):639. doi: 10.1007/s00203-022-03257-2

3. Tabassum N, Blilou I. Cell-to-Cell Communication During Plant-Pathogen Interaction. Mol Plant Microbe Interact. 2022 Feb;35(2):98-108. doi: 10.1094/MPMI-09-21-0221-CR

4. Robb EJ, Nazar RN. Tomato Ve-resistance locus: resilience in the face of adversity? Planta. 2021 Nov 22;254(6):126

5. Gruet C, Muller D, Moënne-Loccoz Y. Significance of the Diversification of Wheat Species for the Assembly and Functioning of the Root-Associated Microbiome. Front Microbiol. 2022 Jan 4;12:782135. doi: 10.3389/fmicb.2021.782135.

PI:196

Efficient Conversion of FastQC Data into Raw Count Table: A Linux-Based Procedure.

Bavita Katiyar[a], Ashutosh Mani[b], Neha Shree Maurya[c]
Department of biotechnology, MNNIT Allahabad, Prayagraj-211004
amani@mnnit.ac.in,

Background:

With the advancement in NGS technologies, the cost of sequencing has reduced significantly over the years, enabling researchers to opt for RNA-sequencing instead of microarrays for transcriptome analysis. After the isolation of mRNA from adenocarcinoma cells; cDNA libraries were constructed and was subjected to Illumina HiSeq 2500 to generate FastQC files.The fastqc files were aligned to the human reference genome (GRCh38).

Review:

The study compares differential Gene Expression of Tumor cells vs Adjacent Normal cells in Stomach Adenocarcinoma Patients. After the alignment of FastQC files with GRCh38 using *HISAT2* aligner, *Samtools* was used to efficiently index and retrieve data from large SAM files to generate BAM file. *StringTie* was used for accurate reconstruction of all expressed isoforms and estimation of their relative abundance. Merging of transcripts was done by *StringTie-merged* while read coverage table was generated using *StringTie-eB*.

Major findings:

Due to availability of many options, there is not a fixed protocol that should be used to analyse RNA-seq data. HISAT2 is more accurate in comparison to TopHat but less than STAR. The pipeline used here provides efficient way to do RNA-seq analysis in small laboratories.

Keywords: - HISAT2, StringTie, Samtools, Adenocarcinoma.

References:

1. https://www.ebi.ac.uk/ena/browser/view/PRJEB45410?show=reads
2. Kukurba KR, Montgomery SB. RNA Sequencing and Analysis. Cold Spring Harb Protoc. 2015 Apr 13;2015(11):951-69. doi: 10.1101/pdb.top084970. PMID: 25870306; PMCID: PMC4863231.
3. Pertea M, Kim D, Pertea GM, Leek JT, Salzberg SL. Transcript-level expression analysis of RNA-seq experiments with HISAT, StringTie and Ballgown. Nat Protoc. 2016 Sep;11(9):1650-67. doi: 10.1038/nprot.2016.095. Epub 2016 Aug 11. PMID: 27560171; PMCID: PMC5032908.
4. Kim D, Langmead B, Salzberg SL. HISAT: a fast spliced aligner with low memory requirements. Nat Methods. 2015 Apr;12(4):357-60. doi: 10.1038/nmeth.3317. Epub 2015 Mar 9. PMID: 25751142; PMCID: PMC4655817.

Session- 3

Biotechnological Intervention in Process Development and Manufacturing

Fungal-pectinases mediated retting of *sesbania aculeata* for extraction of sustainable natural fibers

Shruti Dwivedia[a,*], Ankur Singh[a], and Dinesh Yadav[a]
Department of Biotechnology, Deen Dayal Upadhyaya Gorakhpur UniversityGorakhpur-273009, U.P. India
*dwivedishruti.727@ gmail.com

Background

The soil of different fruit orchards from Gorakhpur Uttar Pradesh was collected and used for soil fungi isolation and elucidation of their biotechnological application potential like retting of natural fibers, fruit juice clarification, and formations of calcium pectate gel sheets. These soil fungi were enzymatically characterized for pectinases (PG, PNL, and PME), and the effect of pH and temperature was studied on them. Among the 22 indigenous isolates, four Soil fungi identified as *A. albamensis*MTCC 13291, *A. foveolatus*MTCC 13310, *F. falciforme* MTCC 13298 and *F. irregulare*MTCC 13296 showed alkaline behavior on pH and were showed promising retting of fibers of *Crotalaria* and *Cannabis*. Pectinases of these isolates were used in the present study for pectinase-mediated retting of fibers of *S. aculeata*.

Review

The pectin-rich fiber, which is primarily located near the middle lamella, has a high degree of elasticity. Filamentous fungi being the natural sources of pectinases are often employed due to their shorter shelf life and mass production of enzymes. *Sesbania* is a legume frequently grown as a green manure crop to enrich the soil with organic matter and nitrogen. This plant produces fibers that are robust, long-lasting, and have a high tensile strength. Retting is a biological procedure that eliminates non-cellulosic substances that have been enzymatically linked to the fiber bundle, leaving only the detachable cellulosic fibers. Water retting is the most common method but requires submerging fibers for a long duration preferably months and yields low-quality fibers. Compared to fibers produced using conventional retting techniques, pectinase-retted fibers can have increased strength. Fibers may become less harmed and more breakage-resistant due to the regulated enzymatic breakdown of pectins. The composite performance was said to be improved by using the best pectinolytic retting formulation.

Major findings

1. Among all four screened isolates *F. irregulare* MTCC 13296 was found most promising isolate.

2. The water retting yielded total fiber in 15 days, water with calcium sequestering agent EDTA reduced time to 10 days.

3. Pectinase-mediated retting using indigenous soil fungi *F. irregulare* MTCC 13296 successfully showed 75% fiber extraction in 48 hours in water.

Keywords: soil fungi, pectinase-mediated retting, natural fibers

References

1. Yadav, S., Maurya, S. K., Anand, G., Dwivedi, R., & Yadav, D. (2017). Purification, characterization and retting of Crotolariajunceafibres by an alkaline pectin lyase from Fusarium oxysporum MTCC 1755. *3 Biotech*, *7*, 1-9.
2. Dwivedi, S., Yadav, K., Gupta, S., Tanveer, A., Yadav, S., & Yadav, D. (2023). Fungal pectinases: an insight into production, innovations and applications. *World Journal of Microbiology and Biotechnology*, *39*(11), 305.
3. Monika, N., Anita, R., & Anupriya, S. (2017). Effect of retting methods on properties of Dhainchafibres. *Asian Journal of Home Science*, *12*(2),

PI: 30

Microbial Amylases Unveiled: A Journey Through Diversity, Optimization, and Applications

Yatika Dixit[a], Arun Kumar Sharma[a*]
[a]Department of Bioscience and Biotechnology, Banasthali Vidyapeeth, Rajasthan

* arunkumarsharma@banasthali.in

Background

Amylases are enzymes crucial for the hydrolysis of starch into simpler sugars, playing a pivotal role in various industrial applications, including food, textile, and pharmaceutical sectors. Due to their diverse ecological niches, microbial sources offer a vast repertoire of amylase-producing strains with unique characteristics. This review focuses on exploring and optimizing amylase from microbial sources, aiming to provide a comprehensive understanding of the current state of research in this field.

Review

The review begins with an overview of the microbial diversity and the factors influencing amylase production, including substrate specificity, pH, temperature, and fermentation conditions. A critical analysis of recent advancements in screening techniques for amylase-producing microorganisms is presented, highlighting the significance of metagenomic approaches and molecular tools in identifying novel strains.

The optimization strategies for enhanced amylase production are thoroughly discussed, encompassing traditional methods such as response surface methodology (RSM) and newer approaches like artificial intelligence-based optimization. Emphasis is placed on the importance of genetic engineering and strain improvement techniques to enhance amylase yields and tailor enzyme properties to meet specific industrial requirements.

The review also addresses the enzymatic characterization of microbial amylases, exploring their biochemical properties, substrate specificity, and stability under different conditions. The structural insights into microbial amylases are discussed, shedding light on the relationship between structure and function.

Major findings

1. **Microbial Diversity:** A diverse range of microbial sources for amylase production, including bacteria, fungi, and archaea, has been explored, highlighting the untapped potential of various environments.
2. **Optimization Strategies:** Novel optimization strategies, including artificial intelligence-based approaches, have shown promising results in enhancing amylase production.
3. **Enzymatic Characterization:** In-depth characterization of microbial amylases reveals their unique biochemical properties, providing valuable information for industrial applications.
4. **Structural Insights:** Understanding the structural aspects of microbial amylases contributes to the design of enzymes with improved properties through rational engineering.

Keywords: Microbial amylase, enzyme optimization, microbial diversity, enzymatic characterization, structural insights

PI - 33

Synergistic effect of co-culture system on phytase production

Vidhi Saxena[a], Dr. Lalit Kumar Singh[a,*]
[a]Department of Biochemical Engineering School of Chemical Engineering Harcourt Butler Technical University
Kanpur, Uttar Pradesh-208002
*lkumar@hbtu.ac.in

Abstract

Plant-available phosphate is often limited in soils, hindering agricultural productivity. Microbial phytases degrade this phytic acid, but their individual efficacy can be low. Synergistic effect of sequential co-culturing bacteria and mold are emerging as a promising strategy to enhance phosphate release.

This study employed a functional genomics approach to elucidate the activity of phytase through bacterial and mold co-culturing and studying their synergistic effect on production. We can sequentially co-culture phosphate-solubilizing bacteria and mold such as *B. licheniformis* and *Aspergillus niger*. Functional genomics tools such as RNA-seq technique can be used to identify differentially expressed genes and assess phytase activity under mono- and co-culture conditions. Phosphate release mechanism can be studied by HPLC or Colorimetric assay.

According to Yuan.et.al (2021) monocultures of *Bacillus licheniformis* yields approximately 20% of phytase enzyme. Through sequentially co-culturing two strains of bacteria and mold could increase the production along with enhanced activity on the substrate over wider range of conditions. RNA-seq analysis can reveal differential expression of genes related to phytase production, secretion, and regulation in both bacteria and mold. Co-culture may induce up regulation of key genes in both bacteria and mold, leading to increased phytase production, secretion, and broader substrate utilization, ultimately optimizing phosphate mineralization. This review paves the way for developing potent microbial consortia for sustainable and eco-friendly agricultural practices.

Keywords: Phytase, Synergism, Bacteria, Mold, Functional Genomics

References:

1. Thamy Lívia, Ribeiro Corrêa, Elza Fernandes de Araújo Fungal phytases: from genes to applications Braz J Microbiol 2020 Sep; 51. DOI: 10.1007/s42770-020-00289-y

2. Hoang Thi, Hong Anh, Esmaeil Shahsavari, Nathan J. Bott, and Andrew S. Ball Application of Co-Culture Technology to Enhance Protease Production by Two Halophilic Bacteria, Marinirhabdus sp. and Marinobacterhydrocarbonoclasticus. Molecules. 2021 Jun; 26(11): 3141. doi: 10.3390/molecules26113141

3. Y Han, DB Wilson, X Lei Expression of an Aspergillus niger Phytase Gene (phyA) in Saccharomycescerevisiae.DOI:10.1128/AEM.65.5.1915-1918.1999 https://pubmed.ncbi.nlm.nih.gov/10223979

4. Cong Chen a, Zeyu Wang b, Min Zhao a, Bohan Yuan a, Jiachao Yao b, Jun Chen b, Dzmitry Hrynshpan c, Tatsiana Savitskaya c A fungus–bacterium co-culture synergistically promoted nitrogen removal by enhancing enzyme activity and electron transfer. Science of the Total Environment. https://doi.org/10.1016/j.scitotenv.2020.142109

PI: 44

Ecological Implications of Pendimethalin Exposure on *Zygogrammabicolorata* Unraveling Effects on Beneficial Insects in Agricultural Ecosystems

Neha Singh[a], NikhilMaheshwari[b], Ayesha Qamar[*]
[a]Section of Entomology, Department of Zoology, Faculty of Life Science, Aligarh MuslimUniversity, Aligarh202002, U.P., India
[b]Department of Biochemistry Faculty of Life Sciences, Aligarh Muslim University, Aligarh 202002, U.P., India
*ayesha.zoology@gmail.com

Background

In the realm of agricultural practices, effective weed control is vital, with herbicides playing a pivotal role. Pendimethalin is a widely used herbicide crucial for managing weeds in major crops like cotton and paddy. Despite its efficacy, the broad-spectrum nature of herbicides poses risks to non-target organisms, including beneficial insects that contribute to a healthy ecosystem. Zygogrammabicolorata, an essential insect, plays a key role in controlling the weed Parthenium hysterophorus, contributing to the overall health of agricultural crops.

Literature Review

While herbicides like pendimethalin are instrumental in weed control, their impact on non-target organisms, particularly beneficial insects, remains a topic of concern. Understanding the effects on the life history and reproductive success of beneficial insects is crucial for sustainable agricultural practices. Existing literature provides insights into the potential consequences of herbicide exposure on insect populations, emphasizing the need for a comprehensive investigation into the biochemical and physiological impacts on key species like *Z. bicolorata*.

Major Findings

Our study focused on evaluating the effects of pendimethalin on the biology of *Z. bicolorata* by exposing the insects to the minimum recommended field dose of the herbicide. The results revealed a significant decrease in fecundity, adult longevity, oviposition days, and hatchability in the exposed group. At the biochemical level, there was a notable decline in antioxidant enzymes—catalase (CAT), superoxide dismutase (SOD), glutathione peroxidase (GPX), and reduced glutathione (GSH). Simultaneously, there was an increase in lipid peroxidation (LPO) levels, indicating heightened oxidative stress in the treated insects. These findings underscore the intricate dynamics of pendimethalinimpact on *Z. bicolorata*, emphasizing the importance of considering the broader ecological implications of pesticide use.

Keywords: *Zygogrammabicolorata*, Weed control, Ecological impact, Oxidative stress, Sustainable agriculture.

PI: 64

Production of starch based biodegradable films incorporated with organic/ inorganic bioactive agents and studying their applications for packaging industries

Rishpreet Kaur[a]* and Indu Chauhan[a]

[a]Department of Biotechnology Dr. B. R. Ambedkar National Institute of Technology
Jalandhar -144008, Punjab

* rishpreetk.bt.22@nitj.ac.in

Abstract

The plastic demand is increasing tremendously, especially in the food packaging industries. Packaging is a renowned method to preserve food and extend the shelf-life of food by acting as the barrier to gas and vapor exchange that allows the sustainable consumption of the food. Plastics used as food packaging material are generally used for a very short period, which leads to 9 million tons of plastic waste accumulating in the environment (Guillard et al., 2018). Most food packages create problems for the environment as they are non-biodegradable. Research has been carried out for the last many decades to use biopolymers in the field of packaging industries due to certain inherent properties such as biodegradability, low toxicity, easy availability, and low cost. One way to deal with the existing problems of conventional plastics is to replace them with biodegradable polymers such as Polylactic acid (PLA), polyhydroxyalkanoates (PHA), thermoplastic starch (TPS), Polybutylene succinate (PBS), etc. Starch is a new and promising raw material for producing biopolymers due to its easy availability and cost(Agarwal et al., 2021). However, the problem associated with biopolymers is their low mechanical and water barrier properties. These properties can be improved by polymer blending, cross-linking, and nano reinforcement. The reinforcement of the nanofillers is considered an efficient method to overcome all the limitations of the starch-based films. The organic and inorganic additives can be incorporated to the films for improving physico chemical properties for application various packaging industries. The organic additives are found to be sustainable and have lower toxicity, dosage limit, and biodegradability than the inorganic fillers. In this research work we have added the cellulose nanofibers along with ZnO nanoparticles and reported tensile strength to be 17.2 Mpa. Also the addition of ZnO nanoparticles imparted the bactericidal properties to the films.

Keywords: Starch, bioplastic, additives, and packaging.

References:

1. Agarwal, S., Singhal, S., Godiya, C. B., & Kumar, S. (2021). *International Journal of Environmental Analytical Chemistry*, *00*(00), 1–20.
2. Guillard, V., Gaucel, S., Fornaciari, C., Angellier-Coussy, H., Buche, P., &Gontard, N. (2018). *Frontiers in Nutrition*, *5*(December), 1–13.]

Exploring the influence of renewable sugar industry waste on ratoon sugarcane for improved jaggery quality

Prasoon Kumar*, Pallavi Singh Arya[a], Manmohan Singh[a] , Priyanka Singh[a]
[a]U.P. Council of Sugarcane Research, Shahjahanpur, U.P., India

* pmishra8173@gmail.com

Abstract

Jaggery, a staple in rural areas, holds profound significance for impoverished communities, playing a crucial role in India's rural economy. Derived from sugarcane juice alongside sugar production, it serves as a key commodity. The sugar industry produces various by-products, including bagasse, molasses, press mud, bagacillo, fly ash, and wastewater, rich in nutrients that enhance organic carbon and nutrient levels for plants. The external attributes of jaggery, encompassing color, texture, and storability, significantly influence consumer preference and marketing. These qualities hinge on matured sugarcane having high sucrose content, low colloids, and cultivation in suitable soil conditions. The use of organic fertilizer enriches the soil, elevating the nutritional and medicinal qualities of jaggery. To investigate the impact of sugar industry by-products, infused with organic content and micronutrients, alongside chemical inorganic fertilizers on jaggery production, a study was conducted in Village-Parajarsa, Nigohi, Shahjahanpur. The experiment comprised ten treatments, including inorganic fertilizers (T1 & T2), integrated treatments (T3 & T4), and diverse organic options like sugar industry by-products and bio-fertilizers (T5-T10). The ratoon cane was harvested and jaggery samples were prepared from the canes of all the treatments and quality parameters were analysed. Notably, treatment T5 exhibited the highest jaggery content in cane 12.4%, jaggery yield 11.7%, and jaggery% juice 21.3%, coupled with the lowest levels of invert sugar (3.3 mg/ml), colour (105), and moisture% (4.9%). Conversely, treatment T1 recorded the lowest jaggery content in cane 10.8%, jaggery yield 9.2%, and jaggery% juice 19.5%. Mineral content analysis (Zn, Fe, Mn, and Cu) in the jaggery prepared from all treatments revealed higher mineral content when sugar industry by-products were applied compared to inorganic chemical fertilizers. These findings suggest that the application of sugar industry by-products and bio-fertilizers enriches the soil with organic matter and micronutrients. Such enriched soils contribute to the cultivation of high-quality sugarcane, resulting in superior jaggery with desirable attributes such as colour, texture, and increased micronutrient content.

Keywords: Sugarcane, jaggery, sugar industry, by-products, bio-fertilizers.

PI:113

Bioengineering of microalgae for production of bioisoprene; a step towards sustainable future

Ariba Hasan[a] , Gaurav kant[a] , Sameer Srivastava[a]*

[a]Department of Biotechnology, Motilal Nehru National Institute of Technology Allahabad,
Prayagraj, Uttar Pradesh, India.
* sameers@mnnit.ac.in

Background

Isoprene also known as 2-methyl-1,3-butadiene ($CH_2=C(CH_3)-CH=CH_2$) is a volatile unsaturated pentahydrocarboncompound.It has low solubility in water and has a low boiling point of 34 °C. In plants, it act as a precursor molecule for the formation of isoprenoids, which comprises a large variety of natural products such as flavors, fragrances, pigments, antioxidants, steroids, and drugs, fat-soluble vitamins, carotenoids and related pigments. It has a wide range of industrial applications ranging from the production of products such as adhesive, tires and synthetic rubbers to use as fuel additive for gasoline, diesel, or jet fuel, act as a prominent feedstock in plastic production and an important polymer building block for the chemical industry.

Review

Plants are the major source of isoprene but its collection from the plant bodies is not feasible because of its high volatile nature, that’s why alternate route i.e, petrochemical method is adopted where isoprene monomer is produced as a byproduct during petroleum cracking. Moreover, the process is not viable and environmentally friendly as petroleum is non renewable resource and its cracking releases large amount of green house gases which causes thining of ozone layer. So,there is a need to develop a method which is sustainbale, eco-friendly and at the same time produces large amount of isoprene without affecting the environment. In this regard biobased (microbial) production process is developed as it has lots of advantages like rapid growth and cultivation at high cell densities, microbes can be grown in enclosed bioreactors that facilitate isoprene recovery from the gas phase, generated wastes in the form of biomass can be utilized for other purposes. It was found through review of literature that from over last ten years lots of microbes(E.coli, Bacillus, cyanobacteria,yeast) were genetically engineered for isoprene synthesis using different approaches like overexpression of rate limiting enzyme of isoprene biosynthesis pathway, inhibition of byproduct formation to divert the flux toward desired precursor, heterologous expression of mevalonate pathway in E.coli, heterologous expression of fused Isoprene synthase(IspS) and isopentenyl diphosphate(IDI). Nowadays microalgae is widely explored for the production of various metabolites as it has advantages of cultivation over other microbes, it can grow on wastewater, it does not require expensive carbon source as they are photoautotrophic organism synthesizes CO2 through photosynthesis.

Major findings

The microalgae as a cell factory is not explored much for the isoprene production So we are planning to metabolically engineered the microalgae using multidimensional approach where heterologous expression of kudzu isoprene synthase and downstream inhibition of Methylerythritol phosphate(MEP) pathway will be used for the first time in microalgae. So in this context some initial work had done where kudzu isoprene synthase gene is successfully cloned in vector .

Keywords: Isoprene, Kudzu isoprene synthase , microalgae, metabolic engineering .

References

1. Kim, J. H., Wang, C., Jang, H. J., Cha, M. S., Park, J. E., Jo, S. Y., ... & Kim, S. W. (2016). Isoprene production by Escherichia coli through the exogenous mevalonate pathway with reduced formation of fermentation byproducts. *Microbial cell factories*, *15*, 1-10.

PI:115

Soil stabilization with an environment friendly biopolymer: A Review

Abhishek Raniwal[a*], Kumar Venkatesh[a]
[a]Department of Civil Engineering, Motilal Nehru National Institute of Technology Allahabad, Prayagraj-211004, U.P., India

*abhishek.2022ge20@mnnit.ac.in

Background

Traditional methods for stabilizing soil involve incorporating substances like cement and lime, but these approaches often lead to considerable environmental contamination. In contrast, biopolymers have emerged as a sustainable, cost-effective, and eco-friendly alternative. This research explores how the type and quantity of biopolymers influence soil's geotechnical properties during stabilization.

Review

A comprehensive review of existing literature is conducted to examine the performance of various biopolymers across different soil types. The study also looks into the biochemical behavior of biopolymers, including their properties, processes, and applications, as well as interactions with soil particles at both the molecular and macroscopic levels. Through this analysis, the most effective bio-stabilization components are identified and analyzed. The research concludes by offering recommendations for selecting appropriate bio-additive types and quantities for soil stabilization based on the specific soil type.

Majorfindings

The findings highlight that the performance of biopolymers is contingent upon their type and percentage, soil characteristics, and the electrostatic forces generated during cementation and hydrogel formation. Notably, Guar gum, Beta-glucan, Gellan gum, Agar gum, and Xanthan gum emerge as effective biopolymers, enhancing mechanical and shear strength while mitigating compressibility, shrinkage, and permeability.

Keywords: Soil stabilization; Biopolymer; Eco-friendlyadditive; Engineering properties.

References

1. Chang, I., Im, J., and Cho, G.-C. 2016. Introduction of microbial biopolymers in soil treatment for future environmentally-friendly and sustainable geotechnical engineering. Sustainability 8(3): 251. doi:10.3390/su8030251.
2. Hadi Fatehi , Dominic E. L. Ong, Jimmy Yu and Ilhan Chang Biopolymers as Green Binders for Soil Improvement in Geotechnical Applications: A Review, Geosciences 2021, doi.org/10.3390/geosciences11070291

Microbial Biotransformation of Vinblastine to Vincristine using an Endophytic Fungus Isolated from *Catharanthusroseus*

Gauri Srivastava[a], Deepak Ganjewala[a]*

[a]Amity Institute of Biotechnology, Amity University Uttar Pradesh, Sector-125, Noida-201303 (UP), India.

* dganjewala@amity.edu, deepakganjawala73@yahoo.com

Background

Over the years, two Vinca alkaloids vinblastine and vincristine, which areisolated from *Catharanthus roseus* have gained recognition in chemotherapy owing to their antitumor properties. Vincristine also known as leurocristine is particularly effective in treating leukemia, lymphoma, myeloma, breast, head, and neck cancer. However, in *C. roseus*its production rate is very low. Enhancing the yields of vincristine could greatly improve cancer healthcare treatments, making them more accessible and affordable.

Review

There are limited studies on the production of vincristine from vinblastine. Hamada and Nakazawa (1991) successfully produced vincristine from vinblastine using cell suspension cultures of *C. roseus*. Kumar and Ahmad (2013) carried out biotransformation of vinblastine into vincristine using an endophytic fungus *Fusarium oxysporum*isolated from *C. roseus*. Birat et al. (2022) recently reported that the fungus *Nigrosporazimmermanii*, found within the leaves of *C. roseus* was also capable of producing vincristine.

Major findings

We developed a biotransformation system using an endophytic fungus isolated from *C. roseus* leaves to produce vincristine from vinblastine. The process was carried out in a 500 ml conical flask with 100 ml PDB, which was inoculated with the fungal culture and substrate at 25-30°C for 10 days. Analysis using LC/MS revealed that ~42% of vinblastine was converted into vincristine after 8 days of incubation. Further, the optimization of the system was carried out for pH, rotation speed, vinblastine (substrate) and culture with an incubation period of 8 days at 30°C. Hence, the study demonstrated the potential of a fungal endophyte as a valuable tool for the production of vincristine from vinblastine. To our knowledge, this is the first report on this particular biotransformation.

Keywords: Anticancer, Vinblastine, Vincristine, Endophytes, Biotransformation

References

1. Kumar, A., and Ahmad, A. (2013). Biotransformation of vinblastine to vincristine by the endophytic fungus *Fusariumoxysporum* isolated from *Catharanthusroseus*. Biocatalysis and Biotransformation 31(2), 89-93.
2. Hamada, H., and Nakazawa, K., (1991). Biotransformation of vinblastine to vincristine by cell suspension cultures of *Catharanthusroseus*. Biotechnology Letters 13, 805-806.
3. Shankar, Naik. B. (2019). Potential roles for endophytic fungi in biotechnological processes: a review. Plant and Human Health, Volume 2: Phytochemistry and Molecular Aspects 327-344.
4. Birat, K.; Binsuwaidan, R.; Siddiqi, T.O.; Mir, S.R.; Alshammari, N.; Adnan, M.; Nazir, R.; Ejaz, B.; Malik, M.Q.; Dewangan, R.P.; et al (2022). Report on vincristine producing endophytic fungus Nigrosporazimmermanii from leaves of *Catharanthusroseus*. Metabolites 12, 1119.

Cloning and Expression of D-Lactate Dehydrogenase (D-*ldh*) Homologs of *Lactobacillus delbrueckiisub* sp. *bulgaricus* in *Lactococcus lactis* for D-Lactic Acid Production

Nirmal Sarkar[a*], Payal Mukherjee[a], Aiyagari Ramesh[a], Senthilkumar Sivaprakasam[a]
[a]Department of Biosciences and Bioengineering, Indian Institute of Technology Guwahati

*s.nirmal@iitg.ac.in

Background

D-lactic acid is a key industrial compound, primarily as a precursor in the synthesis of heat-resistant, biodegradable poly-D-lactic acid bioplastics [1]. This study focuses on enhancing D-lactic acid productionthrough metabolic engineering in lactic acid bacteria. Two D-lactate dehydrogenase (D-*ldh*) homologs, *ldb1010* and *ldb1147*, were cloned from *Lactobacillus delbrueckii*sub sp. *bulgaricus*, and expressed into *Lactococcus lactis* using pNZ8148 as a vector and nisin as the promoter. Experimental studies were conducted in both shake andstatic flask conditions using wild-type and recombinant *L. lactis* strains. These experiments were performed on M17 media, supplemented with 0.5% glucose, to assess the dynamics of cell growth, substrate consumption, and D-lactic acid production.

Review

A few studies have shown that *Lactococcus lactis* can be metabolically engineered with D-*ldh*encoding genes toproduceD-lacticacid. *L. lactis* engineered by heterologous over-expression of D-*ldh*and used to produce D-lactic acid, resulted in 0.67 g/g and 0.44 g/g of DLA yield from lactose and galactose, respectively [2]. D-*ldh* genes from *L. delbrueckii*sub sp. *Bulgaricus* were cloned and overexpressed in *E.coli* that achieved a D-lactic acid titer of 1.94g/L using glucoseas carbon source [3].

Majorfindings

The results indicate a pronounced enhancement in cell growth and D-lactic acid yield under shaking conditions. The specific growth rates for the recombinant *L. lactis* strains with *ldb1010* and *ldb1147* homologs were notably higher in shaking conditions, standing at 0.8349 and 0.5948, respectively. Additionally, these strains exhibited are duced doubling time in shaking conditions, with *ldb1010* showing a rapid doubling time of approximately 49.8 minutes. The recombinant strains also demonstrated improved D-lactic acid titer of 6.13 mg/L and 7.64 mg/L, respectively, within 36 hours, an enhancement of 1.8 and 2.3 times the L-Lactic Acid yield by the same strains. Furthermore, the highest biomass yields for the recombinant *L. lactis* strains with *ldb1010* and *ldb1147* homologsin shaking conditions were 2.43 g/g and 1.13 g/g of substrate, respectively, which outperformed the static conditions. A significant increase in protein concentration was also observed in there combinant strains, with170µg/ml for ldb1010 and 275 µg/ml for *ldb1147*, representing 3.6 and 5.9-fold increases over the wild-type strain. This increased protein expression was corroborated through SDS-PAGE analysis. This study opens pathways for further exploration, including the expression of other D-*ldh* homologs in *L. lactis*, kinetic analysis of substrate utilization, media optimization for maximized cell growth, and bioreactor experiments with optimized media toscaleup D-lacticacid production usingrecombinant *L. lactis* strains.

Keywords: D-lactic acid, *Lactococcuslactis*, *Lactobacillus delbrueckii*sub sp. *bulgaricus*, D-lactate dehydrogenase

References

1. Bozell,J.J.,&Petersen,G.R.(2010).Technologydevelopmentfortheproductionofbiobasedproductsfrombiorefinery carbohydrates—the US Department of Energy's "Top 10" revisited. *Green Chemistry*, *12*(4), 539.https://doi.org/10.1039/b922014c

PI: 137

Combined ultrasound enhanced enzymatic pretreatment and saccharification of corn stalk for generation of monomeric sugar for 2G biofuel generation

Subhodeep Banerjee[a,b], SubharaDey[b], Anusha[d], Tapas Kumar Bandhyopadhyay[c], Rintu Banerjee[a,b,d*]

[a] Advanced Technology Development Centre, Indian Institute of Technology Kharagpur
[b]P.K Sinha Center for Bioenergy and Renewables, Indian Institute of Technology Kharagpur
[c] Department of Metallurgical and Materials Engineering, Indian Institute of Technology Kharagpur
[d] Department of Agricultural and Food Engineering, Indian Institute of Technology Kharagpur

*rb@agfe.iitkgp.ac.in; banerjeesubhodeep9@gmail.com

Background

The global interest in biobased processes is increasing, and significant efforts are being made to create efficient technologies for the utilisation of bioresources.. Maize cultivation allows farmers to conserve 90% of water and 70% of power in comparison to Paddy cultivation. This contributes to an annual production of about 21 MT, makes corn stalk an ideal lignocellulosic waste as 2G biofuel feedstock.

Review

Corn stalks primarily consist of leaves and stems, with the stems being formed of cortex and pith. The untreated Corn Stalk had hemicellulose, cellulose, and lignin levels of 33.6%, 38.7%, and 18.9% correspondingly, that needs to be converted into monomeric sugars for biofuel generation. Ultrasound exposure in a liquid medium produces highly reactive free radicals, which stimulate localised turbulence and microcirculation in the liquid, hence increasing the rates of mass transfer. The integration of laccase and ultrasound techniques results in decreased utilisation of chemicals, energy, and water. These methods show great potential in minimising the environmental footprint and operational expenses associated with traditional industrial processes. If lignocellulosic biomass is effectively saccharified, it has the potential to serve as an excellent raw material for the generation of biofuels.

Major findings

The reduction of lignin polymers in biomass had been reduced to 80.43% which enables greater sachharification efficiency with reducing sugar yield after hydrolysis to 83% of holocellulose being converted to reducing sugars. CCD-RSM based optimization of combined enzymatic pretreatment and saccharification of biomass resulted in efficient removal of lignin, and production of monomeric sugars for fermentation to 2G biofuels like ethanol, butanol and biohydrogen.

Keywords: corn stalk, enzyme, biofuel, ultraosund

References

1. Rajak, R. C., & Banerjee, R. (2016). Enzyme mediated biomass pretreatment and hydrolysis: a biotechnological venture towards bioethanol production. Rsc Advances, 6(66), 61301-61311.
2. Gonçalves, I., Silva, C., & Cavaco-Paulo, A. (2015). Ultrasound enhanced laccase applications. Green Chemistry, 17(3), 1362-1374.
3. Adekunle, A. E., Rabeya, T., Jehadin, F., Asad, M. A., Ayodele, O. O., & Islam, M. S. (2021). Compositional and microstructural changes in compressed hot water pretreated corn stalk. Current Research in Green and Sustainable Chemistry, 4, 100057.
4. Sherpa, K. C., Kundu, D., Banerjee, S., Ghangrekar, M. M., & Banerjee, R. (2022). An integrated biorefinery approach for bioethanol production from sugarcane tops. Journal of Cleaner Production, 352, 131451.

Enzyme-Mediated Pretreatment and Saccharification studies on Cotton Stalk

Subhara Dey[a], Subhodeep Banerjee[a,], Anusha[b], Rintu Banerjee[b,*]
[a]P. K. Sinha Centre for Bioenergy and Renewables, Indian Institute of Technology Kharagpur
[b]Department of Agricultural and Food Engineering, Indian Institute of Technology Kharagpur

*rintuin@gmail.com

Background

The transformation of lignocellulose into sugar is an integral aspect of lignocellulose biorefining, playing a vital role in the efficient utilization of lignocellulosic materials for biofuel production.

Review

The scientific community is increasingly exploring the potential of lignocellulosic biomass, a cost-effective and abundant source consisting of cellulose, hemicellulose, and lignin, for sustainable biofuel production and chemical generation. These feedstocks, sourced from various crops and residues, hold significant promise for second-generation biofuels without compromising food production. Globally, cotton, a major crop, covers 32.6 million hectares, with India alone dedicating 12.4 million hectares to its cultivation. The cultivation of cotton yields byproducts such as seeds, husks, and stalks, which are utilized for various applications. However, cotton stalks, generated in large quantities during harvesting, are typically burned by farmers, leading to the release of pollutants and greenhouse gases. The high holocellulose content in cotton stalks i.e. cellulose content in the range of 40.10 ± 1.55%, hemicelluloses at 13.60 ± 0.64%, makes them a favorable candidate for bio-ethanol production but the presence of a stringent recalcitrant layer of lignin which is approximately 29.40 ± 0.95% is the primary reason for the further valorization of cotton stalk (Binod et al., 2012). This study specifically focuses on the treatment of cotton stalks through the enzymatic method to obtain a high yield of fermentable sugars for subsequent bioethanol production.

Major findings

The present study investigates the efficiency of enzyme-mediated simultaneous pretreatment and saccharification of cotton stalks. Enzymatic treatment of cotton stalk efficiently degraded lignin and holocellulose with maximum reducing sugar yield (mg/g) i.e. 224.68(mg/g) at solid loading 15% (w/v), pH of the broth at 5, at 50 °C for 16 h. Further structural characterization of cotton stalks was done through SEM and FTIR.

Keywords: Lignocellulose, Bioethanol, Cotton Stalks, Cellulase, Laccase

References

1. Binod, P., Satyanagalakshmi, K., Sindhu, R., Janu, K. U., Sukumaran, R. K., & Pandey, A. (2012). Short duration microwave assisted pretreatment enhances the enzymatic saccharification and fermentable sugar yield from sugarcane bagasse. Renewable Energy, *37*(1), 109-116.

2. Chang, V. S., & Holtzapple, M. T. (2000). Fundamental factors affecting biomass enzymatic reactivity. In *Twenty-First Symposium on Biotechnology for Fuels and Chemicals: Proceedings of the Twenty-First Symposium on Biotechnology for Fuels and Chemicals Held May 2–6, 1999, in Fort Collins, Colorado* (pp. 5-37). Humana Press.

PI: 145

Enzyme mediated approach on synthesis of fluorescent graphene quantum dots

Swagata Dutta[a], Rintu Banerjee[a*]
[a]Agricultural and Food Engineering Department, Indian Institute of Technology, Kharagpur-721302, West Bengal, India
*rb@.iitkgp.ac.in

Background

Graphene quantum dots (GQDs) have emerged as promising nanomaterials due to their unique electronic, optical, and chemical properties. Traditional synthesis methods often involve hazardous chemicals and energy-intensive processes, raising concerns about environmental impact and biocompatibility. This study aims to develop a novel green approach for the synthesis of biocompatible fluorescent GQDs, addressing the limitations of conventional methods.

Experimental Study

A sustainable and eco-friendly synthesis strategy was adopted to obtain GQDs with enhanced biocompatibility. Graphite was converted into graphene quantum dots through the use of enzymes, ensuring minimal environmental footprint. To optimize enzyme activity and graphene quantum dot formation, different temperatures and pH levels were tested. Characterization techniques such as transmission electron microscopy (TEM), atomic force microscopy (AFM), Fourier-transform infrared spectroscopy (FTIR), UV vis and fluorescence spectroscopy were employed to assess the structural, morphological, and optical properties of the synthesized GQDs.

Major Findings

- UV-vis absorption spectra showed peaks at around 220 nm and 280 nm and a strong and sharp PL emission peak (λem) at 440 nm was observed at an excitation wavelength (λex) of 350 nm
- The biocompatible fluorescent GQDs synthesized through this approach exhibited remarkable characteristics.
- The fluorescence spectroscopy results demonstrated strong and tunable fluorescence properties, making them suitable for various bioimaging applications.

Keywords: Graphene quantum dots, Green synthesis, Enzyme mediated synthesis, Nanotechnology

References

1. Singh, J., Kaur, S., Lee, J., Mehta, A., Kumar, S., Kim, K. H., & Rawat, M. (2020). Highly fluorescent carbon dots derived from Mangifera indica leaves for selective detection of metal ions. *Science of The Total Environment*, 720, 137604.
2. Saleem, H., Saud, A., & Zaidi, S. J. (2023). Sustainable Preparation of Graphene Quantum Dots from Leaves of Date Palm Tree. *ACS omega, 8*(31), 28098-28108.

PI: 149

Effect of pretreatment on enhanced reducing sugar production from lignocellulosics formethanol synthesis

Devalina Khamaru[a], Rintu Banerjee[a]*
[a]Microbial Biotechnology and Downstream Processing Laboratory, Agricultural and Food Engineering Department, Indian Institute of Technology Kharagpur, Kharagpur-721302, India

*rb@agfe.iitkgp.ac.in,rintuin@gmail.com.

Background

Methanol is being developed as a desirable liquid fuel and raw material for the production of numerousimportant organic chemicals that are now made from feedstocks such as coal, natural gas, and petroleum. So, there is a need to produce methanol from renewable resources. Renewably produced methanol entirelyeliminatesemissionsofsulfur-oxide and particulate matter, reduces emissions of nitrogen oxide by upto 80%, and reduce emissions of carbon-dioxideby upto 95% when compared to traditional fuels.

Review

There are some existing methods to produce bio-methanol from biomass. A complicated process calledgasification transforms carbonaceous biomass into syngas (H_2 and CO), which is then processed to producemethanol. Approximately 31% carbon loss to tars and chars is a major impediment of gasification. Anotherapproach is indirect synthesis of methanol from CO_2 via syngas production. However, CO_2-to-methanol oftenhas drawbacks, such as CO_2-syngas being less reactive than CO-syngas alongwith more water production. Major drawback of electrolysis for directly converting CO_2 into methanol is requirement of huge amount ofhydrogen and energy. So, we aim to synthesize methanol from lignocellulosic agrowaste from methane andcarbon-dioxide, obtained by anaerobic digestion.

Major findings

Despiteanincreaseinrecentpublicationsonthesubject, there are still gaps and short comings that hinder bio-gas production in industrial scale from being widely accepted. Thorough literature review has revealed

1. There is noefficientmanagementsystemofCO_2whichis releasedfrombio-gas productionoperation.
2. For maximum conversion of biogas to syngas to synthesis methanol, need of effective and suitable catalystandreformreactor isverycrucial.

Forusing 100% CO_2, produced from anaerobic digestion we need to increase CH_4 yield and decrease CO_2. By pretreating lignocellulosic substrate enzymatically we are trying to increase the CH_4 yield. The experiments are being carried out to increase the reducing sugar yield and ultimately to increase methanol production.

Keywords: Methanol, Methane, Yield, CO_2

References

1. Mohanty,Pratikhya,etal."Acriticalreviewonprospectsandchallengesinproductionofbiomethanolfromlignocellulosebiomass."*BiomassConversion and Biorefinery*(2021):1-15.
2. Sawatdeenarunat,Chayanon,etal."Anaerobicdigestionoflignocellulosicbiomass:challengesandopportunities."*Bioresourcetechnology*178 (2015):178-186.
3. Chiou,Hsuan-Han,etal."EvaluationofalternativeprocessesofmethanolproductionfromCO2:Design,optimization,control,techno-economic,and environmentalanalysis."*Fuel*343 (2023):127856.
4. Bozzano,Giulia,andFlavioManenti."Efficientmethanolsynthesis:Perspectives,technologiesandoptimizationstrategies."*Progressin Energyand CombustionScience*56 (2016):71-105.

PI: 150

Production of Bacterial cellulose from *Lesfonia. soli*

Baneeprajnya Nayak[a], Rintu Banerjee[a]*
[a]Microbial Biotechnology and Downstream Processing Laboratory,
Agricultural and Food Engineering Department, Indian Institute of Technology Kharagpur,
Kharagpur-721302, India

rb@iitkgp.ac.in,rintuin@gmail.com

Background

Bacterial cellulose (BC) is recognized as a versatile biomaterial with diverse applications. Microorganisms, predominantly bacteria, play a crucial role in the synthesis of BC, which occurs through static or agitated fermentation processes in the presence of suitable media. The microbial production of BC is esteemed as a source of pure cellulose, characterized by high purity and distinct physicochemical characteristics. This makes it suitable for widespread applications in various sectors, including food industries, biomedical sectors, and the formation of bio based polymers and nanocomposites.

Review

The cellulose production in general involves the use of standard Hestrin-Schramm media (HS) media. This media comprises glucose as the carbon source, yeast extract as the nitrogen and mineral source, peptone as another nitrogen source. However, the elevated production cost, primarily attributed to components like yeast extract and peptone, not only renders the process economically unsustainable but also inefficient in meeting the growing global demand for bacterial cellulose in the near future. Thus, an attempt has been made to enhance the bacterial cellulose production by using alternative carbon and nitrogen sources. Further, the carbon and nitrogen sources are being optimized for enhancing the economical feasibility of bacterial cellulose. Unlike traditional media, this study observed an increase in productivity when substituting more expensive ingredients with more cost-effective sources. Furthermore, scale-up studies are currently underway to facilitate the cost-effective industrialization of the process.

Major findings

- The yield of the bacterial cellulose is around 4.5 g/L under static fermentation.
- The optimized media produces higher yields compared to the conventional Hestrin-Schramm media.

Keywords: Bacterialcellulose, cheapsource, L.soli

References

1. Jalili Tabaii, M., &Emtiazi, G. (2015). Comparison of Bacterial Cellulose Production among Different Strains and Fermented Media. *AppliedFoodBiotechnology*,*3*(1),35–41.https://doi.org/10.22037/afb.v3i1.10582
2. Chiaoprakobkij,N.,Seetabhawang,S.,Sanchavanakit,N.,&Phisalaphong,M.(2019).Fabricationandcharacterizationofnovelbacterialcellulose/alginate/gelatinbiocompositefilm.*JournalofBiomaterialsScience, PolymerEdition*,*30*(11),961-982.
3. Kumar,V.,Saran,S.,Pandey,A.,&Soccol,C.R.(Eds.).(2023).*BacterialCellulose:Production,Scale-up,andApplications*.CRCPress.
4. BlancoParte,F.G.,Santoso,S.P.,Chou,C.C.,Verma,V.,Wang,H.T.,Ismadji,S.,&Cheng,K.C.(2020).Currentprogressontheproduction,modification,and applicationsofbacterialcellulose. *Criticalreviewsinbiotechnology*,*40*(3),397-414.

PI: 161

Behavioural Selection in a Canine Olfactory Detection Program using Machine Learning

Riya Deshpande[a,*], Amit Agarwal[a]

[a]Department of Electronics and Communication, VNIT, Nagpur, Maharashtra, 440010.

*riyadeshpande24@gmail.com

Background

Canines possess a sense of smell approximately forty times more sensitive than humans, coupled with a highly developed olfactory system featuring up to 300 million receptors. Their exceptional olfactory abilities enable them to undertake diverse tasks, from detecting illegal substances to aiding the military as trackers. Sniffer dogs excel in identifying explosive residues, while search and rescue dogs play pivotal roles in disaster scenarios. Training programs for working dogs are essential, requiring 6-12 months of rigorous training to ensure precision in critical tasks. However, these programs are expensive and face low acceptance rates, necessitating more efficient approaches. This paper explores the application of machine learning (ML) in improving the selection and training process for working dogs, utilizing a dataset from the Transportation Security Administration's canine breeding and training program. Thirteen supervised ML algorithms are employed to predict a canine's acceptance or elimination from the program based on behavioral traits. To address class imbalance, the Synthetic Minority Oversampling Technique (SMOTE) is employed, generating synthetic data points to enhance model performance.

Review

This work is done as an addendum to the recent research done in the domain of analysis for canine olfactory detection program by Eyre et. al. [1]. The authors have implemented three supervised machine learning algorithms at default settings on the same dataset and shown the most relevant traits for classification at each time-point. The best performance was observed for the Random Forest model giving an accuracy of 87% and AUC of 0.68. Poor performance in differentiating the dogs that were eliminated because they belonged to the minority class has been reported by the authors. Additionally, they have suggested that the accuracy might be improved.

Major findings

After applying Hyperopt on all the models, the gradient boosting machine (GBM) outperforms the majority of the datasets used. The best performance of GBM is found on the 12th month dataset showing an improved accuracy of 96% and AUC of 0.81 as compared to previously used method in [1]. Furthermore, SMOTE is used to overcome the class imbalance problem; however, we observe a trade off with the accuracy. We have also explained the model's behaviour locally and globally using an explainability technique namely SHapely Additive exPlanations (SHAP).

Keywords:

Behaviour classification, canine behaviour, olfactory detection, machine learning, SMOTE.

References

1. Eyre, A.W. et. al. "Machine learning prediction and classification of behavioral selection in a canine olfactory detection program," Sci Rep 13, 12489 (2023). https://doi.org/10.1038/s41598023-39112-7.

PI:175

Electrochemical characterization of an H-type microbial fuel cell (MFC) operated using pure culture of exo-electrogenic microbial strains as biocatalysts

Sangita Karmaker[a] and Radha Rani[a]*

[a]Department of Biotechnology, Motilal Nehru National Institute of Technology, Prayagraj, India,

* radharani@mnnit.ac.in; raadharaani1982@gmail.com

Background

Bio-electrochemical systems (BES) like Microbial fuel cells (MFC) are developed to extract energy from bacterial cells using wastes/other substrates as a carbon source (*Rashid et al.,* 2023). Specialized microorganisms known as exoelectrogens can release electrons externally to an acceptor material (Anode) which can be integrated into a fuel cell system to harness electrical energy stored in these systems. Anodic oxidation of fuel and cathodic reduction of atmospheric oxygen results in the generation of potential difference which gives rise to current that flow through the system.

Review

In this study, pure microbial inoculums of *Pseudomonas gessardii*and *Pseudomonas aeruginosa* were used to operate an H-type MFC in batch mode continuously for 30 days and were used to study the electrochemical behavior and reaction kinetics along with bioelectricity generation (*Mukherjee et al.,* 2021). The performance of MFCs was analyzed by measuring operating voltage (OV), open circuit voltage (OCV) and Polarization using varied external resistance. Electrochemical analyses were also done using Metrohm AUTOLAB potentiostat for cyclic voltammetry (CV), and linear sweep voltammetry (LSV) studies in two and three-electrode setup modes.

Major findings

The MFC performance for the two pure stains had a maximum OCV of 504 mV for *P. gessardii*, followed by 227 mV for *Pseudomonas aeruginosa* respectively. The Polarization study of the two MFC setups revealed a maximum power and current density of 1.05 W/m^2 and 180 mA/m^2 with a volumetric power density of 4200 W/m^3 for *P. gessardii*while *P. aeruginosa* had a maximum power density of 0.168W/m^2.and current density of 20 mA/m^2 Cyclic voltammograms and Linear Sweep voltammetry with two and three-electrode setups for *P. gessardii* and *P. aeruginosa* showed a highest anodic peak current (i_{pa}) of 0.5 mA with cathodic peak current at (i_{pc}) 0.44 mA. The exo-electrogenic strains are important in the functioning MFCs, indicating the efficacy of these microbial strains in electricity generation. This study further highlights its future prospective in developing other technologies through optimizing such techniques for improved functioning using different microbial species.

Keywords: microbial fuel cells, bioelectricity, exoelectrogens, bioelectrochemical systems.

References

1. Rashid, A. A. F. A., Nasir, M. N. M., Bohari, Z. H., Yahaya, M. S., Sulaima, M. F., &Nanyan, A. N. (2023). Electricity Generation through Microbial Fuel Cells Utilizing Leftover Rice as Food Waste. *Journal of Advanced Research in Applied Sciences and Engineering Technology*, *31*(3), 299-316.
2. Mukherjee, A., Zaveri, P., Patel, R., Shah, M. T., & Munshi, N. S. (2021). Optimization of microbial fuel cell process using a novel consortium for aromatic hydrocarbon bioremediation and bioelectricity generation. *Journal of Environmental Management*, *298*, 113546.

Impact of copper stress on the growth traits and levels of lipid peroxidation in Saccharomyces cerevisiae during anaerobic fermentation

Shruti Das and Sangeeta Negi,*
Department of Biotechnology, Motilal Nehru National Institute of Technology Allahabad, Prayagraj, India-211004

* sn5@mnnit.ac.in:

Background

Copper is a necessary micro component that is needed for several enzymes and other biological functions, such as iron absorption.It is generally accepted that copper functions, at least in part, in cells by inducing oxidative stress.Copper-induced oxidative stress in Saccharomyces cerevisiae targets enzymes of the glycolytic pathway. According to studies, high copper concentrations hinder the growth of Saccharomyces cerevisiae, delaying fermentation and lowering alcohol yield.

Methodology

Effect of copper toxicity on *Saccharomyces cerevisiae* strain NCIM 3288 was to be evaluated under anerobic fermentation condition. Cells were treated with copper concentration from 0Mm to 2Mm and checked for substrate utilization and ethanol production post 75hrs of treatment. After 75hrs cells were harvested and analyzed for ROS and change in growth pattern. In order to determine the rise in lipid peroxidation brought on by ROS, measurements of MDA levels, a marker for lipid peroxidation, were made.

Major findings

Post 75hrs of reaction when cells were harvested it was observed that maximum amount of glucose consumption occurred at 1.3Mm of copper concentration post which the consumption of sugar decreased. Ethanol production peaked at 1.2 mM copper concentration, after which there was a trend toward decline, suggesting that the generation of alcohol was inhibited. A tendency of rising dry mass is evident up to 1.2 mM, after which there is a noticeable stagnation. The MDA assay on the lysed cells revealed that MDA levels increased as the media's copper concentration increased. At 2 mM copper concentration, a maximum of 0.464 nmol/ml of MDA was generated.

Keywords: Copper toxicity, oxidative damage, Antioxidant, *Saccharomyces cerevisiae*

References

1. Shanmuganathan, Anupama, et al. "Copper-induced oxidative stress in Saccharomyces cerevisiae targets enzymes of the glycolytic pathway." FEBS letters 556.1-3 (2004): 253-259.
2. Sun, Xiangyu, et al. "Effect of copper stress on growth characteristics and fermentation properties of Saccharomyces cerevisiae and the pathway of copper adsorption during wine fermentation." Food chemistry 192 (2016): 43-52.
3. Howlett, Niall G., and Simon V. Avery. "Induction of lipid peroxidation during heavy metal stress in Saccharomyces cerevisiae and influence of plasma membrane fatty acid unsaturation." Applied and environmental microbiology 63.8 (1997): 2971-2976.

PI: 200

Optimization of intracellular Melatonin Synthesis in *Saccharomyces cerevisiae* under fermentation conditions

Shruti Das and Sangeeta Negi,*
Department of Biotechnology, Motilal Nehru National Institute of Technology Allahabad,
Prayagraj, India-211004

*sn5@mnnit.ac.in

Background

Melatonin (N-acetyl-5-methoxytryptamine) is a pineal gland hormone produced in response to darkness. Melatonin is produced from tryptophan precursor through the following steps hydroxylation, decarboxylation, acetylation, and methylation to produce 5-Hydroxytryptophan, serotonin, N-acetylserotonin, and Melatonin respectively. It is a potent antioxidant taken as a dietary supplement that has been shown to be clinically useful in improving sleep. Melatonin which is a bioactive molecule acts as an antioxidant against various stressors and environmental stress in yeast cells. Melatonin thus plays a protective role in yeast cells by shielding them against increased oxidative stress due to fermentation

Methodology

Saccharomyces Cerevisiae strain NCIM 3288 was cultured and used for fermentation conditions. Primary inoculum was prepared using yeast extract potato dextrose media and the fermentation media was prepared according to 3. The experiment was carried out to maximize the yield of melatonin by optimizing fermentation conditions like time, and ethanol stress under anaerobic conditions. Cells were then lysed using lysis buffer and melatonin Extraction was done using a mixture of Methanol: H2O: HCl in the ratio of 7:2.9:0.01. The UV-spectrometric method was done to quantify melatonin yield.

Major finding

Maximum melatonin production for the saccharomyces cerevisiae strain NCIM 3288 was ~33.12 ug/ml under anaerobic fermentation. Intracellular melatonin was observed to be produced at a substantial amount after 72hrs of reaction setup. According to the experimental results, 30% alcohol stress was required for the yeast strain being studied to produce the highest amount of melatonin.

Keywords: Melatonin, Fermentation, Tryptophan, Antioxidant, Saccharomyces cerevisiae

References

1. Morcillo-Parra, María Ángeles, et al. "Effect of several nutrients and environmental conditions on intracellular melatonin synthesis in Saccharomyces cerevisiae." *Microorganisms* 8.6 (2020): 853.
2. Rodriguez-Naranjo, M. Isabel, et al. "Melatonin is synthesised by yeast during alcoholic fermentation in wines." *Food Chemistry* 126.4 (2011): 1608-1613.
3. Fernández-Cruz, E., et al. "Melatonin and derived L-tryptophan metabolites produced during alcoholic fermentation by different wine yeast strains." *Food chemistry* 217 (2017): 431-437.

PI:211

Use of *Streptomyces* co-culture strategy to produce secondary metabolites: A review

Sushil Singh[a], Ashish Yadav[a], Bhavana Tandon[a], Dr. Rupika Sinha[a, *]
[a]Department of Biotechnology, Motilal Nehru National Institute of Technology, Allahabad, Prayagraj-211004, Uttar Pradesh, India
*rupika@mnnit.ac.in

Background

In microbial co-culture technology, two or more microorganisms are grown together to enhance the efficacy of producing partners concerning the production of targeted metabolite (Luti and Mavituna 2011). Division of labor among the co-culture partners to perform the metabolic functions is the primary reason behind the increased efficiency of the co-culture system compared to axenic culture.

Review

This strategy has been successfully used for the efficient valorization of complex carbohydrate-based wastes and their subsequent use in the production of biofuels. This technology has also been used to discover novel secondary metabolites and enhance the production of desired antibiotics (Adnani, Chevrette et al. 2017).

Major findings

Different co-culture experiment designs have been evaluated for the products of interest, including the direct contact between the cell walls of producer and inducer partners or the interaction by metabolite contact only. Increased production of targeted antibiotics like actinorhodin, undecylprodigiosin has been achieved by co-culture of *S. coelicolor* with *Bacillus subtilis* and *E. coli*, respectively (Pérez, Muñoz-Dorado et al. 2011). This work includes a review on effect of co-culture of *Streptomyces* species with other microbes for production of secondary metabolites.

Keywords: **Axenic-culture; Co-culture; Secondary-metabolites; Antibiotic**

References

Adnani, N., M. G. Chevrette, S. N. Adibhatla, F. Zhang, Q. Yu, D. R. Braun, J. Nelson, S. W. Simpkins, B. R. McDonald and C. L. J. A. c. b. Myers (2017). "Coculture of marine invertebrate-associated bacteria and interdisciplinary technologies enable biosynthesis and discovery of a new antibiotic, keyicin." **12**(12): 3093-3102.

Luti, K. J. K. and F. J. B. E. J. Mavituna (2011). "Elicitation of *Streptomyces coelicolor* with *E. coli* in a bioreactor enhances undecylprodigiosin production." **53**(3): 281-285.

Pérez, J., J. Muñoz-Dorado, A. F. Braña, L. J. Shimkets, L. Sevillano and R. I. J. M. b. Santamaría (2011). "*Myxococcus xanthus* induces actinorhodin overproduction and aerial mycelium formation by *Streptomyces coelicolor*." **4**(2): 175-183.

Impact of Ecological Factors on the seed germination of *Cicer arietinum*

Vaishali Trivedi, A.K. Tewari
Department of Botany, Ewing Christian College, 20013

*trivedivaishali@gmail.com

Background

The presence of proper ecological conditions like temperature, light intensity, pH and characteristics of the soil severely affects the process of seed germination and hence affects the productivity of fertile land (1). Similarly, germination of seeds can be negative photoblastic or positive photoblastic depending upon the requirement of darkness or exposure to light for germination, respectively (2).

Review

For crop production, abiotic factors like wind, water, soil salinity, etc. or activity of biotic factors like activity of earthworm or foraging activity of grazing animals are the major stress factors which hinders the proper germination of seeds (3,4). Thus, to evaluate the impact of various ecological factors like temperature, salinity, pH and seed burial depth, seeds of chickpea (*Cicer arietinum*) were chosen which is generally sown in semiarid environments which may get affected by these ecological factors (5).

Major findings

The result showed the maximum percentage of seed germination at 25/15° C (day/night) and Least percentage at 35/20° C (day/night). The percentage of seed germination declined significantly with increase in the level of salinity. Rate of the germination of seeds of *Cicer arietinum* declined with increase in the depth. Least germination of seeds was reported at pH 5 while maximum germination occurred at pH 7.

Keywords: Ecological Characteristics, Germination Temperature, Sowing Depth, *Cicer arietinum,* Salinity.

References

1. Ren, J., Tao, L., Liu, X. M. (2002). Effect of sand burial depth on seed germination and seedling emergence of *Galligonum* spp. Species. Journal of Arid Environment. 51, 603-611.
2. Bakker, J., C.C. Baskin & J.M. Baskin, Seeds, Ecology, Biogeography and Evolution of Dormancy, and Germination. *Plant Ecology* **152**, 204–205 (2001). https://doi.org/10.1023/A:1011465920842
3. Demir, I., K., Mavi, M., Özcoban and G., Okcu. (2003). Effect of salt stress on germination and seedling growth in serially harvested aubergine (*Solanum melongena* L.) seeds during development. Israel J. Plant Sci., 51: 125-131.
4. Coons, J. M., R.O., Kuehl and N.R., Simons. (1990). Tolerance of ten lettuce cultivars to high temperature combined with NaCl during germination. J. Amer. Soc. Hort. Sci. 115: 1004-1007.
5. Saxena, M.C. (1990) Problems and potential of chickpea production in nineties. In: Chickpea in the nineties: proceedings of the second international workshop on chickpea improvement, 4–8 Dec 1989, ICRISAT Center, Patancheru, India.

Session-4

Biotechnological Intervention in Agriculture and Food sector

PI: 24

Allergenic peptides/proteins of *Anacardium occidentale*: insights on their potential cross-reactivity

Yadvi[a], RashiChugh[a], Ranjit Singh Gujjar[b], Dibyalochan Mohanty[c]and Atul Kumar Upadhyay[a]
[a]Department of Biotechnology, Thapar Institute of Engineering & Technology, Patiala, Punjab, India, 147004.
[b]Division of Crop Improvement, Indian Institute of Sugarcane Research, Lucknow, India
[c] Department of Pharmaceutics (Centre for Nanomedicine), School of Pharmacy, Anurag University, Hyderabad 500088, Telangana, India
* atul.upadhyay@thapar.edu

Background

Food allergies are allergic reactions that are triggered by eating and have an impact on the immune system. Numerous techniques, including traditional and computational methodologies, have been developed for identifying the allergic component in food. In this work, the allergenic potential of cashew proteins was identified, assessed, and validated using *in silico* techniques.

Review

The edible part of most of the tree nuts contain a significant amount of protein in addition to vitamins, minerals, fibre, carbohydrates, and many other nutrients(Smeekens et al., 2018). Tree nut allergies were shown to be the reason for an upsurge in anaphylaxis cases in 2014 by Johnson et al(Johnson J, et al., 2014). They discovered that 373.3% of anaphylaxis instances rose during the course of a ten-year research period. They also noticed that although other tree nut allergies were consistent, cashew sensitivities rose throughout this period.The protein sequences of the tree nuts might differ significantly in terms of similarity, and some of them can have distant associations and be cross-reactive.

Major Findings

Using the consensus ofalignment based algorithm such as Fast Alignment (FASTA) and Basic Local Alignment Search Tool (BLAST) the cross-reactivity of cashew proteins were established with known food allergens. Eleven cashew proteins have shown cross reactivity with both the methods at a significant E-value and percentage identity of 50%. AllergenFP, AlgPred(Sharma et al., 2021), and Allermatch(Vashisht et al., 2023)- allergenicity prediction programmers - identified eight out of eleven cashew proteins as possible allergens based on their physicochemical features. The predicted cashew protein and known food allergens shown to have a sequence alignment conservancy of 66 to 68%. Swiss-model, PSIPRED, and PHD fold service were used to obtain detailed structural insights of the identified allergenic peptide. The anticipated B-cell epitopes for the chosen cashew proteins were modelled using the PepFold 3.5 server, and the resulting structure was then docked with the ClusPro 2.0 server. Detailed analysis with the help of *in silico* tools gives first insight into the cross-reactivity and possible allergenicity of cashew proteins. With this approach, the elusive allergenicity of allergen sources may be evaluated.

Keywords: Cashew allergy: food allergen; Proteome; cross-reactivity

References:

Johnson J, Malinovschi A, Alving K, Lidholm J, Borres MP, N. L. (n.d.). Ten-year review reveals changing trends and severity of allergic reactions to nuts and other foods. *Acta Paediatr.*, *103*(8), 862–867.

Sharma, N., Patiyal, S., Dhall, A., Pande, A., Arora, C., & Raghava, G. P. S. (2021). AlgPred 2.0: An improved method for predicting allergenic proteins and mapping of IgE epitopes. *Briefings in Bioinformatics*, *22*(4). https://doi.org/10.1093/bib/bbaa294

Smeekens, J. M., Bagley, K., & Kulis, M. (2018). Tree nut allergies: Allergen homology, cross-reactivity, and implications for therapy. In *Clinical and Experimental Allergy* (Vol. 48, Issue 7). https://doi.org/10.1111/cea.13163

PI: 34

Integrated Pipeline for Accurate Classification of Soybean Leaf Diseases using Multi-Technique Feature Extraction

Ravindra Yadav[a*], Dr. Anita Seth[a]
IET, DAVV, INDORE

ryadav@ietdavv.edu.in, aseth@ietdavv.edu.in

Abstract: This research explores the classification of soybean leaf diseases through an ensemble method that merges four distinct feature extraction techniques. The methodology involves combining outputs from these four methods in a sequential pipeline. The primary aim is the precise identification and categorization of diseased soybean leaves. Initially, a dataset comprising 500 images was gathered using a 50-megapixel mobile camera (Samsung M-14) in a 2-acre land located at longitude 22.821212748693778 and latitude 75.81044598332882, village Paliya district Indore, Madhya Pradesh. The images were captured between September 15th to September 29th and were manually labeled as healthy or diseased. Subsequently, the dataset was expanded to 3000 images using Generative Adversarial Networks (GANs), and these were also labeled manually. Following standard preprocessing, which included resizing images to 256x256 dimensions, four feature extraction techniques were employed the output of each feature extractor fed to the XGB classifier generating different validation accuracy levels. Customized Kernel 1 gives accuracy of 89.4%, Thresholding technique makes the accuracy level to 91 %, Canny Edge Detection gives accuracy of 85.4%, Gabor Filter with GLCM shown the accuracy 84.4%, Customized Kernel 2 (Pipeline of all the feature extractor employed) gives 93.4 %. Notably, the proposed work achieved the highest accuracy at 93.4% among all methods employed.The research investigates the efficacy of combining multiple feature extraction methods encompassing texture, shape, color, and structural features. The aim is to provide a more comprehensive representation of soybean leaf diseases. This exploration evaluates whether the combined features capture a wider range of disease-related information compared to using individual methods in isolation. The study's approach stands out as a novel and promising method for the disease classification of soybean plants.

Keywords:Leaf disease, feature extraction, GLCM, XGB classifier, Edge detection, GAN,Gabor filter

PI: 39

Modification of Starch Extracted from Dasheen Type of Taro Grown in Joida, India

Ashwath K S[a,*],Prasanna B D[a]

[a]Department of Chemical Engineering (National Institute of Technology Karnataka,
Srinivasanagar Mangalore 575 025, India)

*ashwathks1998@gmail.com

Background

Taro (*Colocasia esculenta*) starch with a small granule size and high amylopectin content is useful in a wide variety of food applications. The objective of this study was to subject the starch extracted from taro tubers to ultrasound treatment followed by annealing treatment and evaluate the physicochemical properties of starch.

Review

Various techniques have been used to modify the physicochemical properties of corn, potato, and rice starches as per food industry requirements. However, no such studies have been conducted on Taro starch so far. Considering the safety and cost-effectiveness of such physical modifications and the unique properties of Taro starch, this study was taken up.

Major findings

Taro starch was subjected to ultrasound treatment at two frequency levels for different time intervals followed by annealing treatment at 50°C for 24 h. The swelling power of treated starch did not increase significantly at 65°C but significantly increased at 100°C. The solubility of modified starches was reduced when compared to untreated starch. Paste clarity and amylose content of the modified starches were reduced significantly. The reduction in amylose content could be attributed to structural rearrangement during annealing treatment. The in-vitro glycemic index increased after treating the starch with ultrasound and annealing.

Keywords: *Colocasia esculenta;* Physical modification; Glycemic index; Ultrasound treatment.

References

1. Kunyanee, K., Van Ngo, T., Kusumawardani, S., &Lungsakul, N. (2022). Ultrasound-chilling assisted annealing treatment to produce a lower glycemic index of white rice grains with different amylose content. Ultrasonics Sonochemistry, *87*, 106055. doi: 10.1016/j.ultsonch.2022.106055
2. Afolabi, T. A., Opara, A. O., Kareem, S. O., &Oladoyinbo, F. O. (2017). In vitro digestibility of hydrothermally modified Bambara groundnut (Vigna subterranean L.) starch and flour. Food Science & Nutrition, *6*(1), 36–46. doi: 10.1002/fsn3.510
3. Kizhakedathil, M. P. J., Belur, P. D., Wongsagonsup, R., Suphantharika, M., Agoo, E. M. G., &Janairo, J. I. B. (2022). Evaluation of Enzymatic and Chemical Treatments to Produce Oxalate Depleted Starch from a Novel Variety of Colocasia esculenta Grown in Joida, India. Starch-Stärke, *74*(1–2), 2000231. Doi: 10.1002/star.202000231
4. Wang, J., Lv, X., Lan, T., Lei, Y., Suo, J., Zhao, Q., Lei, J., Sun, X., & Ma, T. (2022). Modification in structural, physicochemical, functional, and in vitro digestive properties of kiwi starch by high-power ultrasound treatment. *Ultrasonics Sonochemistry*, *86*, 106004.doi: 10.1016/j.ultsonch.2022.106004

PI: 40

Melatonin and gamma-aminobutyric acid modulate cadmium toxicity in the paddy field cyanobacteria *Anabaena* sp. and *Nostoc muscorum*

Sakshi Pandey[a] and Sheo Mohan Prasada*

Ranjan Plant Physiology and Biochemistry Laboratory, Department of Botany, University of Allahabad, Prayagraj-211002, India
***profsmprasad@gmail.com**

Abstract:

In recent years, the rising population is putting pressure on the supply of food commodities, while another side severe alteration in the environment particularly in soil and water due to enhanced anthropogenic activities is negatively impacting the productivity of crops. Paddy is one of the prime staple foods that supports the growth and development of humans in several developing countries. Cyanobacteria are the important inhabitants of paddy fields and contribute as a source of carbon and nitrogen as they can convert atmospheric nitrogen to ammonia and fix carbon dioxide to organics. Hence, they are considered as biofertilizers since time immemorial. Increasing contamination by toxic chemicals such as heavy metals and pesticides of soil and water is directly affecting the crops and also the beneficial microbes, causing a great loss to crop productivity. To minimize such losses, in recent years several attempts have been made by scientists, governments, and agriculturists by applications of molecular manipulations, and exogenous applications of phytohormones and signaling agents. In present investigation, an attempt has been made by exogenous application of signaling molecules such as melatonin (MT) and gamma-aminobutyric acid (GABA) to alleviate the toxicity induced by cadmium (Cd) in two paddy field cyanobacteria *Nostoc muscorum* and *Ananaena* sp. Cadmium caused damaging effects on growth, photosynthetic pigments, PS II photochemistry, and photosynthetic oxygen evolution by accumulating Cd which resulted into excessive generation/accumulation of oxidative biomarkers: H_2O_2, superoxide radicals, and MDA equivalents contents despite of upregulation in enzymatic antioxidants: SOD, POD, and CAT. The exogenously applied MT and GABA considerably alleviated toxicity induced by Cd on these parameters by down-regulating the oxidative biomarkers and further elevating the antioxidant defense system.

Keywords: Heavy metal, photosynthetic pigments, PS II photochemistry

Study of Nutritional value enrichmentin hybrid of black wheat and common wheat varieties

Nidhi Shukla[a], Nand kumar Singh[a]*
Department of Biotechnology, Motilal Nehru National Institute of Technology
Prayagraj U.P 211004, India
*nksingh@mnnit.ac.in

Background

Wheat is one of the important cultivatedcropon a global scale.Major wheat breeding programmes are starting to focus more on quality than quantity.Coloured wheat offers a unique approach to addressing malnutrition by increasing antioxidants like anthocyanin, carotenoids, flavonoids, polyphenols, and other nutritional levels. The pigments carotenoids and anthocyanin are what give kernels their distinctive blue, purple, black, and red hues.Purple and blue wheat were crossed to create black wheat which is a coloured form of wheat. The outer layer of wheat grains contains anthocyanin, which is ultimately gives them their black colour.The primary limitation in black wheat production lies in its comparatively lower productivity when compared to conventional wheat varieties. Furthermore, the adaptability to diverse climatic regions is a crucial factor for gaining popularity in India, that offer different climatic zones.

Review

According to Monasterio et al., 2017The goal of biofortification is to create crop varieties enriched with micronutrients using traditional plant breeding methods. It is crucial to identify genetic resources containing elevated levels of the desired micronutrients and to assess the heritability of the specific traits being targeted. Sharma et al.,2020, assess the anthocyanin biofortification of black, purple, and blue wheat flour, examining their antioxidant potential and antimicrobial activity against prevalent human pathogens.Dhua et al., 2021, elevated grain protein content, increased carotenoid content, and disease resistance in a superior bread wheat variety through molecular breeding. The PsyE1 gene (Y gene) and the GpcB1 gene were employed as innovative sources to augmentboth grain carotenoid and protein content in the commercially elite bread wheat cultivar HD2967.

Major findings

Hybrids were created by breeding technique to improve production and nutrition value of wheat. Crossing had donebetween less yielding black wheat varietyand different common Indian wheat variety. After analysis of morphological parameter, confirmed hybrid grain and their flour were analyzed for different biochemical test to determine and compare the nutrition profile in hybrids and their parents. The result showing that hybrid perform better in term of Anthocyanin content, Total phenolic content (TPC), Antioxidant capacity and reduced gluten protein content in hybrid than parent cultivars. The ultimate result offer high yield and nutrition enriched genotype.

Keywords- Wheat, Breeding, Biofortification, malnutrition, Anthocyanin

References

1.Dhua, et al 2021 Composition, characteristics and health promising prospects of black wheat: A review. Trends in Food Science & Technology

2.Sharm et al., 2020. Evaluation of anthocyanin content, antioxidant potential and antimicrobial activity of black, purple and blue colored wheat flour and wheat-grass juice against common human pathogens. *Molecules*,

Geneticandmolecularcharacterization fordesirableagronomicaltraitsin RILpopulationofrice (*Oryzasativa*L.)

Kaamini Bisht[a] and Nand K. Singh[a]*

Department of biotechnology, Motilal Nehru National Institute of Technology
Allahabad, Prayagraj 211004, India

*nksingh@mnnit.ac.in

Background

This research is centered on the identification of desirable agronomic traitswithin the rice (*Oryza sativa*) Recombinant Inbred Line (RIL) population and the subsequentinvestigationofthegenetic basisgoverningthese traits.

Review

Sequencing-based genotyping is a quick and economical method for high-resolutionmapping, genomic selection, QTL (Quantitative Trait Locus) identification, and populationgenetics (Tomoyuki, et al., 2017; Singh et al., 2018). Single nucleotide polymorphic (SNP)markers are favoured over other molecular markers due to their uniform distribution andwidespread occurrence throughout the genome (Uttam et al., 2022). This makes them the bestoption for creating high-density linkage maps and identifying markers that are closely linkedtothedesiredtrait(Yadavetal.,2019).

Majorfindings

Thefindingsderivedfrombothphenotypiccharacterizationandbiochemicalanalysisrevealedthatcertainplantsdemonstratedearlymaturationandexhibitedamorerobustaroma comparedtobothparentricevarieties.

Keywords: RIL;QTL;SNPs;Marker-assistedselection.

References:

1. Singh, V., Singh, A.K., Mohapatra, T. *et al.* (2018) *Pusa Basmati 1121 – A rice variety with exceptionalkernelelongationandvolumeexpansionaftercooking*,Rice 11,19.

2. Tomoyuki,F; Motoyuki, A.; Kshirod, K.J: Kazuyuki, D.; Stefan, Reuscher.; *Adapting Genotyping-by-Sequencing for Rice F2 Populations*, G3 Genes Genomes Genetics, Volume 7, Issue 3, 1 March 2017,Pages881–893,

3. Uttam, GA.; Suman, K.; Jaldhani, V.; Babu, PM.; Rao, DS.; Sundaram, RM., *Identification of genomicregionsassociatedwithgrainZncontentinpolishedriceusinggenotyping-by-sequencing(GBS).*Plants(Basel).2022Dec28;12(1):144.

4. Yadav, S., Sandhu, N., Singh, V.K. *Et Al.* (2019). *Genotyping-by-sequencing based QTL mapping forricegrainyieldunderreproductivestagedroughtstresstolerance*.SciRep9,14326.

Morphological, cultural, growth characterization and molecular studies of *Alternaria brassicae*strains I-6A1y21 causes leaf spot of mustard.

Shailendra Kumar[a], Prof. H.K. Kehri[a*], Prof. S.M. Prasad[a*]

Myco-pathology laboratory, Department of Botany University of Allahabad,211002

[*]profsmprasd@gmail.com,

Black leafspot disease in mustard caused by *Alternaria brassicae*. Among the various fungal diseasesoccurringonthemustardisoneofthemostdevastatingdiseasesthathasbeenreported to cause 10-70%yield losses in the world. Mustard is the most economically important genus of the family Cruciferae. It is oil seed crop that is grown under a wide range of agro-climatic conditions in India. Variations in morphological, and cultural characteristics among different representatives in Allahabad geographical isolates of *Alternaria brassicae*. This isolate showed high-level variability in vitro with respect to a growth pattern in different culture media, conidial length, width, and number of septa. Conidia of isolate (I-6A1y21) have a number of transverse septa and a number of vertical between 3-6 and 2-4 respectively. Substantial variation was found in mycelial growth and sporulation among these isolates in different culture media. However, Potato Dextrose Agar, oatmeal agar, Czapexdox agar, andV-8juice Agar were best for all the cultures. Conidia of these isolates showed maximum growth in oatmeal agar and minimum in carrot agar. variations in mycelial growth and sporulation were also recorded. It is more similar to the Koran, Meja isolates whereas distantly like Soraon and Phoolpur. Molecular identification was done by using an internal transcribed spacer sequence and the isolates were found to be approximately~ 75% like other isolates and 99.99%similar to *Alternaria brassicae*isolates according to the NCBI database.

Keywords: Alternariabrassicae, strainsI-6A1y21, leafspotdiseases, morphological, cultural, growth, molecular, ITS analysis, Allahabad region.

References

1. GoyalP,ChaharM,MathurAP,KumarA,ChattopadhyayC(2011).Morphologicaland cultural variation in different oilseed *Brassica* isolates of *Alternaria brassicae*from different geographical regions of India. Indian J. Agric. Sci. 81 (11): 1052–1058.
2. NouraniSL,MinassianV,SafaieN(2008).Identification,pathogenicityanddistribution of Alternaria spp. of canola in Iran. Iranian J. Plant Pathol. 44: 33-36.
3. Patni CS, Kolte SJ, Awasthi RP (2005). Cultural variability of *Alternaria brassicae*, causing Alternaria blight ofmustard. Ann. Plant Physiol. 19: 231–42.
4. Saitou N, Nei M (1987). The neighbor-joining method: A new method for reconstructing phylogenetic trees. Mol. Biol. Evol. 4:406-425.
5. SinghD,SinghR,SinghH, YadavRC,YadavN,BarbettiM,SalisburyP,Nimbal S, Chattopadhyay C, Kumar A (2007). Cultural and morphological variability in *Alternariabrassicae*isolatesofIndianmustard(*Brassicajuncea*L.Czern&Coss.). (in)Proceedingofthe12thInternationalRapeseedCongress,26-30March,Wuhan, China 4: 158–60.

PI: 58

Gamma-aminobutyric acid and methyl jasmonate alleviate cadmium toxicity by regulating growth, PS II photochemistry, and oxidative stress in tomato and brinjal seedling

Varunendra Kumar Singh[a] and Sheo Mohan Prasad[a]*

Ranjan Plant Physiology and Biochemistry Laboratory, Department of Botany, University of Allahabad, Prayagraj-211002, India

***** profsmprasad@gmail.com

Background

Vegetables are essentially important for growth and development of humans as they contain minerals, vitamins, antioxidants, etc. In recent years, due to urbanization, the cultivation of vegetables is rapidly increasing in the catchment areas of cities to feed the growing population where soils and water are getting rapidly contaminated (Gelaye et al., 2022). Cadmium (Cd) is one of the toxic heavy metals whose concentration is rising severalfold in soils above the permissible limit (0.8 mg kg^{-1}) (Osmani et al., 2015). Further, for sustainable cultivation of vegetables in these areas an attempt has been made by adopting a model study to investigate the alleviatory role of signaling molecules gamma-aminobutyric acid (GABA) and methyl jasmonate (MeJA) against the Cd toxicity in common vegetables tomato and brinjal.

Review

According to some studies, Cd interacts with nucleic acids, destroys membranes, obstructs electron transport, and inhibits or stimulates enzymes. Crop productivity is lowered because key biological and physiological processes are affected, causing agricultural plants to grow and develop more slowly (Zulfiqar et al., 2022). Exogenous GABA and MeJA have been demonstrated in numerous studies to enhance growth and other parameters, hence decreasing the negative effects of various abiotic stresses on vegetable crops (Habibi et al., 2019).

Major findings

The experiments were conducted in hydroponics where growth medium was supplemented Cd, GABA and MeJA and also with their biosynthetic inhibitors 3-mercaptopropionic acid (MPA) of GABA and diethyldithiocarbamicacid (DIECA) of MeJA wherever required. It is evident from the results that intracellular Cd accumulation negatively affected the growth, photosynthetic pigments and PS II Photochemistry of both the test plants, whereas exacerbation of the oxidative biomarkers (SOR, H_2O_2, and MDA) was noticed due to substantial decrease in the activity of antioxidant enzymes SOD, POD, CAT, and GST. Both GABA and MeJA down regulated Cd accumulation, hence substantial improvements in the activity of enzymatic antioxidants, growth and related parameters were noticed. The application of their biosynthetic inhibitors suggests that GABA appeared to be the main player in alleviation of Cd toxicity.

Keywords: Antioxidative enzymes, Mitigation strategies. Oxidative biomarkers, Photosynthesis, Vegetables

References

Gelaye, Y. (2022). Noxious substance content of vegetables grown in urban and peri-urban areas. Food Mat. Res. 2(1), 1-13.

Osmani, M., Bani, A., & Hoxha, B. (2015). Heavy metals and Ni phytoextractionin in the metallurgical area soils in Elbasan. Albanian J. Agric. Sci., 14(4), 414.

Zulfiqar, U., Jiang, W., Xiukang, W., Hussain, S., Ahmad, M., Maqsood, M. F., Mustafa, A. (2022). Cadmium phytotoxicity, tolerance, and advanced remediation approaches in agricultural soils; a comprehensive review. Front. Plant Sci., 13, 773815.

Habibi, F., Ramezanian, A., Rahemi, M., Eshghi, S., Guillén, F., Serrano, M., & Valero, D. (2019). Postharvest treatments with γ-aminobutyric acid, methyl jasmonate, or methyl salicylate enhance chilling tolerance of blood orange fruit at prolonged cold storage. J. Sci. Food Agric., *99*(14), 6408-6

PI: 135

Green Guardians: Redefining plant resilience against Abiotic Stress during biopolymer encapsulation of Plant Growth Promoting Rhizobacteria.

Shivani Mahra [a], Sneha Tripathi [a], Kavita Tiwari [a], *Shivesh Sharma [a]
[a] Department of Biotechnology, Motilal Nehru National Institute of Technology, Allahabad, 211004, Uttar Pradesh, India
*shiveshs@mnnit.ac.in

Background

The agricultural industry has consistently been at the forefront of technological innovation in recent times. Using a progressive release approach based on encapsulation technology is thought to be an effective way to deliver and store beneficial microorganisms known as Plant growth promoting bacteria. Under varied stress conditions, PGPR plays as a role in enhancing plant health and growth. Regretfully, environmental variables and temperature cause bacterial viability to decline.Several encapsulation techniques have been developed by scientists to improve the effectiveness and survivability of biocontrol agents (De Oliveira et al., 2021). Bacteria encapsulation produces a layer that resembles a wall that regulates the release of microorganisms, shields them, and ensures their capacity to function.

Review

The key to creating bacterial inoculants is to adopt novel formulations and calculate the survival rate of the bacteria (Saberi-Rise et al., 2020). This work introduces a novel formulation that improves their survivability and effectiveness in harsh environmental settings. In this study, alginate and gelatin were combined to encapsulate PGPR, utilizing an ionic gelation- biopolymer approach. The impact of the biopolymer to bacteria mass ratio on the encapsulation process, morphological & bioactivity features of encapsulated bacteria have been thoroughly investigated.

Major Findings

According to the results, the swelling behavior and liquid content increased as the gelatin and alginate concentration did, since 1.5% gelatin concentration was found to have the highest encapsulation efficiency i.e. 91.83% and bacterial release, and this concentration was taken into consideration when mixing it with 2% alginate for the encapsulation. This formulation, which is more effective for plants and is based on encapsulation, seems to be a potential method of delivering PGPR in soil.

Keywords: Encapsulation, Biopolymers, PGPR, Encapsulation efficiency

References

Saberi-Rise, R., & Moradi-Pour, M. (2020). The effect of Bacillus subtilis Vru1 encapsulated in alginate–bentonite coating enriched with titanium nanoparticles against Rhizoctonia solani on bean. *International journal of biological macromolecules*, *152*, 1089-1097.

De Oliveira, J. L., Fraceto, L. F., Bravo, A., &Polanczyk, R. A. (2021). Encapsulation strategies for Bacillus thuringiensis: from now to the future. *Journal of Agricultural and Food Chemistry*, *69*(16), 4564-4577.

PI: 138

Protein rich food formulation for addressing a sustainable global nutrition: a prototype of meat analogue

Priyadharshini Jayaseelan[a], Rintu Banerjee[a]*
[a]Agricultural and Food Engineering Department, Indian Institute of Technology Kharagpur, India
*rb@iitkgp.ac.in

Background

The world's population is predicted to expand drastically in the near future, leading to a surge in the demand for food production systems (Hoehnel et al., 2022). With the increase in the population, an escalated demand for protein is expected as it is a crucial component for sustaining human health and development. The conventional source of protein for the non-vegetarian population is obtained from poultry, red meat, dairy, fish and eggs. Though the animal source of protein provides sufficient nutritional benefits several factors like changing diet patterns, existing resource constraints, meat related diseases and environmental sustainability emphasize the critical need for alternative protein-rich foods on a global scale. Considering the vegetarian and vegan choices the plant-based protein including legumes, soy-products, nuts and seeds offers only a narrow range of essential amino acids individually. Many plant-based foods are less protein-dense and contain anti-nutritional factors, such as protease inhibitors and lectins, which can interfere with protein absorption and digestion.

Experimental set up

This piece of work presents an innovative approach to produce a meat analogue using mushrooms as a primary ingredient, fortified with elevated levels protein by substrate modification. The additives like raw jackfruit paste, along with mushroom powder were used to mimic the texture and nutritional profile of the meat analogue.

Major findings:

The formulated meat analogue were subjected to texture analysis and among the different formulations the F4 (Mushroom Powder: Raw Jackfruit -60:40) showed a closer texture compared to commercially available product and the meat control chicken. Further, its nutritional profile revealed that its protein content was significantly higher than the marketed product of about 35.42%. Comparatively, among the physiological parameters, oil holding capacity and swelling power was higher in the analogue with decent protein post digestion. The formulated meat analogue, an example of a good functional food, showed a positive correlation with the gut micro-biota.

Keywords: Meat analogue, *Pleurotus djamor*, Raw Jackfruit, In-vitro Digestibility, protein, texture profile

Reference:

1. Hoehnel, A., Zannini, E., & Arendt, E. K. (2022). Targeted formulation of plant-based protein-foods: Supporting the food system's transformation in the context of human health, environmental sustainability and consumer trends. *Trends in Food Science & Technology*, *128*, 238–252. https://doi.org/10.1016/j.tifs.2022.08.007

PI: 152

Assessment of Sodium Fluoride (NaF) Impact on *Channa punctatus*: Tissue-Specific Toxicity and Environmental Health Implications

Mohan Kumar[a*], Kundan Patel[a], and G.B. Chand[a]
Department of Zoology, Patna University, Patna, Bihar, India

*mohankumarpup@gmail.com

Background

Excessive fluoride in water poses risks to aquatic life, animals, and humans(1). Fluoride accumulates in the tissues of freshwater fish after entering the food chain and causes severe health implications.

Review

Studies have revealed that fluoride is taken rapidly by bony tissues including operculum, and scales(2). Chronic exposure to high levels of fluoride through water and food can harm body tissues over time, potentially causing skeletal and dental fluorosis, and has also been linked to cartilage damage(3). However, in soft tissues such as the liver and kidney bioaccumulation of fluoride has also been reported up to a lesser extent (2). Sodium fluoride (NaF) toxicity significantly affects the xenobiotic detoxifying organ of the animal body, the liver, and the chief excretory organ, the kidney as marked by a variety of pathological and metabolic changes in them(4)(5). High levels of liver and kidney function enzymes and corresponding histological changes in the hepatic and renal tissues have been reported in the freshwater fish inhabitants of fluoride-contaminated water(6).

Major findings

The current study involved the administration of sodium fluoride (NaF) to the freshwater fish model *Channa punctatus* initially to determine its LC_{50} value. Subsequently, the fish were divided into distinct groups and exposed to three different doses for varying durations. The objective was to investigate the effects of sodium fluoride on aquatic organisms. Serological and histopathological investigations were carried out using blood samples, liver tissue, and kidney tissue. The serological results showed increased levels of ALT, AST, and ALP in blood serum, associated tissue impairment, and cellular damage in the liver of the fish exposed to NaF. NaF administration also caused increased levels in serum urea, creatinine, uric acid, sodium ions, and chloride ions levels and serious histopathological changes in the kidney tissues.

Keywords: Fluoride, Bioaccumulation, Xenobiotics, Fluorosis, LC_{50}, Serological, Histopathological.

References

1. Zhou Y, Liu K, Yan F, Berger E. Two cases of skeletal fluorosis from the historic cemetery at Zhangwan, Henan Province, China. Int J Osteoarchaeol. 2023 Nov 1;33(6):1052–63.
2. Rani DrA. Estimation of fluoride bioaccumulation in different tissues of Channa punctatus from water bodies of Lucknow region. J EntomolZool Stud. 2021 May 1;9(3):362–5.
3. Wang Y, Li A, Mehmood K, Hussain R, Abbas RZ, Tariq Javed M, et al. Long-term exposure to the fluoride blocks the development of chondrocytes in the ducks: The molecular mechanism of fluoride regulating autophagy and apoptosis. Ecotoxicol Environ Saf [Internet]. 2021 [cited 2024 Feb 8];217:112225. Available from: https://doi.org/10.1016/j.ecoenv.2021.112225
4. Pal P, Kumar Jha N, Pal D, Kumar Jha S, Anand U, Gopalakrishnan AV, et al. Molecular basis of fluoride toxicities: Beyond benefits and implications in human disorders. [cited 2024 Feb 8]; Available from: http://creativecommons.org/licenses/by/4.0/
5. Azab AE, Albasha MO, Jbireal JM, Adwas AA. Sodium Fluoride Induces Hepato-Renal Oxidative Stress and Pathophysiological Changes in Experimental Animals. Open J Apoptosis. 2018;07(01):1–23.
6. Perera T, Ranasinghe S, Alles N, Waduge R. Effect of fluoride on major organs with the different time of exposure in rats. Environ Health Prev Med [Internet]. 2018 May 16 [cited 2024 Jan 26];23(1). Available from: /pmc/articles/PMC5956923/

PI: 153

Harnessing the potential of multi-omics approaches to improve yield and related traits in leguminous crops

Sandhya Sharma[a]*, Kishor Gaikwad[a]
[a]ICAR- National Institute for Plant Biotechnology, New Delhi. 110012

*nipbsandhya@gmail.com

Background

The growing food demands and increasing urbanization are putting pressure on higher productivity from already shrinking land areas. The field of Omics has generated enormous information on crop genomics which has enhanced our understanding of crop physiology, stress physiology, and response mechanisms.

Review

In the wake of climate change, this field is contributing greatly towards developing stress-resilient crops with improved nutritional composition. The multi-omics approaches have played a significant role in the identification of genes and gene loci regulating yield attributes and nutritional quality.

Major findings

The application of genomics and transcriptomics in pigeon pea and cluster bean has resulted in the generation of linkage maps, identification of QTLs, and candidate genes related to agronomically relevant traits. Among yield-related traits, the number of clusters/plants, number of pods/clusters, number of seeds/pods, seed size, and seed weight are important. Among these, seed number per pod (SNPP) and pods/ cluster are especially important and are a target for breeders. Further, it has been possible to identify the function/ role of different genes in the metabolic pathways and utilize this information in the development of improved crop varieties at a rapid pace. Here, we have highlighted the progress and contribution of OMICS approaches to study the genes/ pathways contributing to yield (SNPP) in legumes with special emphasis to pigeon pea.

Keywords: Nutritional traits, crop productivity, pigeon pea, cluster bean, multi-omics.

References

1. Yang, Y., Saand, M.A., Huang, L., Abdelaal, W.B., Zhang, J., Wu, Y., Li, J., Sirohi, M.H. and Wang, F., 2021. Applications of multi-omics technologies for crop improvement. Frontiers in Plant Science, 12, p.563953.

2. Arpita, K., Sharma, S., Srivastava, H., Kumar, K., Mushtaq, M., Gupta, P., Jain, R. and Gaikwad, K., 2023. Genome-wide survey, molecular evolution and expression analysis of Auxin Response Factor (ARF) gene family indicating their key role in seed number per pod in pigeonpea (C. cajan L. Millsp.). International Journal of Biological Macromolecules, 253, p.126833.

PI:159

Screening, isolation and characterization of heavy metal tolerant (HMT) microbes having plant growth promoting potential

Aanand Kumar[a], Radha Rani[a]*
Department of Biotechnology, Motilal Nehru National Institute of Technology, Prayagraj
India

*radharani@mnnit.ac.in; raadharaani1982@gmail.com

Background

Abiotic stresses especially heavy metal (HMs) contamination poses a serious threat to agricultural productivity and ecosystems (Mishra et al. 2017). Microbes with plant growth-promoting (PGP) properties have been thoroughly explored for enhancing plant cultivation in contaminated soils by reducing the toxic effects of pollutants (Etasami 2018).

Review

In this study, multi metal-tolerant bacterial strains (A, B1, B2, B3, RS1, and RS2) having PGP potential were screened and isolated. These bacterial cultures exhibit PGP properties like N fixation; indole-3-acetic acid (IAA), hydrogen cyanide (HCN), siderophore, ammonia production, ACC deaminase (ACCD) activity, and phosphate solubilization, etc.

Major finding

IAA production in strains A, B1, B2, B3, RS1, and RS2 ranged from 6 to 237.2 µg/ml, while, releasing free phosphate from calcium triphosphate varied in the range of 4.1 to 34.1 ppm. Moreover, ACCD activity in strains A, B1, RS1, and RS2 varied between 4.3 and 20.6 µM α-ketobutyrate $hr^{-1}gm^{-1}$protein, and strains B2, B3, RS1 showed ammonia production ranging from 17 to 39.1 μMml^{-1}. All the strains showed high tolerance towards metals like Zn, Cu, As, Cr, Pb, Cd, etc. Based on morphological and biochemical characterization, the isolates A, B1, RS1, and RS2 were tentatively identified to be *Rhizobium sps.*, *Cronobactersps.*, *Kosakoniasps.*, and *Enterobacter sps, respectively. These* strains can be used as inoculants in metal-stressed conditions decrease metal toxicity in the soil and increase plant health and soil fertility (Vyas et al. 2022).

Keyword: Heavy metal, stress tolerance, Plant growth promoting bacteria, phytohormone.

References

1. Mishra, J., Singh, R. and Arora, N.K., 2017. Alleviation of heavy metal stress in plants and remediation of soil by rhizosphere microorganisms. *Frontiers in microbiology*, *8*, p.1706.
2. Etesami, H., 2018. Bacterial mediated alleviation of heavy metal stress and decreased accumulation of metals in plant tissues: mechanisms and future prospects. *Ecotoxicology and environmental safety*, *147*, pp.175-191.

Vyas, P., Rana, A.K. and Kaur, M., 2022. Rhizospheric bacteria as soil health engineer promoting plant growth. In *Rhizosphere Engineering* (pp. 45-64). Academic Press.

PI: 167

Evaluation of Oxidative Stress Indicators in some plants cultivated in the Prayagraj, Uttar Pradesh, India.

Sandhya Kushwaha*, Tripti Aggarwal, Shweta Singh, Jyoti Madhesia, Ujla Minhas*
Department of Biochemistry, Faculty of Science, University of Allahabad, Prayagraj-211002, UP, India,
* ujlaminhas@rediffmail.com

ABSTRACT

Background

Oxidative stress is a pathological condition which arises due to imbalance between reactive oxygen species produced and body’s antioxidant defense to neutralize them. This stress has been linked in the pathogenesis of several diseases in animals as well as plants. The present study was designed with an aim to investigate oxidative stress marker in some common indigenous plants of Prayagraj, Uttar Pradesh.

Review

Oxidative stress arises from an imbalance between reactive oxygen species (ROS) production and the biological system's antioxidant capacity. All organisms maintain a reducing environment in their cells, regulated by enzymes that require metabolic energy. Disruption of this balance leads to the generation of peroxides and free radicals, damaging cellular components like proteins, lipids, and DNA. While ROS are essential for normal plant physiology, excessive production under stress can harm cells (Mittler 2016). ROS also serve as signaling molecules, triggering apoptosis. Climate change-induced abiotic stress exacerbates ROS production, particularly in organelles like mitochondria, chloroplasts, and peroxisomes, impacting crop productivity negatively (Nadarajah, 2020).

Major findings

Catalase activity and lipid peroxidation levels were assessed in the fresh leaves of *Azadirachta indica* (Neem), *Ficus religiosa*(Peepal), *Ocimumtenuiflorum*(Tulsi) and *Mentha*(Pudina/Mint). High catalase activity and lipidperoxidation, a marker of oxidative stress, in the leaves of Azadirachta indica (Neem), Ficus religiosa (Peepal) was observed which reflect stress induced physiological state. Ocimumtenuiflorum (Tulsi), Mentha (Mint) displayed better oxidative stress homeostasis. This was a brief report; a more comprehensive examination involving additional variables is required for further investigation.

Key words: Oxidative stress, *Azadirachta indica, Ficus religiosa, Ocimumtenuiflorum, Mentha,* catalase, Lipidperoxidation

References

1. Mittler R. ROS Are Good. Trends Plant Sci. 2017 Jan;22(1):11-19. doi: 10.1016/j.tplants.2016.08.002. Epub 2016 Sep 23. PMID: 27666517.
2. Nadarajah KK. ROS Homeostasis in Abiotic Stress Tolerance in Plants. Int J Mol Sci. 2020 Jul 23;21(15):5208. doi: 10.3390/ijms21155208. PMID: 32717820; PMCID: PMC7432042.

PI: 183

Role of selenium in sustainable agriculture: A Review

Preeti Vishwakarma[a*], Shivesh Sharma[a], Joyabrata Mal[a]
[a]Department of Biotechnology, Motilal Nehru National Institute of Technology Allahabad, Prayagraj, Uttar Pradesh, 211004

*km.2022rbt04@mnnit.ac.in

Background

Selenium (Se) is an essential microelement and is pivotal for human health. It is an important constituent of several selenoproteins including selenocysteine (SeCys) and selenomethionine (SeMet) and is involved in various physiological and metabolic processes. Se is present in environments in their different organic and inorganic forms. It has a beneficial role in plant growth promotion and mitigation of various environmental stresses when present in trace amounts. Se regulates the reactive oxygen species (ROS) and stimulates the production of antioxidative defense mechanisms in dose dependent manner. However, Se can generate toxicity and adverse effects too in plants depending on its chemical form and dose. Recently, Se nanoparticles (Se NPs) has been emerged as a suitable approach to overcome the adverse effects of Se and improved the crop production in a sustainable way due to their unique physical and chemical properties (Sarkar, et al. 2023).

Review

Se-oxyanions i.e. selenite and selenate can enhance plant growth and development under different abiotic stresses (Yin, et al. 2019). However, Se NPs appears to be more advantageous in terms of promoting growth and increasing tolerance against abiotic stresses due to their high bioavailability, biocompatibility, and less toxicity than any other form of selenium (Nasirzadeh, et al. 2022). However, at higher concentration, both Se-oxyanions and Se NPs shows phytotoxicity and result in the reduction of plant growth and development (El-Ramady, et al. 2014).

Major findings

The major findings concluded that Se has an important role in maintaining plant physiological and biochemical responses and helps in crop improvement through enhancing growth, yield, and quality. Thus, Se can be used as fertilizer as well as fortifying agent in crop improvement. Although biogenic Se NPs are more environmental friendly and have been found to mitigate the different abiotic stresses and enhance plant tolerance, reports on applications of biogenic SeNP in agriculture is still limited.

Keywords: selenium, nanotechnology, nanoparticle, agriculture

References

El-Ramady, H. R., et al. (2014). "Selenium and nano-selenium in agroecosystems." Environmental Chemistry Letters **12**: 495-510.

Nasirzadeh, L., et al. (2022). "Foliar-applied selenium nanoparticles can alleviate soil-cadmium stress through physio-chemical and stomatal changes to optimize yield, antioxidant capacity, and fatty acid profile of wheat (Triticum aestivum L.)." Journal of Soil Science and Plant Nutrition **22**(2): 2469-2480.

Sarkar, J., et al. (2023). "A state-of-the-art systemic review on selenium nanoparticles: Mechanisms and factors influencing biogenesis and its potential applications." Biological Trace Element Research: 1-37.

Yin, H., et al. (2019). "Selenium forms and methods of application differentially modulate plant growth, photosynthesis, stress tolerance, selenium content and speciation in Oryza sativa L." Ecotoxicology and environmental safety **169**: 911-917.

PI 188

Impacts of Metal-Contaminated Soils on Agricultural produces through measurement of Magnetic Susceptibility

Himanshu Hanumant Singh[a*], Ram Pal Singh [b]
[a]Department of Civil Engineering Motilal Nehru National Institute of Technology Allahabad, Prayagraj-211004, UP, India
[b]Department of Civil Engineering Motilal Nehru National Institute of Technology Allahabad, Prayagraj-211004, UP, India

*himanshu.2022en09@mnnit.ac.in

Background

The increasing prevalence of metal-contaminated soils poses a significant threat to global agricultural productivity, food safety, and environmental sustainability. the magnetic susceptibility of metal-contaminated soils is crucial, as it can provide valuable insights into the potential repercussions for agricultural produces.

Review

In this study, transfer of metals from contaminated soils to crops, results into adverse health risks with the consumption of metal-laden agricultural products. Understanding the pathways through which metals accumulate in edible plant tissues is crucial for developing effective strategies to mitigate the impact on human health.

Major findings

The results have implications for both soil science and agronomy, offering valuable insights for policymakers, environmental scientists, and farmers. The research emphasizes the need for integrated approaches to address the complex challenges posed by metal contamination in agricultural systems.

Keywords: Magnetic susceptibility, Metal contamination, Heavy metals, Sustainable agriculture.

References

1. S. Khan, Q. Cao, Y. M. Zheng, Y. Z. Huang, and Y. G. Zhu, “Health risks of heavy metals in contaminated soils and food crops irrigated with wastewater in Beijing, China,” Environmental Pollution, vol. 152, no. 3, pp. 686–692, (2008)
2. Mattigod, S. V., and A. L. Page. "Assessment of metal pollution in soils." Applied environmental geochemistry 1 (1983).
3. Neli V. Jordanova, Diana V. Jordanova, Ludmila Veneva, Kitka Yorova, and Eduard Petrovsky “Magnetic Response of Soils and Vegetation to Heavy Metal Pollution: A Case Study” Environmental Science & Technology (2003) 37 (19), 4417-4424 DOI: 10.1021/es0200645.
4. Xu, Y., Fang, Z. & Tsang, E.P. In situ immobilization of cadmium in soil by stabilized biochar-supported iron phosphate nanoparticles. Environ Sci Pollut Res 23, 19164–19172 (2016). https://doi.org/10.1007/s11356-016-7117-z.

PI: 192

View of Insect Parasitoid community structure of leaf miner *Chromatomyiahorticola* and *Liriomyza brassicae* (Diptera: Agromyzidae) on *Pisum sativum* in Prayagraj.

Deepti Mondol[a], Ashwani Kumar[b]
[a]Department of Zoology, Ewing Christian College, Prayagraj, India-211003,
[b]Department of Entomology, SHUATS, Prayagraj, India- 211007
* deeptimondol12@gmail.com

Background

A survey of parasitoids community structure of leaf miner *Chromatomyiahorticola* and *Liriomyzabrassicae* (Diptera: Agromyzidae) was carried out in the research field of SHUATS Allahabad from October to March 2009-2011. The relative abundance of leaf miner and rate of parasitism were also determined.

Review

Three species of natural enemies were found on insect pest of pea of which Diglyphus sp. was recorded major one[1.]Biological control has been applied by some countries using information on the parasitoids biology[2,3,4]. At least 23 parasitoids species have been used in biological control programs to Diptera: Agromyzidae in Senegal, California, Hawaii, Barbados, Marianas, Tonga, Taiwan and Guam[5].

Findings

Parasitoids such as leafminer have long been known to play a chief role in reducing impending pest populations. The pupae collected from the leaves were transferred into the specimen tubes (1"×4") to record pupal parasitism and to identify the species of parasites. The data of the number of healthy and parasitized pupae was recorded to determine the percent parasitism during different time intervals. Upon emergence the leaf miners and the parasites were counted and separated. The average percentage population of parasites of *Chromatomyiahorticola* for the year 2009-2010 and 2010-2011 is 10% in both the years and that of *Liriomyzabrassicae* for the year 2009-2010 and 2010-2011 is 9.8% and 8.5% respectively. The parasitization rate was very low during the main peak of the pest in mid winters, but increased considerably later in the season. It is determined that these parasitoids play a significant role in reducing the population of leafminer during the late winter. Ten species of parasitoids were identified. Four species of the family Eulophidae were observed in *Chromatomyiahorticola*namely *Diglyphusisaea*(Walker), *Diglyphusguptai* (Subba Rao), *Pediobius indicus* Khan, *Chrysonotomyiarexia*Narendran. Two species of family Pteromalidae were *Epicleruskeralensis*Narendran, *Sphegigasterbrunneicornis* (Ferriere) and *Herbertia indica* Burks was from Tetracampidae.Whereas in *Liriomyzabrassicae*species *Opius phaseoli*, *Diglyphusisaea* and *Opius exiguous* were found. The larval parasite *Diglyphusisaea*(Walker), which emerged as the second dominant parasite on *Liriomyzabrassicae* has turned out to be the key parasite of *Chromatomyiahorticola*. The population of parasitoids indicates the potential use of it for biological control programs. The high diversity of parasitoids supports the supposition that leafminer flies are of neotropical origin. The severely pesticide-based pest management practices should take more advantage of the lushness of parasitoids by enhancing its efficacy through the adoption of integrated pest management.

Key Words: *Chromatomyiahorticola, Liriomyzabrassicae, Pisum sativum,* parasitoid.

References

1. Yadav, S. K., and Patel, S. (2015). Insect-pest complex on *Pisum sativum* l. and their natural enemies at Pantnagar. Journal of Plant Development Sciences Vol. 7 (11), 839-841.

2. Chow, A., and Heinz, K.M. (2004). Biological Control of Leafminers on Ornamental Crops. In: Heinz KM, van Driesche RG, Parrella MP, editors. Biocontrol in Protected Culture. B Ball Publishing, Batavia, IL; 21-38.

PI:195

Isolation, Screening, and compatibility assessment of rhizospheric Plant Growth Promoting Rhizobacteria, forconsortia formation incrop improvement

Maneesh Maurya[a],* Shivesh Sharma[a]
[a]Department of Biotechnology, Motilal Nehru National Institute of Technology, Allahabad,211004, Uttar Pradesh, India
*shiveshs@mnnit.ac.in

Background

The emphases on sustainable production systems and diversification have resulted in a significant shift in India's agricultural policy during the past few decades. Ever since the pleasant environment of microorganisms around plant roots, known as the rhizosphere, was discovered, rhizosphere research has been generating unexpected and intriguing research ideas. Plant Growth Promoting Bacteria (PGPRs) are valuable microbes that colonize the plant rhizosphere and increase plant growth by several different mechanisms. As a biofertilizer, PGPR enables a sustainable replacement for chemical fertilizer.

Review

The aim of this study was to collect rhizospheric soil samples, isolation and screening of PGPR activity of Zea mays & Vigna radiata rhizobacteria, compatibility assessment, Biocontrol activity against plant pathogens, and formulation of consortia among compatible bacterial strains. PGP traits such as IAA production assay, HCN production, siderophore synthesis, ammonia production, and ACC deaminase activity is demonstrated by isolated PGPB.

Findings

The results of this study demonstrated that, out of 15 bacterial isolates, each isolates exhibit ammonia production activity, isolates although M6, Z3, and Z4 produced highest IAA concentration and M6 and M8 shown siderophore production activity. Cross streaks method was used to perform the compatibility assay. All isolated bacterial strains were compatible to each other except M5 with M7 and M8. Formulations of consortia among compatible strains have formed. Biocontrol activity was performed by dual culture methods by M1, M4 and Z7 strains infected with Aspergillus niger and M4, M5, Z4 and Z5 infected by Fussarium spp. Formulated consortia of compatible bacterial strains, M4, M5, Z4 and Z5 were used for rice seed priming, which enhanced the germination of rice seedling. This study found a potential novel and advantageous, biofertilizer composition that supports plant growth and development, to decrease the use of synthetic fertilizers.

Keywords: PGPR, Biocontrol, Sidrophore, Consortia, Compatibility, *Fussarium*.

References:

1. Molina-Romero,D.,Baez,A.,Quintero-Hernández,V.,Castañeda-Lucio,M.,Fuentes-Ramírez,
2. L. E., Bustillos-Cristales, M. D. R., ... & Muñoz-Rojas, J. (2017). Compatible bacterial mixture,tolerantto desiccation, improves maizeplantgrowth.PloS one, 12(11),e0187913.
3. Geetha, K., Venkatesham, E., Hindumathi, A., & Bhadraiah, B. (2014). Isolation, screening andcharacterization of plant growth promoting bacteria and their effect on Vigna Radita (L.) R.Wilczek.*IntJ CurrMicrobiolApplSci*,*3*(6), 799-899.3
4. Penrose,D.M.,&Glick,B.R.(2003).MethodsforisolatingandcharacterizingACCdeaminase-containing plant growth-promoting rhizobacteria. *Physiologia plantarum*, *118*(1), 10-15.
5. Maheshwari, D. K., Dubey, R. C., Agarwal, M., Dheeman, S., Aeron, A., & Bajpai, V. K. (2015). Carrier based formulations of biocoenotic consortia of disease suppressive *Pseudomonas aeruginosa* KRP1 and *Bacillusl icheniformis* KRB1. *Ecological Engineering*, *81*, 272-277

.

Session-5

Biotechnological Intervention in Interdisciplinary Approach in Design and Innovation

Photosynthetic Production of Farnesene by Engineered Cyanobacteria

Akhil Rautela[a] and Sanjay Kumar[a*]

[a]School of Biochemical Engineering, IIT (BHU) Varanasi, Varanasi-221005, U.P., India

* sanjaykr.bce@iitbhu.ac.in

Background

Advancements in synthetic biology tools for the engineering of cyanobacteria to produce jet biofuels have been a point of attention for many researchers. Petroleum-based jet fuels and natural gases produce toxic greenhouse gases that adversely affect living beings. Therefore, alternative fuel molecules must be sought. The aviation industry contributes 2-3% of man-made CO_2 emissions alone. Sustainable aviation biofuels are high-energy molecules used to power aircraft that could be a great alternative to petroleum-based jet fuels. The International Renewable Energy Agency (IRENA) has highlighted ‘biofuel for aviation’ to promote biofuel-based aviation transportation. Jet engines cannot be replaced by low-carbon emission technology due to high manufacturing costs and long lifespans; “drop-in” biofuels, which can be used without modifying existing jet engines, are required. In recent years, farnesene has been identified as a novel aviation biofuel molecule by researchers.

Review

Farnesene is mainly synthesized by higher plants via MEP and MVA pathways. Moreover, they can be synthesized chemically. Thermal cracking of crude oil leads to the production of isoprene, which, when trimerized, produces farnesene. Photosynthetic production of farnesene by cyanobacteria from CO_2 is a carbon-neutral process, so these can play a very important role as sustainable and renewable energy sources. Cyanobacteria lack the farnesene synthase gene. However, they are equipped with an MEP pathway. Heterologous expression of the farnesene synthase gene can be done in cyanobacteria to produce farnesene. The doubling time of cyanobacteria lies between 4 to 5 hours. Fast-growing cyanobacteria such as *Synechococcus elongatus* UTEX 2973 has a doubling time of approximately 2 h at ambient conditions. Engineering fast-growing cyanobacteria will lead to a higher yield of farnesene.

Major findings

UTEX 2973 was first engineered with a codon-optimized *Malus domestica* farnesene synthase gene (AFS) through an integration vector strategy. The strain could not produce the quantifiable amount of farnesene for the first three days. However, on days 5 and 6, due to the accumulation of farnesene, a production of 0.41 ± 0.08 mg/L was obtained. UTEX *AFS* strain was engineered with the *dxs* gene (UTEX *AFS::dxs*). This only moderately increased the farnesene production to 0.49 ± 0.05 mg/L. It can be presumed that IPP and other intermediates were being accumulated and not being converted to farnesene. Later, UTEX *AFS* was engineered with the *idispA* gene generating UTEX *AFS::idispA* strain. There was a significant increase in the production of farnesene in UTEX *AFS::idispA* strain (2.76 ± 0.06 mg/L). A notable improvement in the growth of UTEX *AFS::idispA* was also observed. Further, both *dxs* and *idispA* genes were overexpressed in UTEX *AFS* strain, resulting in UTEX *AFS::dxs::idispA* strain, which produced the highest farnesene level of 12.87 ± 0.7 mg/L in 5 days, equivalent to 12.48 mg/g DCW. With a productivity of 2.57 mg/L/day, UTEX *AFS::dxs::idispA* emerges as the superior photosynthetic farnesene producer compared to the existing literature. This study could serve as a foundation for engineering any terpene synthase gene into UTEX 2973 by further modulating the genetic elements that control gene expression.

Keywords: Biofuel; CO_2 sequestration; cyanobacteria; farnesene; MEP pathway; Synechococcus elongatus UTEX 2973

References

1. Yu, J., Liberton, M., Cliften, P.F., Head, R.D., Jacobs, J.M., Smith, R.D., Koppenaal, D.W., Brand, J.J. and Pakrasi, H.B. (2015). *Synechococcus elongatus* UTEX 2973, a fast growing cyanobacterial chassis for biosynthesis using light and CO_2. Sci. Rep. 5, 1–10. https://doi.org/10.1038%2Fsrep08132
2. Yadav, I., Rautela, A. and Kumar, S. (2021). Approaches in the photosynthetic production of sustainable fuels by cyanobacteria using tools of synthetic biology. World J. Microbiol. Biotechnol. 37, 1–17. https://doi.org/10.1007/s11274-021-03157-5

T Signaling of gamma-amino butyric acid and nitric oxide in mitigating ultraviolet-B radiation induced toxicity in two paddy-fields cyanobacteria

Aparna Pandey and Sheo Mohan Prasad*

Ranjan Plant physiology and Biochemistry Laboratory, Department of Botany, University of Allahabad, Allahabad- 211002, India
*profsmprasad@gmail.com

Abstract

Background

Enhanced anthropogenic activities are resulting into several threating changes in the environment. One of such effect is depletion of ozone layer, thereby resulting into enhanced solar ultraviolet-B (UV-B) radiation which is causing substantial reduction in crop productivity directly and also negatively affecting the growth of beneficial microbes such as cyanobacteria in the paddy fields.

Review

The gamma-amino butyric acid (GABA) and nitric oxide (NO) are essential signaling molecules which have been studied for stress regulation in plants, however, their interaction in cyanobacteria remains yet to be investigated.

Major findings

The signaling role of role GABA and NO has been studied in regulating UV-B impact on growth and physiology of two paddy field cyanobacteria *Anabaena* sp. PCC 7120 and *Nostoc muscorum* ATCC 27893. The UV-B exposure significantly ($p<0.05$) declined the growth and negatively impacted on nitrogen metabolism i.e., NO_3^- and NO_2^- uptake, NR, NiR, GS and GOGAT activities (except GDH activity). Reverse to this, UV-B stress accelerated the enzymatic anti-oxidant (SOD, POD, CAT, and GST) activity and raised the levels of non-enzymatic anti-oxidants (proline, cysteine and NP-SHs), however, the negative effect of UV-B prevailed in test cyanobacteria. The exogenous supplementation of GABA / NO alleviated the UV-B stress induced damage to growth and the nitrogen metabolism as a result of further rise in the activity / contents of antioxidants. To study the role of NO in GABA mediated stress regulation, NOS-inhibitor and NO scavenger were employed which critically masked the exogenous GABA's response, hence clearly demonstrated that GABA mediated stress regulation involves NO signaling which acts as downstream to GABA.

Keywords: **Abiotic stress, alleviation, defense system, nitrogen uptake, signaling.**

References:

Babele, P.K., Singh, G., Singh, A., Kumar, A., Tyagi, M., Sinha, R.P. (2017). UV-B radiation and temperature stress-induced alterations in metabolic events and defense mechanisms in a bloom-forming cyanobacterium *Microcystis aeruginosa*. Acta Physiol. Plant 39 (11), 248. https://doi.org/10.1007/s11738-017-2540-4.

Jiang, Y. (2023). Application of gamma-aminobutyric acid and nitric oxide on turfgrass stress resistance: Current knowledge and perspectives. Grass Res 3, 3. https://doi.org/10.48130/GR-2023-0003

Khan, M., Ali, S., Al Azzawi, T.N.I., Yun, B.-W. (2023). Nitric oxide acts as a key signaling molecule in plant development under stressful conditions. Int J Mol Sci. 24, 4782. https:// doi.org/10.3390/ijms24054782

PI.:78

Centrifugal pump: a review study

Dipali Singh
UG Student Department of Mechanical Engineering, FoET, University of Lucknow,
Lucknow 226031
*ds5299181@gmail.com

Abstract

Considering all the changes and demands in the current era, we all are growing and moving towards less power-consuming devices in the agricultural, industrial, and many fields. Water is a vital component in the agricultural system and mainly supply of water in the fields can be done with the equipment known as a pump. The basic requirements of plants are air, water, and sunlight. There are many types of pumps, out of which we will discuss about the centrifugal pump in this review paper. A centrifugal pump is the most versatile mechanical rotodynamic equipment in fluid operation whose application ranges from agricultural to industrial. The main function of the pump is to convert electrical energy into hydraulic energy. In other words, we can say that the job of the pump is to raise the water to some height. An electric motor powers the centrifugal pump and does the function of transferring fluid to a storage above tank via a flow control valve. With the rapid development in the engineering industry, there are a lot of changes in the construction and parameters of the pump. The design of the centrifugal pump is focused on its performance and efficiency. Further research and developments are engaged to improve these technologies and also keep in mind the cost to ensure effective solutions which is the basic principle of engineers.

Keywords: Centrifugal pump, water, performance

Assessment of behavioral changes of sandstone under sulphuric acid environmental conditions

Kushlendra Lal Kharwar[a*], Anupam Rawat[b], Sushant Verma[c], Surjeet Pal[d], Hemant kumar Singh[e]

[a,b,c,d,e]Department of Civil Engineering, Motilal Nehru National Institute of Technology Allahabad, Prayagraj, 211004, India

*Email id: kushalkharwar@mnnit.ac.in

Abstract

Sulfuric acid is harmful for sandstone rocks and sandstone-related structures. One of the main sources of sulfuric acid in sandstone is acid rain. Sulfuric acid reacts with the minerals and elements of sandstone and causes surface erosion. The long-term occurrence of deterioration can become a serious problem for the stability of sandstone structures. Non-destructive tests are powerful tool for analyzing the behavior of structures. The EMI technique is one of the various non-destructive tests used to determine the damage, severity, and service life of a host specimen. In this experimentation work, the sandstone cylindrical specimen and PZT sensor have been used to analyze the behavioral phenomena in an acidic environment. The signatures were continued, measured from the starting day until the one-year duration. Further uniaxial compressive strengths have been compared with the standard uniaxial compressive strengths. Moreover, damage phenomena have related with the XRD and SEM. This research paper is helpful for analyzing the environmental, structural, and health impacts of acidic rain.

Keywords: Acidic environment, PZT, EMI technique, Sandstone

Structure health monitoring of stone structures with piezoelectric sensors for bacterial deterioration

Sushant Verma[a*], Anupam Rawat[b], Radha Rani[c] Kushlendra Lal Kharwar[d], Surjeet Pal[e], Hemant kumar Singh[f]
[a,b,d,e,f]Department of Civil Engineering, Motilal Nehru National Institute of Technology Allahabad, Prayagraj, 211004, India
[c]Department of Biotechnology, Motilal Nehru National Institute of Technology Allahabad, Prayagraj, 211004, India

*sushantverma841@gmail.com

Abstract

Stone weathering refers to the gradual deterioration and alteration of stone surfaces over time due to natural environmental factors and various other processes, like pollution and biological activity. Among the various processes involved in stone weathering, microbial deterioration is the least understood decay mechanism, for stone monuments. In the past few decades, the non-destructive test (NDT) has been used to monitor the health of structures. Hence, the EMI technique using a piezoelectric sensor to determine the biodeterioration of the stone structure. This technique can determine the incipient damage, location, and severity of the damage. For the assessment, the stone cylindrical samples and a piezoelectric patch which was applied to the surface. After applying the sensor, the sample was dipped in sulfur-oxidizing bacteria (SOB). This research paper contains the physical and chemical properties of the stone sample and the deterioration of the sample done by SOB using X-ray diffraction and scanning electron microscopy (SEM). Further, the loss in compressive strength of the standard sample and the deteriorated sample has been compared. Moreover, statistical analysis have used to determine the damage to the sample.

Keywords: Sandstone, Sulfur oxidising bacteria, NDT, EMI Technique

PI: 87

Study of bacterial deterioration of aerated concrete using EMI technique

Surjeet Pal[a*], Anupam Rawat[b], Kushlendra Lal Kharwar[c], Sushant Verma[d], Hemant Kumar Singh[e]
[a,b,c,d,e]Department of Civil Engineering, Motilal Nehru National Institute of Technology Allahabad, Prayagraj, 211004, India
*ersjp148@gmail.com

Abstract

Nowadays, the use of aerated concrete is widely spread across structures because of its light weight properties. Aerated concrete is made by adding an air-entraining agent to cement mortar and concrete. They are generally used in high-rise buildings as partition walls to reduce the weight of the structure, and they also provide high insulation against temperature and sound. There are various ways to make light-weight aerated concrete. In the experimentation, aluminium powder is used as an air-entraining agent with different concentrations. The same specimen is used to determine the bacterial deterioration done by sulfur-oxidizing bacteria. This deterioration is checked using non-destructive testing; hence, the EMI technique with a piezoelectric sensor is used for analysis. Further physical and chemical properties of the standard specimen and the deteriorated specimen have been compared using x-ray diffraction and compressive tests.

Vector Construction in cyanobacteria for improvisation of farnesene production

Rishika Chatterjee, Akhil Rautela and Sanjay Kumar*
School of Biochemical Engineering, IIT (BHU) Varanasi, Varanasi-221005, U.P., India
*sanjaykr.bce@iitbhu.ac.in

Background

Terpenoids are plant's secondary metabolites. All terpenoids are made through two major pathways methyl erythritol 4-phosphate (MEP) and mevalonate (MVA). Plants have both pathways whereas cyanobacteria and bacteria have MEP pathways. Isopentenyl pyrophosphate (IPP) and its interconvertible isomer dimethylallyl pyrophosphate (DMAPP) in the pathway proceeds to produce farnesyl pyrophosphate(FPP), which is converted to farnesene by farnesene synthase enzyme. Farnesene (3,7,11-trimethyldodeca-1,3,6,10-tetraene), a linear sesquiterpenoid exists in two isomers α and β-farnesene. Farnesene finds extensive applications in various industries, including biofuel, cosmetics, pharmaceuticals, tire and polymer industries. It is a potential precursor molecule for the generation of biofuel. Also, considered a jet category fuel. Burning jet fuels increases greenhouse gas (GHG) emissions, which is around 2% of global CO_2 emissions annually, the aviation industry aims to reduce CO_2 emissions by 50% by 2050 as compared to 2005's GHG level. So, there is a need to explore alternative carbon-neutral fuel sources. Microorganisms are promising hosts for the ecofriendly production of farnesene, and plenty of literature is available on the product's microbial synthesis. However, the current focus is on investigating the photosynthetic synthesis of farnesene. For this purpose, cyanobacteria are being used which grow rapidly and easily without much effort. On this account researchers have introduced innovative techniques to manipulate cyanobacteria, aiming to enhance the production of the desired product.

Review

Various metabolic engineering literature indicates that bottleneck genes are overexpressed to further increase the desired product. The the same concept is presented in a study shows that on increasing the copy number, insertion of *IDI* and *IspA*genes in yeast *Pichia pastoris* increases α-farnesene production. Similarly, in *Yarrowia lipolytica*two copies of *IDI* and *IspA*are integrated chromosomally to enhance the β-farnesene production. Moreover, in the same organism, two FS and *ispA* are incorporated and exhibit better α-farnesene production. Previous research studies exhibited that increasing the copy number of key genes is an efficient yield-enhancing strategy.

Major findings

Based on our previous study, it was noted that the UTEX *AFS* strain was modified by the incorporation of*dxs* and *idispa* genes at NSII and NSIII neutral sites for the production of farnesene [6]. However, (UTEX *AFS::dxs*) exhibited a moderate increase in production. Another strain generated (UTEX *AFS::idispA)* had a significant increase in production. Further, the copy number of two genes that is *AFS* and *idispA* was increased, by targeting *AFS* gene at the NSII site while *idispA* gene was inserted at NSIII site of the plasmid (pBbE1k-*RFP*), resulting in two constructs namely pBbE1cNSII-*AFS* and pBbE1cNSII-*idispA* with antibiotic chloramphenicol resistance gene. Similarly, *AFS* was incorporated at NSIII site with a kanamycin resistance gene and a pBbE1kNSIII-*AFS* vector was generated. Further, the three constructed vectors were introduced in UTEX 2973 by triparental conjugation.

Keywords: MEP pathway, MVA pathway, farnesene, UTEX2973, triparental conjugation, vector construction.

References

1. Liu, Y., Jiang, X., Cui, Z. *et al.* Engineering the oleaginous yeast *Yarrowia lipolytica* for production of α-farnesene. *Biotechnol Biofuels* **12**, 296 (2019).

Computational Insights into Coagulation Factor IX: A Machine Learning Approach for SNP Data Analysis

Vikalp Kumar Singh[a*], Maheshwari Prasad Singh[b] and Ashutosh Mani[c.]

[a]Department of Computer Science and Engineering, National Institute of Technology, Patna, Bihar 800005-India.

[b]Department of Computer Science and Engineering, National Institute of Technology, Patna, Bihar 800005-India.

[C]Department of Biotechnology, Motilal Nehru National Institute of Technology Allahabad, Prayagraj, India-211004

* vikalps.phd20.cs@nitp.ac.in

Background

Single nucleotide polymorphisms (SNPs) constitute individuals' most widespread form of genetic variation and play a pivotal role in various genetic disorders. The Human Genome Variation Society (HGVS) nomenclature is widely adopted for SNP data characterization. The analysis of SNP data is vital for the exploration of mutation-based disorders. In computational analyses, encoding mechanisms like one-hot encoding are commonly employed, generating extensive datasets that demand significant computational resources. A position-specific mutation (PSM) encoding mechanism was introduced in pursuit of heightened accuracy and computational efficiency.

Review

In this research,the PSM encoding method employed in processing the EAHAD SNP dataset associated with Hemophilia B, a disorder resulting from mutations in Coagulation Factor IX, leading to severity levels categorized as Mild, Moderate, and Severe. The SNP dataset underwent pre-processing using the traditional one-hot encoding (OHE) method and the concurrent implementation of the PSM method. Classical supervised machine learning classifiers, including K-Nearest Neighbors (KNN), Random Forest, AdaBoost, and Support Vector Machine (SVM), were utilized for prediction, with their performance compared in terms of Accuracy, Training Time, and Testing Time.

Major findings

The results showcased the superiority of the PSM encoding method over traditional OHE in all evaluated aspects, in the context of Hemophilia B SNP dataset. Training time demonstrated aimprovememt of approximately 91-97% across all classifiers, except for KNN, which saw an improvement of 78%. Prediction time showed improvements of approximately 94-99% across all classifiers, except for Random Forest, which exhibited a 44% improvement when using the PSM-encoded dataset compared to the OHE-processed dataset. The PSM-encoded dataset exhibited notably higher classification accuracy, with Random Forest achieving an accuracy of 72.09%, while AdaBoost performed slightly lower at 69.833%. Conversely, AdaBoost achieved the highest accuracy among classifiers in the OHE-processed dataset, reaching 71.79%. Future endeavors aim to consistently apply the PSM approach to SNP datasets, aiming for improved classification, enhanced semantic representation of data and reduced computational time.

Keywords: Haemophilia B, Factor IX, PSM, OHE , Machine learning,

References:

[1] Singh VK, Maurya NS, Mani A, Yadav RS. Machine learning method using position-specific mutation based classification outperforms one hot coding for disease severity prediction in haemophilia 'A'. Genomics. 2020 Nov;112(6):5122-5128. doi: 10.1016/j.ygeno.2020.09.020. Epub 2020 Sep 11. PMID: 32927010.

To Combat Antimicrobial Resistance by disrupting *S. aureus* biofilm by drug loaded and surface adsorbed DNase or Tween-80 adsorbed solid lipid nanoparticles

Sarita[a], Manish Gaur[a], Mohd. Sohail Akhtar[b], Awadh BihariYadav[a*]
[a]Center of Biotechnology, University of Allahabad, Prayagraj, UP, India
[b]Molecular and Strucutral Biology, Central Drug Research Institute, Lucknow, UP, India

* awadhyadav@allduniv.ac.in

Background

Antimicrobial resistance (AMR) is a threat to humanity because it reduces the effectiveness of current medications and makes it more challenging to address previously attainable diseases. Biofilm formation is one of the major causes of AMR. The extracellular matrix of the biofilm forms a protective coating around bacteria, making them resistant to antibiotics. The purpose of this study was to investigate whether gentamicin-loaded solid lipid nanoparticles (SLNs) along with surface adsorbed tween-80 or DNase I as adjunct therapy could be used to disrupt *Staphylococcus aureus* biofilms in vitro and further facilitate the penetration of antibiotics inside bacterial biofilms.

Review

According to a report by the Center for Disease Control and Prevention (CDC), 2.8 million antibiotic resistance infections and 35000 deaths occured in the United States in 2019. In a different study, it was found that 65-80% of drug resistance cases were caused by biofilm formation. In another study, it was found that we need 100-1000 times higher antibiotic concentrations are required to kill bacteria residing in the biofilm.

Major findings

The SLNs were synthesized by double emulsion method in the size range 287.3 ± 7.4 nm to 292.4 ± 2.36 and the zeta potentials in the range of -25.6 ± 0.26 mV to -13.16 ± 0.51 mV respectively. The surface morphology and size of SLNs were further characterized using scanning electron microscopy. The encapsulation efficiency of gentamicin was 16.85 ± 0.84%. The compatibility of the drug with the excipient was confirmed by Fourier transform infrared spectroscopy, and the degree of crystallinity was determined by X-ray diffraction (XRD) analysis. SLNs showed sustained release of the drug for up to 360 h. SLNs were easily taken up by A549 cells, with minimal or no toxicity. The present study showed that tween-80 or DNase I-adsorbed SLNs efficiently disrupted *S. aureus* biofilms and possessed no or minimal toxicity against cells and red blood cells (RBCs). *S. aureus* biofilm disruption was dose-dependent. The free drug had 65.34±6.71% disruption whereas DNase adsorbed drug loaded SLNs had 86.28±6.23% disruption at equivalent amount of drug.

Keywords: Antimicrobial resistance, DNase I, *S. aureus* biofilm, Solid lipid nanoparticles, Tween-80.

References

Centers for Disease Control and Prevention (U.S.). *Antibiotic Resistance Threats in the United States, 2019*; Centers for Disease Control and Prevention (U.S.), **2019**. https://doi.org/10.15620/cdc:82532.

Lee, H. W.; Kharel, S.; Loo, S. C. J. Lipid-Coated Hybrid Nanoparticles for Enhanced Bacterial Biofilm Penetration and Antibiofilm Efficacy. *ACS Omega* **2022**, *7* (40), 35814–35824. https://doi.org/10.1021/acsomega.2c04008.

Popularisation of Government's Agricultural Policies through Scientific Cartoons for Rural India

Rohit Shukla[a], Vani Mishra[b], Anupam Dikshit[c] and Rohit Kumar Mishra[a]*
aCentre of Science and Society, Under IIDS, University of Allahabad, Prayagraj-211002, India
bDept. of Biotechnology, Motilal Nehru National Institute of Technology (MNNIT), Prayagraj-211004, India.
* rohit_ernet@yahoo.co.in

Abstract

Agriculture is the backbone of rural India, which plays an essential role in the economy and livelihood of millions of people. Although government agricultural policies have a crucial role in shaping the agricultural environment, it is still difficult for rural people to understand them effectively. Therefore, the main aim of the present work is to explore the innovative application of scientific cartoons (Scientoons) as a means of communication to popularize government agriculture policies among rural Indians. For this purpose, a series of scientifically accurate and culturally relevant cartoons are designed to convey complex agricultural policies like Pradhan Mantri Fasal Bima Yojana (PMFBY), Pradhan Mantri Krishi Sinchai Yojana (PMSKY), Soil Health Card Scheme, National Mission on Agricultural Extension & Technology (NMAET), PM-KUSUM Scheme, e-National Agriculture Market (e-NAM), Paramparagat Krishi Vikas Yojna (PKVY) and Kisan Credit Card (KCC) scheme in a visually engaging and easily understandable manner. To draw and assemble these scientific cartoons Autodesk SketchBook version 5.1.0 and M.S. Powerpoint 2016 version 14.0.4734.1000 were used. The findings reveal that scientific cartoons significantly enhanced policy awareness and understanding among the rural population, bridging the information gap that often hinders policy implementation. This study not only sheds light on the efficacy of scientific cartoons in disseminating government agricultural policies but also provides valuable insight into the dynamics of policy communication in rural India. This study holds the potential to inform policy-making and communication strategies for government agencies, NGOs and others engaged in rural development and policy promotion.

Keywords: Rural India, Agriculture policies, Scientific cartoons, Policy communication, Rural development, etc.

Antibiofilm activity of Lemon grass phytochemical against *Staphylococcusaureus* biofilm

Reema Singh[a] , SaritaMaurya[a] , AwadhBihariYadav[a,*]
Centre of Biotechnology, University of Allahabad, Prayagraj, UP, India
*awadhyadav@allduniv.ac.in

Background

Antimicrobial resistance (AMR) poses a significant threat to the global public health. AMR causes severe illnesses; extended hospital stays, higher medical expenses, and make infections incurable. AMR is developed by bacteria for various reasons, such as mutation, excessive use of antibiotics, and biofilm formation. Biofilm formation provides covering to the bacteria to protect themselves from the surrounding hostile environment. The purpose of this study was to identify promising phytochemicals from lemon grass (Cymbopogon citratus) that possess antibiofilm properties.

Review

Mature biofilms are 1000 times more resistant than planktonic bacteria and protect their populations from nutritional deficiencies, pH shifts, mechanical stress, and shear force on the bacteria. Some drugs and phytochemicals can interact with the proteins and cell membrane structures of bacteria, causing damage to microorganisms. In the past few years, biofilm formation by bacteria has drawn attention for the development of new therapies that can target bacteria and reside in the biofilm. Furthermore, research on the anti-biofilm potential of different compounds give hope to overcome AMR by targeting bacterial biofilms using phytochemicals of plant origin.

Major findings

Lemongrass phytochemicals were extracted using different solvents (methanol, ethanol, ethyl acetate, and water) to dissolve the powder, and different components were extracted using a soxhlet apparatus. The extracted fraction was concentrated under reduced pressure by using a rotary evaporator. The GCMS data of the plant extracts showed different phytochemicals present in different amounts in different fractions. In GC-MS analysis, we identified nearly 60– 100 compounds in different fractions of the plant extract. We also identified 10-15 potential phytochemical compounds based on earlier published work of researchers that might possess antibiofilm and antimicrobial activity based on retention time and % of peak areas in different fractions of C. citratus leaves. We also quantified flavonoids, phenolics, and tannins in different fractions using biochemical assays. The extract fraction inhibited biofilm formation by the methanolic extract (92±1.39 %), ethanolic extract (89±0.62 %), ethyl acetate (87±1.51 %), and aqueous extract (86±1.89 %). Biofilm disruption activity was 94±0.14% for the methanolic extract, 86±0.00% for the ethanolic extract,90±1.19% for the ethyl acetate and 83±0.44% for the aqueous extract.

Keywords:Biofilm,*Cymbopogon citratus*,Disruption,GC-MS, *S.aureus*

References

1. Mirghani,Ruba,etal."Biofilms:Formation,drugresistanceandalternativestoconventionalapproaches."*AIMSmicrobiology* 8.3 (2022): 239.
2. Guimarães,Rafaela,etal."AntibiofilmpotentialofmedicinalplantsagainstCandidaspp.oralbiofilms: A review."*Antibiotics* 10.9 (2021): 1142

PI: 124

Synthesis of Titanium di-oxide nanoparticles from leaf extract of *Pogostemoncablin*Benth. and their potential antifungal activity

Mohee Shukla[a,*] , Satya Narain[a]

[a]Duthie Herbarium, Department of Botany, University of Allahabad, Prayagraj-211002, India

*moheeshukla011@gmail.com

Background

In Recent yearsdermal infections caused by fungi have increased severely and affect people's daily life. Traditional antifungal compounds are responsible for side effects and resistance in fungi, so better and non-toxic alternatives are needed. Currently nanotechnology is widely used in the pharmaceutical field and established as a good antifungal agent [1].

Review

There are many metallic NPs such as Ag, Au, TiO_2, ZnO etc. which have good antifungal activity. TiO_2 NPs can be a promising antifungal agent due to widely uses in cosmetics like creams, nail paints, and sunscreen [2]. There are many studies reported synthesis of metallic nanoparticles using plants extract of jasmine flower [3], *Piper nigrum*, *Coriandrum sativum*, *Syzygium aromaticum* [4] etc.

Major findings

This study used TiO_2 nanoparticles (NPs) against four human pathogens *Trichophyton rubrum, Trichophyton mentagrophytes, Microsporumgypseum,* and *Candida albicans.* Green and chemical synthesis methods were used for the synthesis of TiO_2 nanoparticles. In green synthesis, we used aqueous leaf extract of *Pogostemoncablin*Benth. The formation of TiO_2 nanoparticles is confirmed by UV–Visible Spectroscopy, Scanning Electron Microscopy (SEM), Transmission Electron Microscopy (TEM), Fourier Transform Infrared (FTIR) and X-ray Diffraction (XRD) Analysis. The minimum inhibitory concentration (MIC) values of green synthesized NPs for *T. mentagrophytes* were0.076 mg/ml, for *T. rubrum* 0.463 mg/ml, for *M. gypseum* 0.094 mg/ml and for *C. albicans* 0.824 mg/ml. The chemically synthesized TiO2 NPs had MIC of 0.347 mg/ml for *T. mentagrophytes,* 0.894 mg/ml for *T. rubrum*, 0.142 mg/ml for *M. gypseum* and 2.05 mg/ml for *C. albicans.* This study concluded that Green synthesized TiO_2 NPs showed good inhibition against all four pathogens.

Keywords: Dermatophytes, TiO_2 NPs, Nanotechnology, green synthesis

References:

1. Gräser, Y., Monod, M., Bouchara, J. P., Dukik, K., Nenoff, P., Kargl, A., ... & De Hoog, S. (2018). New insights in dermatophyte research. *Medical mycology*, *56*(suppl_1), S2-S9.
2. Jassal, P. S., Kaur, D., Prasad, R., & Singh, J. (2022). Green synthesis of titanium dioxide nanoparticles: Development and applications. *Journal of Agriculture and Food Research*, 100361.
3. Aravind, M., Amalanathan, M., & Mary, M. S. M. (2021). Synthesis of TiO 2 nanoparticles by chemical and green synthesis methods and their multifaceted properties. *SN Applied Sciences*, *3*, 1-10.
4. Bhullar, S., Goyal, N., & Gupta, S. (2021). Rapid green-synthesis of TiO 2 nanoparticles for therapeutic applications. *RSC advances*, *11*(48), 30343-30352.

PI:128

Design of optimized treatment method for degradation of parent compound 1H-Benzotriazole using ozonation as advanced chemical treatment process

Niranjani Soman[a, b], Atul Vaidya [a, b,*]
[a]CSIR-NEERI (National Environmental Engineering Research Institute), Nagpur, Maharashtra, India
[b]AcSIR (Academy of Scientific and Innovative Research), Ghaziabad, Uttar Pradesh, India
*atul.n.vaidya1264@gmail.com

Background

1H-Benzotriazole (BTA) belongs to the class of Emerging Contaminants and Endocrine Disruptors; they have also been enlisted under the category of Persistent organic pollutants (POPs) in the Stockholm Convention. The main objective of this study was to degrade non-biodegradable UV absorbent using the technique of ozonation as an advanced oxidation process. All the conventional treatment methods like chlorination, biodegradation, and even some tertiary stage treatment methods are found to be inadequate in treating this contaminant. AOPs proved to be a promising technology for treating such difficult contaminants which are very hazardous if left untreated. AOP is a green and environment friendly method of treatment as it generates negligible to zero by products and is considered as economically feasible process, with very high treatment efficiencies, especially for contaminants like BTAs.

Review

BTAs are found in concentrations as low as 100-1000µg/l and upto 500-600 ng/l which makes it difficult to remove from the effluents (Shi et al. 2019). It induces severe adverse conditions like hepatotoxicity, neurotoxicity, liver dysfunction, nervous disorders, and endocrine system disrupting effects in humans and other vertebrates. Its negative effects on aquatic organisms are also, are well established (Chen et al. 2019). In plants, it is seen that due to uptake of traces of BTAs along with other nutrients, plant root and shoot growth is stunted, and flower and fruit bearing capacity gets reduced (Wu et al. 1998). Bioaccumulation of BTAs is seen in both terrestrial and aquatic food chains. Some of the common traditional treatment methods used to treat BTAs are Biodegradation, Photodegradation, Chlorination, Plant Uptake (Shi et al. 2019). However, such conventional treatment methods are found inadequate in completely eliminating BTAs, hence, an effective and optimized treatment method needs to be developed (Saha et al. 2022).

Abstract

Heterocyclic persistent organic pollutant i.e. (POP) 1H-Benzotriazole (BTA) is commercially available parent compound of the class of Benzotriazole, also known as UV stabilizer or UV light absorbing xenobiotic contaminant (<98 % purity), 10 and 100 ppm standard synthetic solutions prepared in distilled water were considered for the lab-scale study. Pure ozonation was performed on these solutions for the degradation study. During the experiment, essential parameters like pH of the synthetic wastewater, temperature of the solutions, ozone dosages, and time intervals for ozone exposure were noted. It was found that, at a very low ozone dosage range of 0.023 gm/hr to 1 g/hr, 1H-BTA completely degraded within the first five minutes. In order to enhance the effects of ozonation, a packed bed column was designed and tested for the same solutions. Quantification of 1H-BTA in the treated sample was done using triple Quadrapole GC-MS (GC-MS TQFM). The results obtained indicated that degradation in the column requires less time (reduced to a few seconds from five minutes) and better ozone mixing and absorption in the liquid. The efficiency of the degradation process was found to be increased by almost 60 % -70 % with the help of column. This developed method can be successfully applied for future research on degradation of 1H-BTA and other related hazardous compounds.

Major Findings

- Packed Bed Column design was found to be very effective in treatment of 1H-BTA using ozonation
- Pure ozonation was found to be effective and the degradation efficiency was increased
- Lower dosages of ozone showed good results in terms of degradation
- By - products formed were negligible and no surplus output of unabsorbed ozone was obtained.

Keywords:1H-Benzotriazole; Ozonation; Packed Bed Column; Degradation; Efficiency.

References:

Shi, Z. Q., Liu, Y. S., Xiong, Q., Cai, W. W., & Ying, G. G. (2019). Occurrence, toxicity and transformation of six typical benzotriazoles in the environment: A review. *Science of the Total Environment*, *661*, 407–421. https://doi.org/10.1016/j.scitotenv.2019.01.138

Song, S., Ruan, T., Wang, T., Liu, R., & Jiang, G. (2014). Occurrence and removal of benzotriazole ultraviolet stabilizers in a wastewater treatment plant in China. *Environmental Science: Processes & Impacts*, *16*(5), 1076. https://doi.org/10.1039/c3em00483j

PI:131

Automated deep learning based monkeypox classification usingskin lesion images

Saurabh Kumar Kaushal[1*], Vinod kumar yadav[2*], Pooja Verma[3], and Rajitha Bakthula[4]

* saurabhkaushal0909@gmail.com

Background

The MonkeyPox virus is a member of the Poxyviridae family of viruses. The virus is transmitted to humans through physical contact among humans or animals, or by touching contaminated object. The outbreak of Monky-Pox virus began in 2022, which infected nearly about more than 83,000 people and also caused the death of more than 200 people. An initial symptom because of the virus in an infected person includes fever, shivering, skin rashes, headache and muscle aches. Among the different modality shown by the virus one is skin rashes. Hence, skin rashes are used as an input method in our proposed non invasive method based on deep learning. The proposed method will help in identification of the virus in a person.

Review

Researcher Haque et al. [1] implemented five deep learning models MobileNetV2, EfficientNetB3, DenseNet121, VGG19 and Xception for classifying monkey pox with anaccuracy of 83.89%. In the research [2] researcher Abdelhamid et al. [2] train many pre-trained models for classifying monkey pox. The best accuracy they got by training Googlenet for two-classclassification (monkey pox and non-monkey pox) was 89%.Ali et al [3] proposed three models were combined to form an ensemble. ResNet50 gets the highestoverall accuracy of 82.96(±4.57%), followed by VGG16 81.48(±6.87%) and the combine system 79.26(±1.05%). Sahin et al. [4] trained pre-trained models for classifyingmonkey pox. The best accuracy they got by training Mobilenet for two-classification (monkey pox and non- monkey pox) was 91.1% [4]. Although the authors used several deep learning model mentioned in the past mentioned above but the accuracy achieved by the authors is very low.

Major Findings:

Because of the less accuracy achieved by the researcher in the past a deep learning model is proposed. The proposed model was trained on many monkeypox and non monkeypox images. In our proposed method we also used DCGAN for generating the new images. Hence, our proposed model achieved a high accuracy of 97.5%. The proposed achieved 4-5% accuracy higher than the vision transformer model [6].

References:

1. Haque, Md, Md Ahmed, Razia Sultana Nila, and Salekul Islam. ”Classification of human monkeypox disease using deep learning models and attention mechanisms.” arXiv preprint arXiv:2211.15459 (2022)
2. bdelhamid, Abdelaziz A., El-Sayed M. El-Kenawy, Nima Khodadadi, Seyedali Mirjalili, Doaa Sami Khafaga, Amal H. Alharbi, Abdelhameed Ibrahim, Marwa M. Eid, and Mohamed Saber. ”Classification of monkeypox images based on transfer learning and the Al-Biruni Earth Radius Optimization algorithm.
3. Ali, Shams Nafisa, Md Ahmed, Joydip Paul, Tasnim Jahan, S. M. Sani, Nawsabah Noor, and Taufiq Hasan. ”Monkeypox skin lesion detection using deep learning models: A feasibility study.” arXiv preprint arXiv:2207.03342 (2022)
4. Sahin, Veysel Harun, Ismail Oztel, and Gozde Yolcu Oztel. ”Human monkeypox classification from skin lesion images with deep pre-trained network using mobile application.” Journal of Medical Systems 46, no. 11 (2022): 79
5. Kundu, Dipanjali, Umme Raihan Siddiqi, and Md Mahbubur Rahman. ”Vision transformer based deep learning model for monkeypox detection.” In 2022 25thInternational Conference on Computer and Information Technology (ICCIT),pp.1021-1026. IEEE, 2022

Protein rich food formulation for addressing a sustainable global nutrition: a prototype of meat analogue

Priyadharshini Jayaseelan[a], Rintu Banerjee[a]*
[a]Agricultural and Food Engineering Department, Indian Institute of Technology Kharagpur, India
*rb@iitkgp.ac.in

Background

The world's population is predicted to expand drastically in the near future, leading to a surge in the demand for food production systems (Hoehnel et al., 2022). With the increase in the population, an escalated demand for protein is expected as it is a crucial component for sustaining human health and development. The conventional source of protein for the non-vegetarian population is obtained from poultry, red meat, dairy, fish and eggs. Though the animal source of protein provides sufficient nutritional benefits several factors like changing diet patterns, existing resource constraints, meat related diseases and environmental sustainability emphasize the critical need for alternative protein-rich foods on a global scale. Considering the vegetarian and vegan choices the plant-based protein including legumes, soy-products, nuts and seeds offers only a narrow range of essential amino acids individually. Many plant-based foods are less protein-dense and contain anti-nutritional factors, such as protease inhibitors and lectins, which can interfere with protein absorption and digestion.

Experimental setup

This piece of work presents an innovative approach to produce a meat analogue using mushrooms as a primary ingredient, fortified with elevated levels protein by substrate modification. The additives like raw jackfruit paste, along with mushroom powder were used to mimic the texture and nutritional profile of the meat analogue.

Major findings

The formulated meat analogue were subjected to texture analysis and among the different formulations the F4 (Mushroom Powder: Raw Jackfruit -60:40) showed a closer texture compared to commercially available product and the meat control chicken. Further, its nutritional profile revealed that its protein content was significantly higher than the marketed product of about 35.42%. Comparatively, among the physiological parameters, oil holding capacity and swelling power was higher in the analogue with decent protein post digestion. The formulated meat analogue, an example of a good functional food, showed a positive correlation with the gut micro-biota.

Keywords: Meat analogue, *Pleurotus djamor*, Raw Jackfruit, In-vitro Digestibility, protein, texture profile

Reference

2. Hoehnel, A., Zannini, E., & Arendt, E. K. (2022). Targeted formulation of plant-based protein-foods: Supporting the food system's transformation in the context of human health, environmental sustainability and consumer trends. *Trends in Food Science & Technology*, *128*, 238–252. https://doi.org/10.1016/j.tifs.2022.08.007

Enzyme-Mediated Pretreatment and Saccharification studies on Cotton Stalk

Subhara Dey[a], Subhodeep Banerjee[a,], Anusha[b], Rintu Banerjee[b,*]
[a]P. K. Sinha Centre for Bioenergy and Renewables, Indian Institute of Technology Kharagpur
[b]Department of Agricultural and Food Engineering, Indian Institute of Technology Kharagpur

*rintuin@gmail.com

Background

The transformation of lignocellulose into sugar is an integral aspect of lignocellulose biorefining, playing a vital role in the efficient utilization of lignocellulosic materials for biofuel production.

Review

The scientific community is increasingly exploring the potential of lignocellulosic biomass, a cost-effective and abundant source consisting of cellulose, hemicellulose, and lignin, for sustainable biofuel production and chemical generation. These feedstocks, sourced from various crops and residues, hold significant promise for second-generation biofuels without compromising food production. Globally, cotton, a major crop, covers 32.6 million hectares, with India alone dedicating 12.4 million hectares to its cultivation. The cultivation of cotton yields byproducts such as seeds, husks, and stalks, which are utilized for various applications. However, cotton stalks, generated in large quantities during harvesting, are typically burned by farmers, leading to the release of pollutants and greenhouse gases. The high holocellulose content in cotton stalks i.e. cellulose content in the range of 40.10 ± 1.55%, hemicelluloses at 13.60 ± 0.64%, makes them a favorable candidate for bio-ethanol production but the presence of a stringent recalcitrant layer of lignin which is approximately 29.40 ± 0.95% is the primary reason for the further valorization of cotton stalk (Binod et al., 2012). This study specifically focuses on the treatment of cotton stalks through the enzymatic method to obtain a high yield of fermentable sugars for subsequent bioethanol production.

Major findings

The present study investigates the efficiency of enzyme-mediated simultaneous pretreatment and saccharification of cotton stalks. Enzymatic treatment of cotton stalk efficiently degraded lignin and holocellulose with maximum reducing sugar yield (mg/g) i.e. 224.68(mg/g) at solid loading 15% (w/v), pH of the broth at 5, at 50 °C for 16 h. Further structural characterization of cotton stalks was done through SEM and FTIR.

Keywords: Lignocellulose, Bioethanol, Cotton Stalks, Cellulase, Laccase

References

3. Binod, P., Satyanagalakshmi, K., Sindhu, R., Janu, K. U., Sukumaran, R. K., & Pandey, A. (2012). Short duration microwave assisted pretreatment enhances the enzymatic saccharification and fermentable sugar yield from sugarcane bagasse. Renewable Energy, *37*(1), 109-116.
4. Chang, V. S., & Holtzapple, M. T. (2000). Fundamental factors affecting biomass enzymatic reactivity. In *Twenty-First Symposium on Biotechnology for Fuels and Chemicals: Proceedings of the Twenty-First Symposium on Biotechnology for Fuels and Chemicals Held May 2–6,*

PI:173

AgroTech App–Harnessing Precision Agriculture for Bountiful Harvests

Dr. R.Arthy[a], K.Akila[a*], D.Charanya[a], S.Baby[a]
S.Dharun[a]
Department of Information Technology, Kamaraj College of Engineering and Technology

*akilakarmegam17@gmail.com

Background

The proposed automatic irrigation system is designed to support the agricultural cultivation and maintenance phases by using technology (IoT, soil moisture sensors) to intelligently manage water use.

Review

Various studies propose smart irrigation systems, combining IoT and AI, utilizing sensors like DHT-11, Moisture sensor, and LDR, employing algorithms like PLSR for efficient water usage in agriculture. A paper introduces a cloud-based platform for irrigation control, utilizing moisture sensors and Node MCU, optimizing watering schedules through real-time soil moisture data, weather predictions, and crop-specific parameters, promoting water conservation and sustainable agriculture.

Major findings

The continual evolution of technology, particularly in the realm of the Internet of Things (IoT) there are significant challenges in growing agricultural food in high temperatures. The proposed automated irrigation system designed to overcome the limitations of existing methods. This system uses soil moisture sensors to determine the moisture level of the plant at a specific time. If the moisture level falls below a predefined threshold, the system automatically waters the plant until the moisture level reaches the desired threshold.

Keywords:Automated IrrigationSystem, SoilMoistureSensor, WaterConservation, UrbanAgriculture

References

1. RakhiAkhare(2023).AIANDIOTBASEDIRRIGATIONSYSTEMUSINGSOILMOISTURE.DOI:10.37896/sr10.6/025

2. V.SreelathaReddy,S.Harivardhagini,andG.Sreelakshmi(2024).IoTandCloudBasedSustainable SmartIrrigationSystem.E3SWebofConferences472,01026

A short Review on Electrospun Cellulose nanofibrils/Metal Oxide hybrid Nano-composites

Divyanshu Singh[1*], Binayaka Nahak[1], Dheeraj Ahuja[2*]
[1]Mechanical Engineering Department, Motilal Nehru National Institute of Technology, Allahabad, Prayagraj-211004, India
[2]Chemical Engineering Department, Motilal Nehru National Institute of Technology, Allahabad, Prayagraj-211004, India
divyanshusingh2131@gmail.com

Abstract

The development of advanced nanocomposites materials has gained a significant attention in recent years due to their unique properties and diverse applications. There are various techniques for the development of nanocomposites such as in-situ, extrusion, solvent evaporation, electrospinning etc. Among these techniques, electrospinning has garnered increased attention in the recent past as it results in the formation of ultrathin sheets. A significant progress has been made in the field of electrospunnanofibers based composites for numerous applications. However, development of hybrid nanofibers by incorporation of nanomaterials leads to the formation of a material with combination of collective properties. The product developed with the introduction of these properties make them suitable to be utilized for different applications such as theranostics, filtration, catalysis, and tissue engineering etc. Increasing ecological and environmental concern has diverted the interest of research for the development of biobased materials.

This review starts with the background of electrospun based nanocomposites, proceeding with the utilization of bio-based materials and detail description about the cellulose nanofibers, its isolation techniques and applications. Thereafter, the focus will be on the functionalization of cellulose nanofibers using different nanomaterials for the development of hybrid nanocomposites. Finally, review will sum up with the applications of electrospun hybrid nanocomposites with conclusion and future trends.

Keyword: Electrospinning, hybrid nanocomposites; cellulose nanofibrils; nanomaterials

Session- 6

Biotechnological Intervention in Environmental issues and Sustainability

Biodegradation of Acetonitrile by Aerobic Granular Sludge

Anuroop Singh[a], G. Kiran Kumar Reddy[a,b], Y.V.Nancharaiah[a,b*]
[a]Biofouling and Biofilm Processes Section, WSCD, Chemistry Group, Bhabha Atomic Research Centre, Kalpakkam 603102, India.
[b]Homi Bhabha National Institute, Anushakti Nagar, Mumbai-400094, India.
*yvn@igcar.gov.in,venkatany@gmail.com.

Background

Acetonitrile (ACN) is a versatile bulk chemical used for production of chemicals and in analytical laboratories. Due to wide use in research labs and industries, ACN-laden wastewater is generated. It can enter the sewer lines, sewage and can impact the biological processes in the wastewater treatment plant. Moreover, it is desirable to treat the CAN-laden wastewater from industries and laboratories to avoid pollution and environmental toxicity.

Review

Biodegradation of ACN by axenic bacterial cultures and mixed cultures such as activated sludge and biofilms have been reported. It is also known that biodegradation of ACN releases nitrogen compounds (i.e., ammonium, nitrite and nitrate). Therefore, biodegradation can increase carbon and nitrogen load in the wastewater. In the last decade, bacteria-la dengranular sludge has emerged as a sustainable option for biological wastewater treatment[1,2]. Although the effect and fate of toxic pollutants is an emerging field, there are no reports on the effect and fate of ACN on granular sludge reactors. Hence, we aimed to investigate the effect and fate of ACN in the context of granular sludge sequencing batch reactors. Furthermore, cultivation of bacteria-laden granules using ACN as sole carbon source was investigated with an aim to develop a biological treatment technology.

Major findings

Formation of compact granules was observed within 12 days of bioreactor operation using ACN as the sole C and N source. Gradually, ACN concentration was increased to evaluate its biodegradation and stability of granules. At an organicloadingrateof1.4 to 2.8 KgCODm^{-3}d^{-1}, COD removal was >95%. However, further increase in loading rate to 5.6 KgCODm^{-3} d^{-1} led to filamentous growth and breakage of granules.ACN removal was coincided by COD removal and increase in ammonium concentrations. Formation and removal of acetamide, an intermediate of ACN, was observed. Based on experimental data, biodegradation pathway of ACN was proposed. *Paracoccus*sp. and *Rhodococcus*sp. capable of growing on CAN were isolated from the granules. These strains were able to tolerate and degrade up to 4560 and 2280 mg L^{-1} ACN, respectively. Data shows that bacteria-laden granules can tolerate and achieve complete mineralization of acetonitrile.

Keywords: Acetonitrile biodegradation, aerobic granular sludge, sequencing batch reactors, acetamide, wastewater treatment.

References

1. Nancharaiah, Y.V., Reddy, G.K.K.(2018).Aerobic granular sludge technology: Mechanisms of granulation and biotechnological applications. Bioresource Technology 247, 1128-1143.

PI: 42

Effect of Salinity on the Ecophysiology of *Synechococcus elongatus* PCC7942

Priyul Pandey, Soumila Mondal, Rinkesh Gupta, Sapna Tiwari, Anjali Gupta, Deepa Pandey, ShailendraP Singh*
Centre of Advanced Study in Botany, Institute of Science, Banaras Hindu University,
Varanasi-221005,India
*spsingh@bhu.ac.in

Background

Cyanobacteria are considered essential oxygen-producing photosynthetic organisms and play vital roles in sustaining earth ecosystems. It encompasses their wide-ranging ecological impact as primary producers in diverse habitats. An optimum level of radiant energy is required to drive photosynthesis efficiently. The commercial utilization of cyanobacteria requires large-scale cultivation using marine water, and therefore, fluctuating light environment-dependent variation in the salinity could affect their fitness and productivity. High light, UVR (280–400 nm), and salinity stress induce the production of reactive oxygen species (ROS)that can inactivate enzymes, damage cellular components, including DNA, RNA and proteins, and give rise to lipidperoxylic radicals and lipid hydroperoxides.

Review

Synechococcus elongatus PCC 7942 has been used to study various biological processes like carbon concentration, circadian rhythms, iron balance, nutrient availability, and photosynthesis. Recently, it has gained attention as a model organism for metabolic engineering considering its importance in biofuel and valuable chemicals production. However, the investigation into how salinity stress affects ecophysiology of this cyanobacterium under fluctuating light conditions, which is crucial for large-scale cultivation, is lacking.

Major findings

To address this gap, we conducted a study to examine the ecophysiology of *S. elongatus* PCC7942 under varying light conditions. We investigated the influence of salinity stress in thepresence or absence of different quality and quantity of light using diurnal and continuous photoperiods. Our findings highlighted a light-dependent impact of salinity stress on the ecophysiology of this cyanobacterium.

Keywords: Biofuel, Cyanobacteria, Ecophysiology, Salinity

References

Kumar, V., Mondal, S., Gupta, A., Maurya, P. K., Sinha, R. P., Häder, D. P., & Singh, S. P.(2021). Light-dependent impact of salinity on the ecophysiology of *Synechococcuselongatus*PCC 7942: Genetic and comparative protein structure analyses of UV-absorbing mycosporine-likeaminoacids(MAAs) biosynthesis. *EnvironmentalandExperimentalBotany*, *191*,104620.

Mitigation of Lead Acetate Toxicity in Rice (*OryzasativaL.*) by Dextran Polysaccharide

Mariyam Fatima, Nand K.Singh*
Department of Biotechnology, Motilal Nehru National Institute of Technology Allahabad, Prayagraj, U.P., 211004, India

******nksingh@mnnit.ac.in*

Background

Rice (*Oryza sativa* L.) globally faces growth threats from abiotic stresses like salt, drought, and heavy metals (HMs, e.g., Pb, As, Cr, Cd, Hg) contaminating paddy soil, a significant source of HM exposure for humans. Lead (Pb) is particularly hazardous, impacting plant processes including seed germination, seedling growth, root/shoot ratio, cell membrane permeability, chlorophyll contents, and causing growth abnormalities. Dextran polysaccharide, an EPS (exopolysaccharide), acts as a biostimulant, enhancing stress tolerance and promoting biofilm formation and root colonization by beneficial bacteria, providing a protective barrier against abiotic stress and boosting plant growth and nutrient uptake.

Review

Excessive lead in plants reduces rice biomass, inhibits chlorophyll, photosynthesis, disrupts mineral uptake, and impairs respiratory activities (Ashraf et al., 2015). Awan et al. (2015) found lead stress hampers seedling vigor, decreases chlorophyll, germination rate, root/shoot length, and dry weight. Catalase/peroxidase activity increases with rising lead acetate concentration (Murugalakshmikumari et al., 2014). Dextran is proposed by Park et al. (2009) for acute heavy metal poisoning, environmental cleanup, and soil conditioning.

Major Findings

Lead toxicity negatively impacted morphological properties (fresh weight, dry weight, root length, and shoot length), while dextran treatment yielded positive outcomes compared to the control. Increasing lead concentration led to a decrease in chlorophyll content, but dextran- treated plants exhibited improved chlorophyll levels. MDA content increased with rising lead concentration, yet dextran treatment significantly reduced MDA levels. Catalase and peroxidase activities increased with lead concentration, with dextran-treated plants showing higher antioxidant levels.

Keywords: Rice (*Oryza sativa* L.), Lead acetate, Abiotics tress, Dextran, Biostimulant

References

1. Ashraf, U., Kanu, A.S., Mo, Z., Hussain, S., Anjum, S.A., Khan, I., Abbas, R.N. andTang, X., 2015. Lead toxicityin rice: effects, mechanisms, and mitigation strategies—a mini review. *Environmental Science and Pollution Research*, *22*, pp.18318-18332.
2. Awan, S., Jabeen, M., Imran, Q.M., Ullah, F., Mehmood, Z., Jahngir, M. and Jamil, M., 2015. Effects of leadtoxicityonplantgrowthandbiochemicalattributesofdifferentrice(*Oryzasativa*L.) varieties. *Journal of Bio-Molecular Sciences*, *3*(1), pp.44-55.
3. Murugalakshmikumari, R. and Ramasubramanian, V., 2014. Studies on the impact of lead acetate on the growth and biochemical characteristics of *Abelmoschus esculentus* (L.) Medicus. *International Journal of Science and Environmental Technology*, *3*, pp.591-596.
4. Park, J.K. and Khan, T., 2009. Other microbial polysaccharides: Pullulan, scleroglucan, elsinan, levan, alternant, dextran. In *Handbook of hydrocolloids* (pp. 592-614). Woodhead Publishing.

High density polyethylene (HDPE) Plastic Polymer Biodegradation by Using *Aspergillus flavus*

Snejuti Barua*, Dr. Indu Chauhan
*Department of Biotechnology, Dr. B.R. Ambedkar National Institution of Technology
Jalandhar, Punjab- 144008, India
* snejutib.bt.22@nitj.ac.in

Background

Plastics are one of the emerging environmental problem and potential contaminant currently affecting animals, humans worldwide because of lack of proper plastic waste disposal system. Numerous synthetic polymers are now produced on a global scale as a result of technological advancements. Plastics are highly use in manufacturing and packaging industries like carry bags, bottles, food container, toys. These are mostly made of polyethylene.

Review

The growth of fungi on the plastic surface use plastic as a source of carbon (Srikanth et al., 2022). While many different varieties of fungi are known to produce different types of enzymes, only a small number of them have the ability to break down plastics.*Aspergillus flavus* possesses the capacity to produce numerous extracellular enzymes like cutinase(Tan et al., 2021) hydrolase(Khan et al., 2020), peroxidase, catalase which has the potential to induce corrosion, fragmentation on the plastic surface by cleaving the polymer chain and due to this short intermediate metabolic products are formed which will easily mineralized by fungal cell. The objective of this work is to discuss the increase in high density polyethylene degradation rate by using fungus in combination with physical, chemical treatment.

Major findings

Polyethylene are highly crystalline and hydrophobic in nature. Due to complicated 3D structure, and hydrophobic nature plastics are stubborn in nature and not easily go under degradation. Bioremediation using fungi can be a potential approach to reduce the toxicity of plastic waste.

Keywords: **Biodegradation, *Aspergillus flavus*, Polyethylene**

Reference

1. Srikanth, M., Sandeep, T., Sucharitha, K., Godi, S., 2022. Biodegradation of plastic polymers by fungi: a brief review. Bioresour. Bioprocess. 9 (1), 1–10.
2. Tan, Y., Henehan, G.T., Kinsella, G.K., Ryan, B.J., 2021. An extracellular lipase from Amycolatopsismediterannei is a cutinase with plastic degrading activity. Comput. Struct. Biotechnol. J. 19, 869–879.
3. Khan, S., Nadir, S., Dong, Y., Schaefer, D.A., Mortimer, P.E., Gui, H., Khan, A., Yu, M., Iqbal, S., & Sheng, J. (2020). Biodegradation of polyester polyurethane by *Aspergillus flavus* G10. bioRxiv

PI 50

Phytochemical *screening of methanolic and benzene extract of stem and leaves of Dichrostachys cinerea (L.)*

Istuti Srivastava [a*] and Dr. Sanjay Kumar Mishra [a]
[a]Department of Botany, Ewing Christian College (University of Allahabad) Prayagraj, Uttar Pradesh, 211003
[*] sri.istuti22@gmail.com

Background

With the increasing world population, insufficient drug distribution, the high cost of modern medicines, and the detrimental effects of various synthetic treatments, herbal therapy is becoming increasingly in demand. For a very long time, the medicinal plants have been used worldwide to treat human diseases (1). There are many invasive species which might serve as a source of bioactive compounds of great medicinal value, but often remain unnoticed and under explored. Thus in view of this urge, the present study was conducted to determine the various active components present in stem and leaf extracts of *Dichrostachys cinerea* using techniques like FTIR, GC-MS and antioxidant activity was tested using DPPH method. By isolating and identifying these bioactive compounds new drugs can be formulated to treat various diseases and disorders (4).

Review

Dichrostachys cinerea (*L.)*Wight et Arn. (Fabaceae) earlier known as Mimosaceae, known as sickle bush, Chinese lantern tree, is a semi-deciduous to deciduous fast growing tree. It is one of the very useful wild medicinal plants used in folk medicine across Asia and Africa. Its bark is used to prepare concoction for treatment of dysentery, headache and elephantiasis(2). Phytochemical studies on *D. cinerea* revealed the abundance of secondary metabolites like sterols, alkaloids, tannins, triterpenes, polyphenols, phenolic acid, flavanoids are responsible for the biological properties attributed to the plant, flavonoids are responsible for anti-oxidative action, flavonoids serve as health promoting compound as a results of its anion radicals, while saponins have inhibitory effect on inflammation and remarkable activity in cancer prevention. The presence of these phenolic compounds in *D. cinerea* extracts attribute to its antioxidative properties and thus the benefit of this plant in herbal medicament. Phenols have been found to be useful in the preparation of some antimicrobial compounds such as dettol and cresol (1).Phytochemical screening is very important in identifying new sources of therapeutically and industrially important compounds.

Major findings

GC-MS analysis of the volatile components of the aerial part showed the presence of chemical class like oxygenated compounds-terpenoids, long chain, aromatic and heterocyclic compounds while non-oxygenated compounds chemical groups are terpenoids, long chain, aromatic compounds (4).From the different chromatographic and spectroscopic techniques led to the isolation of phenolic compounds and aglycones (2). Methanolic extract shows high antioxidant capacity in the DPPH assay and antioxidant activity is observed due to the presence of flavanoids and tannins.

Keywords-*Dichrostachys cinerea, phytochemical, bioactive compounds, therapeutic, FTIR*

References-

1.Neondo J.O, Mbithe CM, Njenga PK, Muthuri CW(2012)Phytochemical characterisation, antibacterial screening and toxicity evaluation of Dichrostachys cineraria, International Journal of Medicinal Plant Research Vol 1(4)

2.Reham T.El –Sharawy, Ahmed Elkhateeb, Mona M.Marjouk, Rasha R.Abd El-Latif, Salah Eldeen Abdelrazig, Mohammed A.El-Ansari(2017) Journal of Applied Pharmaceutical Science Vol .7(09) 219-223.doi:10.7324/JAPS.2017.70930.

3. Anita A, Malar Retna A (2016) A study on the bioactive compounds present in leaves of Dichrostachys cinerea. Green Chemistry & Technology Letters 2(20-25) doi:10.18510/gctl.2015.214

4. Abou Zeid AH, HifnawyMS, Mohammed RS, Amany A. Sleem (2014) Volatile Constituents and Anticonvulsant Activity of the Aerial Parts of Dichrostachys cinerea*(L.)*SciJ 2(2), 196-200

5. Saez SJM, Alfayate JAE (2020) Sicklebush (Dichrostachys cinerea) as a Medicinal Plant. Journal of Animal Production 32(3).

PI 53

Isolation and identification of naphthalene tolerant and degrading *klebsiella pneumoniae* sjk2 from contaminated site

Shanky Jindal[a] and Kamal Krishan Aggarwal[a]*
[a]University School of Biotechnology, Guru Gobind Singh Indraprastha University, Dwarka Sector 16C, Delhi-110078

* kkaggarwal@ipu.ac.in

Background

Naphthalene belongs to the class of polyaromatic hydrocarbons (PAHs) with two aromatic rings joint in a linear arrangement. It is one of the 16 priority PAH compounds associated with hazardous and toxic effects and carcinogenic properties. Due to its negative impacts on the environment and human health, attention has been given to regulate its use and bioremediation from the environment.

Review

Bacterial degradation of naphthalene is considered a promising strategy to remediate it using microbes from different sources. However, to withstand high levels of contamination in the environment, a tolerant bacterium is required for the effective and long-term remediation of naphthalene.

Major findings

In the present study, a naphthalene-degrading bacterium was isolated from petroleum oil-contaminated soil. The isolated strain can tolerate and degrade 0.25 g/L concentration of naphthalene. The 16S rRNA gene sequencing revealed it as *Klebsiella pneumoniae* and was designated as SJK2. The bacterial growth curve in the presence of various concentrations of naphthalene showed maximum growth on day 3 at 0.1 g/L concentration followed by 0.15 g/L naphthalene concentration. GC-MS analysis showed 99.35% degradation of naphthalene at 0.25 g/L concentration on day 3 and complete degradation by day 15. Dioxygenase activity showed by the isolated strain indicated that it followed both *ortho*- and *meta*- cleavage pathways for naphthalene degradation. The results indicated the potential of the isolated strain to degrade naphthalene. Further understanding of the isolated strain at the genomic and proteomic levels will contribute to the development of naphthalene bioremediation strategies.

Keywords: Klebsiella pneumoniae SJK2, GC-MS, Naphthalene bioremediation, dioxygenases, tolerant bacteria

References

Abo-State, M. A. M., Riad, B. Y., Bakr, A. A., and Aziz, M. F. A. (2017). Biodegradation of naphthalene by *Bordetella avium* isolated from petroleum refinery wastewater in Egypt and its pathway. J. Radiat. Res. Appl. Sci. 11, 1-9. https://doi.org/10.1016/j.jrras.2017.10.001.

Sakshi, Singh, S. K., and Haritash, A. K. (2023). Bacterial degradation of mixed-PAHs and expression of PAH-catabolic genes. World J. MicrobiolBiotechnol 39, 47. https://doi.org/10.1007/s11274-022-03489-w.

PI: 69

Bioremediation of produced water using fungi and microalgae

Agendra Gangwar[a], Dr. Sanjay Kumar[a,*]

[a]School of Biochemical Engineering (IIT (BHU) Varanasi, Varanasi, Uttar Pradesh 221005)

*Corresponding author email id: sanjaykr.bce@iitbhu.ac.in

Background

Global petroleum hydrocarbon contamination poses a significant worldwide issue, occurring at various points in the oil and gas extraction process. Produced water (PW) is considered the major stream of wastewater generated at the time of oil and gas exploration. Environmental sustainability relies on the transformative reclamation of PW, as current physical and chemical treatment methods exhibit limitations like harmful byproducts, increased energy usage, and environmental risks. In contrast, biological treatment is essential for environmental protection, utilizing natural processes to remove contaminants and ensure sustainable water reuse with minimized ecological impact.

Review

Fungal treatment harnesses the remarkable biodegradative abilities of fungi, such as white rot fungi, *Aspergillus*, and *Penicillium* to break down complex organic compounds and contaminants present in produced water. These organisms have shown an impressive capacity to degrade hydrocarbons and phenolic compounds. Filamentous fungi, *Aspergillus* sp. have been receiving considerable attention as potential candidates for the degradation of a wide range of petroleum hydrocarbons from wastewater.

Phycoremediation, on the other hand, focuses on the cultivation of microscopic photosynthetic organisms that have the unique ability to absorb and assimilate nutrients, including nitrogen and phosphorus, from produced water. This approach not only cleanses the water or sequesters carbon but also generates valuable microalgal biomass, which can be harvested and repurposed for biofuel production, animal feed. The most commonly employed microalgae strains for this purpose include *Chlorella* sp., *Nannochloropsis*, *Scenedesmus* and *Dunaliella*sp..

Major findings

We investigated petroleum hydrocarbon degradation from two types of simulated produced water (SPW) without prior pretreatment by fungi (*Aspergillus fumigatus* (NAIMCC-F-00266) and *Aspergillus Oryzae*) and microalgae (*Chlorella vulgaris* BDU GD003 and *Duneliella* sp. BDU 10113) monoculture. The results indicate that fungi can efficiently remove COD by 40-60% in both types of SPW in 7 days while microalgae remove COD by 30-55% in 30 days. Maximum COD reduction (60.17 ±6.03 %) was achieved by Aspergillus oryzae. All the microorganisms used in this study show growth inhibition due to the presence of petroleum hydrocarbon while *Chlorella vulgaris* shows no growth inhibition and enhanced growth followed by 55.78 ± 4.43 % COD reduction. *Aspergillus oryzae* and *Chlorella vulgaris* can be considered as the prospective organisms for PW bioremediation.

Keywords:Mycoremediation; Petroleum hydrocarbon; Phycoremediation; Produced water; Saline water

References

1. de Andrade, F. P., da Silva Gonçalves, A. H., De Farias Silva, C. E., Macário, L. R., da Silva, J. V. O. N., da Gama, B. M. V., ... and Tonholo, J. (2023). Treatment of oil-produced water using a fungus–microalga consortium. Energy, Ecology and Environment, 1-15. doi: 10.1007/s40974-023-00307-3

PI.:85

Antibiotic residues in aquatic environment: antimicrobial resistance development and bioremediation: a review

Dr. Shefali Gupta[a], Adhi Singh[a*], Shamroz Abrar[b]
[a] Department of Industrial Microbiology, Sam Higginbottom University of Agriculture, Technology and Sciences, Naini, Prayagraj-21007, Uttar Pradesh, India
[b] Department of Molecular and Cellular Engineering, Sam Higginbottom University of Agriculture, Technology and Sciences, Naini, Prayagraj-21007, Uttar Pradesh, India

* aadhisingh621@gmail.com

Abstract:

Antibiotic overuse and their unprocessed disposal are putting the environment and its inhabitants in danger of a catastrophic health emergency. Numerous diverse bacteria and antibiotic-resistance genes are prevalent in the environment, which calls for rapid action in order to effectively remove antibiotics. There are chemical and physical removal techniques, but the production of harmful byproducts has focused the attention of researchers on bioremediation as a sustainable and environmentally benign way to remove antibiotics from the environment. Despite the application of numerous efficient and successful bioremediation techniques, antibiotic residues continue to constitute a serious danger on a global scale. Recent advances in molecular biology may provide an improved method for creating microbe-metabolite biodevices and creating novel strains with desirable traits. This chapter provides an overview of the effects of antibiotics on the environment, the mechanisms through which resistance develops, and several bioremediation techniques.

Keywords: Antibiotic, Antibiotic resistance, Bioremediation

References

1. Apreja, M., Sharma, A., Balda, S., Kataria, K., Capalash, N. and Sharma, P. (2021). Antibiotic residues in environment: antimicrobial resistance development, ecological risks, and bioremediation. *Environmental Science and Pollution Research*, 29(3), pp.3355–3371. doi:https://doi.org/10.1007/s11356-021-17374-w.
2. Danner, M.-C., Robertson, A., Behrends, V. and Reiss, J. (2019). Antibiotic pollution in surface fresh waters: Occurrence and effects. *Science of The Total Environment*, 664, pp.793–804. doi:https://doi.org/10.1016/j.scitotenv.2019.01.406.

Degradation of fungicide Carbendazim using isolated soil bacteria in monoculture and co-culture: A sustainable approach

Moumita Das[a], Sumer Singh Meena[a], Anee Mohanty[a*]
[a]Department of Biotechnology, Dr B R Ambedkar National institute of technology
Jalandhar-144008

* mohantya@nitj.ac.in

Background

Excessive use of Carbendazim for extended periods leads to their accumulation in the agricultural soil, which is further taken by the plants and transfer along the food chain causing serious environmental and health concerns followed by neurotoxicity (Ma et al., 2023), carcinogenicity(Fan et al., 2021), toxicity to aquatic animals(Andrade et al., 2015). Certain soil bacteria has the ability to use these compounds as a carbon source and turn them into non-toxic or less toxic compounds.

Review

Treating Carbendazim contaminated agricultural soil with soil bacteria is a sustainable and eco-friendly approach. In this study isolation of plant growth promoting soil bacteria was done from a field that had received carbendazim treatment. After serial dilution of collected samples in Minimal Salt Media (MSM) with increasing concentration of carbendazim, couple of colonies were isolated. Spectrophotometric analysis and HPLC were done for both of the strains in mono culture and co-culture. Further a few tests were done to check plant growth promoting activity of the isolated strains.

Major findings

In this study it is observed that the degradation activity is higher in co-culture than mono culture and the isolated strains shows different plant growth promoting activity.

Keywords: Carbendazim, Neurotoxicity, Degradation, Spectrophotometric analysis, Co-culture.

References

1. Andrade, T. S., Com, T., Henriques, J. F., Almeida, A. R., Machado, A. L., Koba, O., Giang, P. T., Soares, A. M. V. M., & Domingues, I. (2015). *Carbendazim exposure induces developmental, biochemical and behavioural disturbance in zebrafish embryos*.
2. Fan, R., Zhang, W., Li, L., Jia, L., Zhao, J., Zhao, Z., Peng, S., Yuan, X., & Chen, Y. (2021). Individual and synergistic toxic effects of carbendazim and chlorpyrifos on zebrafish embryonic development. *Chemosphere, 280*. https://doi.org/10.1016/j.chemosphere.2021.130769
3. Ma, X., Chen, X., Hou, H., Liu, D., Liu, X., Wang, P., & Zhou, Z. (2023). Low Dose of Carbendazim and Tebuconazole: Accumulation in Tissues and Effects on Hepatic Oxidative Stress in Mice. *Toxics*, *11*(4). https://doi.org/10.3390/toxics11040326

PI: 95

The Magic of Microbes in Sustainable Plastic Degradation: Nature's Cleanup Crew

Joshi Monalisa[a]

Department of Biotechnology, Dr. B. R. Ambedkar National Institute of Technology
Jalandhar, Punjab-144008, India

*joshimm.bt.22@nitj.ac.in

Background

Due to its low cost and wide range of applications, plastic has evolved from a scientific marvel to a global environmental concern in less than a century. The primary problem is that plastics are disposed of persistently, which puts the environment at risk as they move through habitats and get into food chains.

Review

Conventional disposal techniques, such as landfilling and incineration, are damaging to the environment and not sustainable. Sustainable substitutes, such as microbial breakdown and biodegradable plastics, are now the main focus (Kour et al., 2023). Though the production of bioplastics is more expensive than that of synthetic plastics, there are several benefits, such as environmental sustainability and public acceptance, that make them a good substitute. Plastics would otherwise take hundreds of years to decompose, but microorganisms greatly speed up this process. Using microorganisms extensively is crucial to effectively breaking down solid waste and emphasizes how important they are to the production and disposal of plastics (Venkatesh et al., 2021).

Major findings

This paper mainly investigates how microorganisms use enzymatic processes to break down plastics, offering insights into possible environmentally benign remedies as well as physicochemical degradation techniques.

Keywords: Plastic pollution, microbial degradation, enzymatic degradation mechanism, degradation techniques

References

1. Kour, H., Khan, S. S., Kour, D., Rasool, S., Sharma, Y. P., Rai, P. K., Singh, S., Chaubey, K. K., Rai, A. K., & Yadav, A. N. (2023). Microbes mediated plastic degradation: A sustainable approach for environmental sustainability. *Journal of Applied Biology and Biotechnology*, *11*(3), 9–19. https://doi.org/10.7324/JABB.2023.110515

PI:110

Biochemical fingerprinting of organic compost for edible mushroom production

Pradeep Sahu[a], Vani Mishra[b], Rohit Kumar Mishra[a*]
[a]Centre of Science and Society, IIDS, University of Allahabad, Prayagraj 211002.
[b]Department of Biotechnology, Motilal Nehru National Institute of Technology (MNNIT), 21004, Prayagraj

* rohit_ernet@yahoo.co.in

Background

Agaricus bisporus (J.E. Lange) Imbach and *Pleurotus ostreatus* (Jacq. Ex fr.) P. Kumm is the most widely produced mushroom species for human consumption in the world since it is easily cultivated on lignocellulosic (wheat straw) or agricultural waste generated during cereals harvesting.

Review

In many researches it has been found that addition of organic ingredient can enhance the production and quality of mushroom. Therefore, the main purpose of the present work to enriched the lignocellulosic wastes selected for composting by several organic resources such as brans, seed cake, manures, bacterial bio-fertilizer and weed to formulate new organic compost. Addition of new formulated substrate materials with other combinations can promotes the biological efficiency of mushrooms.

Major finding

To identify the quality of newly formulated organic compost, the ratio of carbon to nitrogen was calculated. The spectroscopic analysis such as GC-MS and ICP-MS of mushroom compost has been carried out to examine quality, maturity and nutritional level of newly formulated compost. GC-MS gives clear representation of chemical composition and compounds while ICP-MS study shows a different level of minerals. The results of different analysis technique show that newly formulated compost is more potent than traditional compost for growth promotion of mushroom species.

Keywords: GC-MS, ICP-MS, organic, weed, composting.

References:

Donini, I. P., Bernardi, E., Minotto, E., & Do nascimento, J. S. (2009). Cultivation of shimejii on elephant grass substrate supplemented with different kinds of bran. *Scientia Agraria*, *10*(1), 67-74.

PI:111

Strategies for the improvement in the production of validamycin A

Ashish Yadav[a], Dr. Rupika Sinha[a*]
[a]Department of Biotechnology, MNNIT Allahabad, Prayagraj-211004, Uttar Pradesh, India

* rupika@mnnit.ac.in

Background

Validamycin is an agricultural antibiotic. It is used to protect crops against certain fungal diseases. It is produced mainly by *Streptomyces hygroscopicus* subsp. *limoneus* and subsp. *jingangensis*(Liao, Wei et al. 2009). Due to its low cost, low drug resistance, and effective control properties, it has broader acceptance in agriculture. Validamycin is a group of eight members from validamycin A-G. In which validamycin A is the main and most active member. So, Validamycin A is the main quality parameter for the commercial formulations of validamycins.

Review

Different attempts have been made to enhance the production of validamycin A, such as adding ethanol, furfural, hydrogen peroxide (H_2O_2), and oxygen carrier in the fermentation medium (Feng, Jiang et al. 2016). Temperature and pH shock-based elicitation approaches have also been studied for the above purpose (Jiang, Sun et al. 2018). The impact of media component concentrations, such as nitrogen, was also assessed using statistical tools. Genetic engineering-based enhancement approaches also have been used for the above purpose. Most of the above studies were conducted at the flask level, except for some reactor-level studies.

Major findings

All the above approaches significantly enhanced the production of validamycin A compared to the control. Among the media modification-based approaches, adding ethanol in the fermentation media resulted in the maximum production of validamycin A, which was 18 g/L (Zhou, Ma et al. 2012). A genetic engineering-based approach resulted in the 22 g/L production of the validamycin A (Zhou, Wu et al. 2011). The nanoparticle and microbial co-culture-based elicitation approach has yet to be used to enhance the production of validamycin A, which can also be used in future studies.

Keywords: Agricultural antibiotic, Fermentation medium, Genetic Engineering.

References:

1.Feng, J., J. Jiang, Y. Liu, W. Li, R. Azat, X. Zheng, W.-W. J. J. o. I. M. Zhou and Biotechnology (2016). "Significance of oxygen carriers and role of liquid paraffin in improving validamycin A production." **43**(10): 1365-1372. doi: 10.1007/s10295-016-1822-y.

2. Jiang, J., Y.-F. Sun, X. Tang, C.-N. He, Y.-L. Shao, Y.-J. Tang and W.-W. J. B. t. Zhou (2018). "Alkaline pH shock enhanced production of validamycin A in the fermentation of *Streptomyces hygroscopicus*." **249**: 234-240. doi: 10.1016/j.biortech.2017.10.012.

3. Liao, Y., Z.-H. Wei, L. Bai, Z. Deng and J.-J. J. J. o. b. Zhong (2009). "Effect of fermentation temperature on validamycin A production by *Streptomyces hygroscopicus* 5008." **142**(3-4): 271-274. doi: 10.1016/j.jbiotec.2009.04.015.

4. Zhou, W.-W., B. Ma, Y.-J. Tang, J.-J. Zhong and X. J. B. T. Zheng (2012). "Enhancement of validamycin A production by addition of ethanol in fermentation of *Streptomyces hygroscopicus* 5008." **114**: 616-621. doi: 10.1016/j.biortech.2012.03.124.

5. Zhou, X., H. Wu, Z. Li, X. Zhou, L. Bai and Z. J. M. e. Deng (2011). "Over-expression of UDP-glucose pyrophosphorylase increases validamycin A but decreases validoxylamine A production in *Streptomyces hygroscopicus* var. *jinggangensis* 5008." **13**(6): 768-776. doi:10.1016/j.ymben.2011.10.001.

PI:117

Ecological assessment of river ghaghara by macrophytes

Prishita Singh[a*], Prateek Srivastava[a]
[a]Department of Botany, University of Allahabad

* prishita_phd2021@allduniv.ac.in

Background

Rivers provide the majority of the world's biodiversity and are crucial to human civilization. However, they are among the world's most threatened ecosystems (Sabater et al., 2013). Biomonitoring is an important approach for assessing and monitoring the health of these ecosystems (Soininen and Könönen, 2004). Macrophytes are commonly employed in river bioassessment because they provide early indicators of eutrophication and organic contamination (Hughes et al. 2012). The goal of this research is to document both short- and long-term ecological consequences on river ecosystems.

Review

Riparian plant communities are associated with ecosystem function and may be examined using biotic indices such as The Macrophyte Biological Index for Rivers (AFNOR 2003), River Macrophyte Index, and riparian forest quality. However, macrophyte indices have only been employed in a few studies, and creating regionally suitable quantitative tools is critical for river ecosystem health.

Major findings

In March 2023, researchers evaluated the water quality and biological variety of aquatic plants in active channels and on the banks of the rivers Ghaghara. The multivariate data was shown using principal component analysis (PCA), and CA was used to identify a cluster of comparable pollution locations dispersed over the river stretch. For Ghaghara, four clusters were identified from the March sample sites, highlighting potential site similarities/dissimilarities. Seventy distinct taxonomic groupings were identified along the Ghaghara. The river's alkaline pH and high levels of dissolved oxygen at several sample points resulted in a large number of macrophytic species. The current study demonstrated the macrophyte potential for ecological evaluation of the Ghaghara River.

Keywords: Biomonitoring, Macrophyte, Ghaghara

References

1. Soininen, J. and Könönen, K., 2004. Comparative study of monitoring South-Finnish rivers and streams using macroinvertebrates and benthic diatom community structure. Aquatic Ecology, 38: 63-75.
2. Sabater S, Elosegi A & Dudgeon D (2013) River conservation: going against the flow to meet global challenges. In: Sabater S, Elosegi A (eds) River conservation: challenges and opportunities. Bilbao, Spain, Fundación, pp 15–38
3. Hughes R.M., Herlihy A.T., Gerth W.J. & Pan Y (2012) Estimating vertebrate, benthic macroinvertebrate, and diatom taxa richness in raftable Pacific Northwest rivers for bioassessment purposes. Environment Monitoring and Assessment 184: 3185-3198.

Water quality evaluation of ghaghara river using multivariate analysis and water quality index

Abhishek Kumar Sharma[a]*, Prateek Srivastava[a]

[a]Department of Botany, University of Allahabad

* abhishek_phd2021@allduniv.ac.in

Background

Ghaghara, plays a crucial role in supporting diverse ecosystems and providing water for agricultural, industrial, and domestic purposes. However, increasing anthropogenic activities and urbanization in the river basin have raised concerns about the water quality. One of the best methods for characterizing the quality of water is the Water Quality Index (WQI), which has been used to describe the acceptability of various water sources for human consumption. WQI makes use of the data on water quality and assists in adjusting the regulations that are developed by different environmental monitoring organizations. This study focuses on the application of the WQI as a comprehensive tool to assess and communicate the overall state of water quality along the Ghaghara River.

Review

Brown et al. produced the water quality index using the Delphi technique by carefully choosing parameters, creating a standard scale, and giving the parameters weights. This index, often known as the NSFWQI, was endorsed by the National Sanitation Foundation (NSF). Due to its thorough nature, it has been referenced in several studies (Brown et al. 1970) monitoring agencies. Multivariate statistical methods have many applications such as classification, modelling and interpretation of large data sets which allow the reduction of dimensionality (Singh et al. 2009, 2013).

Major findings

Principal component analysis (PCA) was used to present the multivariate data and identify gradients across locations. CA was used to identify a cluster of comparable pollution locations scattered over the river stretch. The Ghaghara river water was usually alkaline and increased downstream, although there was no significant geographical variance ($p > 0.05$). The pH value is within the recommended range by BIS for drinking water. The obtained data were standardized and weighted to provide sub-indices for each parameter, which were then aggregated to determine the WQI for each sample point The estimated WQI values were divided into distinct water quality classes like pristine, less polluted, moderate and heavily polluted sites giving a clear picture of the river's overall condition at individual sites.

Keywords: WQI, CPCB, BIS

Reference

1. Brown R. M., McClelland N. I., Deininger R. A. and Tozer R., (1970) “A Water Quality Index”. Do we dare? Water and Sewage Works.
2. Singh, S., et al., 2009. Spatial–Temporal monitoring of groundwater using multivariate statistical techniques in Bareilly district of Uttar Pradesh, India. *Journal of Hydrology and Hydromechanics*, 57, 45 54.doi:10.2478/v10098-009-0005-1

PI: 129

Cross-linked enzyme aggregates: A simple and effective method for hydroxamic acid synthesis using immobilized amidase from *Bacillus smithii* IIIMB2907

Ananta Ganjoo[a, b] and Vikash Babu[a, b]*

[a]CSIR-Indian Institute of Integrative Medicine, Canal Road, Jammu, Jammu & Kashmir 180001, India

[b]Academy of Scientific and Innovative Research (AcSIR), Ghaziabad 201002, India

*vikash@iiim.res.in, Tel.: +91 191-2584999 Ext. 374: fax: +91 191-2586333

Background

Immobilization of enzymes is one of the major techniques used for designing an efficient process for synthesizing industrially important chemicals. Further, for a robust immobilized enzyme to be industrially acceptable it should be stable over a broad range of pH and temperature, tolerant to organic solvents, and reusable[1].

Cross-linked enzyme aggregates (CLEAs) are one such type of biocatalysts wherein crude protein extracts/pure enzymes are precipitated in an aqueous buffer using an agent followed by cross-linking with a bi-functional reagent, usually a dialdehyde such as glutaraldehyde or dextran polyaldehyde[2]. This method over the years has proven to be cost-effective and simple whilst having broad applicability.

Review

Amongst different classes of enzymes, the amidase superfamily has been used in the synthesis of pharmaceutical drugs as it is a versatile biocatalyst[3]. As per literature, different methods have been used such as covalent immobilization on epoxy resin[4], immobilization on butyl sepharose column[5], immobilization by entrapment in polyacrylamide gels, covalent binding on Eupergit C and Amberlite-XAD57[6]. However, these methods resulted in low protein binding and activity. Furthermore, the use of modified resins in turn adds to the cost of the process. Hence, the use of CLEAs has been significant in the present industrial scenario as it significantly enhances the shelf life and operational stability of the enzyme. CLEAs also help in making the process cost-efficient with easy recovery and reusability[7, 8].

Major findings

The present study focuses on the development of an efficient process for the large-scale synthesis of hydroxamic acids using immobilized cell-free extract of *Bacillus smithii* IIIMB2907. Further, optimum conditions for immobilization were observed and validated using one factor at a time analysis and response surface methodology based on the Box-Behnken design of experiments. Cell-free extract of *Bacillus smithii* IIIMB2907 was immobilized by physical aggregation of the enzyme using 5% precipitant i.e., bovine serum albumin, followed by chemical cross-linking with 0.8% glutaraldehyde to form insoluble CLEAs at 7 pH. This method was also successfully scaled up from 0.75 mL reaction to 1 L enzyme reactor for subsequent cycles wherein, maximum acyl-transferase activity of 26.22 U was observed.

Keywords: Amidase, *Bacillus smithii*, Immobilization, Glutaraldehyde, Bovine serum albumin

PI:130

The human health risk implications by the heavy metals and polycyclic aromatic hydrocarbons among the residing population nearby Gomti River, Lucknow, India

Neha Gondial* and Sandhya Bharti
[a]Fish Physiology and Ecotoxicology Laboratory, Department of Zoology
Babasaheb Bhimrao Ambedkar University, Lucknow, Uttar Pradesh, India

*nehagondial06@gmail.com

Abstract

The study is determined about the health risk assessment of human beings along the river Gomti around the stretch of 30 km in state capital Lucknow, India. The river water samples were collected as per APHA-AWWA (2008) from the five equidistant sites Ghaila Pul, Mehndi Ghat, Shaheed Smarak, Kukrail Junction, Bande Dam for the analysis of the eleven heavy metals (Al, Cr, Fe, Co, Ni, Cu, Zn, As, Mo, Cd, Pb and sixteen aromatic hydrocarbons Naphthalene, Acenaphthylene, Fluorene, Acenaphthene, Phenanthrene, Anthracene, Fluoranthene, Pyrene, Benzo(a)anthracene, Chrysene, Benzo (k) fluoranthene, Benzo(b) fluoranthene, Benzo (a) pyrene, Dibenzo (ah) anthracene, Indeno(1,2,3-cd)pyrene, Benzo(g,h,i) perylene through ICP-MS and GC/MS respectively. The concentrations of these factors were compared with BIS (2012) and USEPA .The health risk assessment implications were applied to calculate the potential risk of carcinogenic and non-carcinogenic factors. The ingestion and dermal pathways were selected for the exposure among children and adult population for the evaluation of the potential carcinogenic risk among them. The study found that the children were more susceptible through ingestion pathway rather than the adults in dermal pathway and the fifth site was highly contaminated of the Gomti River in Lucknow.

Keywords: PAHs, heavy metals, health risk assessment, carcinogenic and non-carcinogenic risk

PI: 134

Petroleum hydrocarbon degradation using microbial strain: A Review

Anmol Kumari[a], Dr. Anjana Pandey[a*]

[a*]Department of Biotechnology, Motilal Nehru National Institute of Technology Allahabad (MNNITA), Prayagraj U.P. 211004, India

*anjanap@mnnit.ac.in

Background

One of the serious issues of environmental pollution is petroleum hydrocarbon degradation. Petroleum hydrocarbons are a group of chemicals that contains toxic compounds for human and the environment as the compounds will retain in the environment for a very long time. These chemicals belong to the family of neurotoxic and carcinogenic organic compounds. Oils spills mainly deplete the quality of water bodies in which the ground water and the marine water is affected which results in disturbance of the marine environment.

Review

Microorganisms such as bacteria, yeast and fungi are reported in the degradation of petroleum hydrocarbon aerobically. The most frequently isolated bacteria from hydrocarbon contaminated environment is*Pseudomonas* among the other hydrocarbon utilising bacteria. The sources of petroleum hydrocarbons in the environment are automobile workshops, petrol bunks, crude oil refinery, car washing garages etc. In order to minimise the effect of petroleum hydrocarbon their degradation is important. The removal of hydrocarbons contaminants can be done by physical and chemical method but their effect is limited and costly also. Therefore, cost effective and sustainable approach is necessary in the degradation of petroleum hydrocarbons by the biological means in which microorganisms are used to degrade the hydrocarbons which include bacteria, yeast, fungi and algae. At the last of this review article different techniques are also mentioned that are used in the biodegradation of petroleum hydrocarbon contaminants. Techniques play important role in the identification of degraded compounds.

Major findings

Different strains of ***Pseudomonas***such as *P. fluorescens* AB56, *P. putida* AB58, *P. aeruginosa* AB11, *P. putida* AB67, *P. alcaligenes* AB 44 and *Bacillus subtilis* have the potential to degrade the petroleum hydrocarbon and it is confirmed by various techniques such as FT-IR, GC-FID, HPLC etc.

Keywords: Petroleum hydrocarbon, neurotoxic, carcinogenic, sustainable approach, degradation, cost- effective.

References:

1. Darsa, K. V., Thatheyus, A. J., &Ramya, D. (2014). Biodegradation of petroleum compound using the bacterium Bacillus subtilis. Science International, 2(1), 20-25.
2. Tanti, B., &Buragohain, A. K. (2013). Biodegradation of petroleum tar by Pseudomonas Spp. from oil field of Assam, India. Bioremediation journal, 17(2), 107-112.
3. Ravi, A., Ravuri, M., Krishnan, R., Narenkumar, J., Anu, K., Alsalhi, M. S., ...&Rajasekar, A. (2022). Characterization of petroleum degrading bacteria and its optimization conditions on effective utilization of petroleum hydrocarbons. Microbiological Research, 265, 127184

PI: 147

Preventing hazardous impact of stone dust incorporating environment friendly solution

Shivendra Singh Chauhan [a], Kumar Venkatesh[a], Utkarsh Deep Kamal[a,*]
[a]Department of Civil Engineering, Motilal Nehru National Institute of Technology
Allahabad, Prayagraj-211004, UP, India

*utkarsh.2022ge12@mnnit.ac.in

Background

When stone dust (SD) is discarded into the environment without treatment, it poses several difficulties. This waste is one of the leading sources of a variety of health risks. Proper waste disposal or utilization in other remediation measures can only eliminate risks in the environment.

Silty soils (SS) pose some issues inconstruction because of the low bearing capacity. This can be overcome with the use of stone dust.

Review

To improve the qualities of SS, an array of SD must be introduced to the soil, which prepares the way for soil property augmentation. Diverse waste elements such as bottom fly ash, rice straw ash, and baggase ash have shown increase in the distinctive qualities of soils. This report presents an examination of laboratory experiments conducted on stone dust (SD) in silty soil.

Major findings

A series of experiments were carried out by increasing the proportion of SD from 6% to 24%, with each increase of 6%. Based on the results, it was discovered that the unconfined compressive strength (UCS) of SS increased, and the optimal quantity of SD was 18%.

Keywords: Silty soil, Stone dust, Unconfined compressive strength

References:

Chauhan SS, Venkatesh K (2023) Stabilizing clayey soil in subgrade with waste ash. Natl. Acad. Sci. Lett.

PI: 156

Unveiling the Protective Role of exogenously supplied Si and NO in Alleviating Chromium Stress in *Brassica juncea*

Samarth Sharma[a], Shivesh Sharma[a,*]
[a]Department of Biotechnology, Motilal Nehru National Institute of Technology Allahabad,
Prayagraj, 211004, UP, India

*siveshs@mnnit.ac.in

Background

Hyperaccumulation of heavy metal in agricultural land has hampered yield of important crops globally. It has consequently deepened concerns regarding the burning issue of food security in the world. Among heavy metals, Chromium (Cr) is not needed for plant growth and found to pose detrimental effects on plants. Present study highlights the role of exogenous application of sodium nitroprusside (SNP, exogenous donor of NO) and silicon (Si) in alleviating detrimental ramification of Cr toxicity in Brassica juncea.

Review

NO is gaseous transmitter molecule which regulates cell signaling. Various studies has proved that it improves plant growth under abiotic stress by enhancing antioxidant defence system of plants (Singh *et al.*, 2016; Khan *et al.*, 2021; Sharma *et al.*, 2023) and boosting photosynthesis (Khan *et al.*, 2021; Ahmad *et al.*, 2021). Similarly, Si helps in improving tolerance among plants against various stresses (Ashfaque *et al.*, 2017; Vishwakarma*et al.*, 2020; Khan *et al.*, 2022). Si alleviates metal toxicity (Sena*et al.*, 2022) as it immobilizes and chelates metal present in soil to reduce its bioavailability, thereby restricting its uptake and subsequent transfer to shoots. Although the role of Si and NO have been investigated by researchers for growth promotion under Cr stress, but the synergistic effect of combined application of Si and NO on plants under stressful conditions is not well documented. Also, there is no study available which investigates the synergistic role of Si and NO in mitigating Cr stress in *Brassica juncea.*

Major findings

The exposure of *B. juncea* to Cr (100 µM) under hydroponic system hampered the morphological parameters of plant growth like length and biomass and physiological parameters like carotenoid and chlorophyll contents. It also resulted in oxidative stress by disrupting the equilibrium between ROS production and antioxidant quenching leading to accumulation of ROS such as hydrogen peroxide (H_2O_2) and superoxide ($O_2^{\bullet -}$) radicle which causes lipid peroxidation. However, application of Si and SNP both individually and in combination counteracted oxidative stress due to Cr by regulating ROS accumulation and enhancing antioxidant metabolism. As the alleviatory effects were more pronounced in plants treated with combined application of Si and SNP; therefore, our findings suggest that dual application of these two alleviators can be used to mitigate Cr stress.

Keywords: Heavy metal, stress, antioxidant, ROS, gene expression

References:

1. Ahmad, A., Khan, W. U., Shah, A. A., Yasin, N. A., Naz, S., Ali, A., ... &Batool, A. I. (2021). Synergistic effects of nitric oxide and silicon on promoting plant growth, oxidative stress tolerance and reduction of arsenic uptake in *Brassica juncea*. Chemosphere, 262, 128384.

PI:162

Phytochemical analysis and Antibacterial activity of *Terminalia bellirica* leaf extracts

ShivangiSingh*, Jalaj Kumar Gour

Department of Biochemistry, Faculty of Science, University of Allahabad, Prayagraj-211002

*shivangisinghvns2018@gmail.com,jalaj19biochem@gmail.com

Background

Plants have been a key component of traditional medicine for ages due to their therapeutic properties. Antimicrobial resistance is major issue in India. Bahera or *Terminalia bellirica*has been reported to havemedicinal properties and with this in mind we have worked on the plant to investigate its antibacterialactivity.

Review

Plant extracts have shown antibacterial activities against avariety of bacteria responsible for diseases. Bacteria not only cause significant damage to humans as pathogens but also cause losses via food spoilage (1). The plant extracts contain phytochemicals in it and these phytochemicals can be responsible for the activities such as antimicrobial, and antioxidant activities (3).

Majorfindings

The extracts prepared with solvent -Petroleum ether, ethyl acetate and methanol has shown positive results for presence of different phytochemicals. The plant extract was tested for its activity against different bacteria at varying concentrations and it has shown that *Terminalia bellirica*can inhibit the bacterial population. Further investigation of extract–microbial relationship can tell us more about the action of plant extract on bacterial population.

Keywords: ***Terminaliabellirica*, Plantextract, Antibacterial, Phytochemical.**

References:

1. Gonelimali FD, Lin J, Miao W, Xuan J, Charles F, Chen M, Hatab SR. Antimicrobial Properties andMechanismofActionofSomePlantExtractsAgainstFoodPathogensandSpoilageMicroorganisms.Front Microbiol.2018Jul24;9:1639.

2. BalouiriM,SadikiM,IbnsoudaSK.Methodsforinvitroevaluatingantimicrobialactivity:Areview.JPharmAnal.2016Apr;6(2):71-79.

3.SaeedN,KhanMR,ShabbirM.Antioxidantactivity,totalphenolicandtotalflavonoidcontentsofwholeplant extractsTorilisleptophyllaL.BMC ComplementAlternMed.2012Nov16;12:221.

PI: 184

Biological treatment of pharmaceutical compound: Pure vs Mixed culture

Rishu Kumari Singh[a*], Y.V.Nanchariah[b], Joyabrata Mal[a]
[a]Department of Biotechnology (Motilal Nehru National Institute of Allahabad- 211004, Teliyarganj, Prayagraj, Uttar Pradesh)
[b]Water and Steam Chemistry Division (BBPS, BARCF Kalpakkam-603102, Chengalpattu, Tamil Nadu)

*rishu.2023rbt14@mnnit.ac.in

Abstract

Pharmaceutical compounds (PCs) are chemicals used in human and veterinary medicine to prevent or treat various health conditions. Commonly types of PCs include antibiotics, anti-inflammatories, analgesics, antidepressants, antiepileptics, lipid-lowering drugs, β-blockers, antiulcer drugs, and antihistamines. However, their environmental impact is a growing concern due to their widespread use, unregulated discharge, inefficient removal system. They can easily pass through cellular membranes and remain active in the environment for long time and potentially harm to non-target organisms. (Guo, Qi, & Liu, 2017). Hence, it is important to a have effective treatment technology for PC-laden wastewater.

PC-laden wastewater can be treated by physio-chemical or biological treatment. However biological methods involving biosorption and/or biodegradation of PCs are getting more popular than physio-chemical methods for their effectiveness, sustainability, and economic benefits. Although various biological treatment techniques are employed, including pure culture and activated sludge process, but moving bed biofilm reactor, membrane bioreactor, up-flow anaerobic sludge blanket (USAB) reactor, aerobic granular sludge (AGS) system is getting more attention in PC-laden wastewater treatment system (Saidulu, Gupta, Gupta, & Ghosal, 2021).

Several strains of *Streptomyces spp.*(MIUG 4.88, MIUG 4.89, SNA, LP1 and LP2) were tested for their ability to biodegrade PCs such as Carbamazepine (CBZ), Sulfamethoxazole (SMX), sulfadiazine (SD), sulfamethazine (SMT), 17α Ethinylestradiol, and 4-nonylphenol. Out of 19 tested strains, only two CBZ-tolerant strains (MIUG 4.89 and SNA) were able to remove 35% of CBZ (Popa et al., 2014). *Acinetobacter sp.* shows biodegradation of SMX, SD, and SMT. However, while mineralization of SMX was 99%, for SD (17%) and SMT (20%) it was significantly poor (Wang, Hu, & Wang, 2018).

AGS in Sequencing Batch Reactor (SBR) systems can remove antibiotics from wastewater, but reports on their effectiveness is limited. In a lab-scale system, increasing biomass concentration improved removal efficiency from 82% to 90%. AGS can degrade 17α Ethinylestradiol and 4-nonylphenol, but removal of CBZ was minimal.({Kent, 2019 #93}). Initially, adsorption is the primary removal mechanism, but degradation rates improve as the sludge acclimatizes to 17α Ethinylestradiol, 4-nonylphenol, and CBZ. The PCs also had minimal effect on the AGS's removal capabilities of COD, nitrogen, or phosphate.

Studies aims to develop an understanding of the effects of sulfamethoxazole–erythromycin–tetracycline (ETS), sulfamethoxazole–tetracycline (ST), erythromycin–sulfamethoxazole (ES) and erythromycin–tetracycline (ET) combinations on the anaerobic treatment of pharmaceutical industry wastewater. Bacteria had a competitive advantage over archaea under all antibiotic combinations. The ET combination showed better performance compared to the other reactors. However, antibiotic concentrations strongly affected the microbial community and its composition which might impact the overall wastewater treatment efficiency {Aydın, 2015 #96}.

Although, biological treatment of PC-laden wastewater are still limited, using only pure cultures does not accurately reflect the behavior of microorganisms in natural environments where different types of bacteria work together to break down hydrocarbons (Cerqueira et al., 2011).

Keywords: Pharmaceutical compounds; Wastewater treatment; Biological treatment.

PI: 185

Phytoremediation of industrial waste water using a constructed wetland

AkhilPandey[a], Radha Rani[a]*

[a]Department of Biotechnology, Motilal Nehru National Institute of Technology Allahabad,
Prayagraj 211004

Background

The growing industrialization is a major concern nowadays because the effluents of industrial waste contain variety of contaminants like heavy metals, chemicals, toxins, and hazardous material which poses a serious challenge to environmental management (Guittonny-Philippe, et al 2015). This study reviews the potential of constructed wetlands (CW) for the removal of toxic pollutants from industrial waste water In an eco-friendly and sustainable manner.

Review

Some of the important factors affecting the performance of a CW for removal of BOD, COD and toxic pollutants include, the design, flow pattern, substrate composition, macrphytic species used and the microflora of the complete ecosystem. Furthermore, it is imperative to assesses the ecological impact and long-term sustainability of CWs as a phytoremediation process, taking into account variables like plant health, biodiversity, microbial diversity, and the resilience of the wetland ecosystem as a whole (Hassan et al. 2021).

Major findings

Application of phytoremediation techniques in artificial wetlands has shown a remarkable potential for effective removal of organic chemicals, heavy metals, and other contaminants commonly found in industrial effluent. Several wetland plants are well reported hyperaccumulators, and many of them, have significant capacity for absorbing and transforming pollutants. An artificial wetland not only can be used for waste water treatment but also it offers an eco-friendly, economic and aesthetic solution for the same along with an advantage of landscape beatification.

Keywords: Phytoremediation, artificial wetland, heavy metal, macrophytes, contaminants

Reference:

1. Hassan I, Chowdhary S, Prihartato P, Razzak S, (2021), Wastewater Treatment Using Constructed Wetland: Current Trends and Future Potential, Processes 9(11), 1917.
2. Guittonny-Philippe, A., Petit, M.E., Masotti, V., Monnier, Y., Malleret, L., Coulomb, B., Combroux, I., Baumberger, T., Viglione, J. and Laffont-Schwob, I., 2015. Selection of wild macrophytes for use in constructed wetlands for phytoremediation of contaminant mixtures. *Journal of environmental management*, *147*, pp.108-123.

PI: 187

A Case Study on Fly Ash Utilization for Sustainable Environment

Apratim[a*], Rakesh Chandra Vaishya[b]
[a]Department of Civil Engineering, Motilal Nehru National Institute of Technology Allahabad, Prayagraj-211004, UP, India
[b]Department of Civil Engineering, Motilal Nehru National Institute of Technology Allahabad, Prayagraj-211004, UP, India

*apratim.2022en03@mnnit.ac.in

Background

Combustion of coal in coal fired power plant results into generation of Fly ash. Particularly it is the residual part after burning of coal. Fine particles that can be termed as suspended matter generated with flue gasses are collected in filter bags or Electrostatic precipitators. Ash has special property that it will not burn further decomposition or by-product is not possible.

Review

A case Study is carried out on the generation and utilization of Fly ash from LANCO Thermal Power Plant Anpara, Uttar Pradesh. A detailed analysis was done on the effects of fly ash formation in the surrounding areas and its control on sustainable Environment.

Major findings

The total generation of Ash is 1704199MT in which, 1363359 MT is fly Ash. The current utilization is just 11.67%.

Form this study it is concluded that

1. The area of ash pond is lower as 380 Ha is combined with UPRVUNL. So LANCO group need to increase ash pond area.
2. Mine fills have potential or capacity to consume large quantity of Fly ash.
3. Indian fly ash is alkaline in nature so it improves the quality of soil by reducing acidity of soil and increasing the yield in terms of grain and fodder.

Keywords: Fly ash, Sustainable Environment, Ash Pond.

References:

1. Lokeshappa, B., and Dikshit, A.K., 2011, Disposal and management of coal fly ash, Proc. ICLST, 11-14

PI: 194

Production, Characterization & Kinctics of patially purified laccase from *Pleurotus Citrinopileatus* and its application in Bioremediation of Azo Dyes

Ankita Kushwaha[a], M.P. Singh[b,*]

[a]Centre of Biotechnology, Nehru Science Centre, University of Allahabad
[b] Centre of Biotechnology Nehru Science Centre, University of Allahabad

*eshacompact15@gmail.com

Background

In the present investigation the efficiency of laccase (benzene-diol:oxygenoxidorductase, EC1.10.3.2) from *Pleurotus citrinopileatus*assessed for the decolorization of azo dyes.

Review

Laccase has been partially purified by using 80% ammonium sulphate solution.

Major findings

Total activity, total protein, specific activity and purification fold for the partially purified laccase were found to be 40.38 U, 293.33mg/100ml, 0.91U/mg and 2.84 respectively. The pH, temperature optima of laccase were 5.0 and 50 ºC respectively, while the enzymes was most stable at pH 4.0 and temperature 30ºC, when exposed for one hour. The Km of the partially purified laccase for substrate guaiacol, DMP (2, 6 dimethoxyphenol) and syringaldazone (3,5 dimethoxy-4 hydroxybenzaldehyde azine) were 60,95,26 respectively. This laccase has been tested for the use in the bioremediation of azo dyes in the absence of mediator molecule. Dye namely Congo red was tested More than 80% decolorization was observed within half and hour and their lower Km value indicates that efficiency of the enzymes is very high. The results were promising due to quicker decolorization in the absence of mediators that it can be used as a valuable biocatalyst for quick bioremediation of azo dye.

Keywords: Laccase, Azo dye, *Pleurotus citrinopileatus,* decolorization, bioremediation, Congo red

References

1. Coll, M.P., Fernandez-Abalos, J.M., Villanueva, JR., San tamaria, R. and Perez, P. (1993) Purification and characterization of phenoloxidase (Laccase) from the lignin— Degrading basidiomycete PM I (CECT 2971). Applied Environmental Microbiology, 59, 2607-2613.
2. Dhawan S, Lal R &Kuhad R.C. eEthidum bromide stimulated hyperlaccase production from birds nest fungus *Cyathusbulleri*. Letters in Applied Microbiology. 2003, 36:64-67.
3.Lowery O.H. ,RosebroughN.J.,Farr A.L.& Randall R,J. Protein measurement with the folin phenol ragent. Journal of Biological Chemistry.1951, 193: 265-275.
4. Sahay R., Yadav R.S.S. & Yadav K.D.S. Purification and Characterization of laccase Secreted

Assessment of Land Use Land Cover and Environmental Indicators of Ghaghara River

Amit kumar Pandey, H.K. Pandey, R.P. Singh
Department of Civil Engineering, Motilal Nehru National Institute of Technology
Allahabad, Prayagraj-211004, UP, India.

*amit.2022en05@mnnit.ac.in

Background

Ghaghara river is a trans boundary river which originates near Lake Manasarovar in TibetanPlateau. It joins the Sharda River in India at Brahma Ghat after travelling through theHimalayas in Nepal. Himalaya having the no tributaries and joining river Ganga in Bihar. Itlies between 25◦ 30′ 00" N to 31◦00′ 00" N latitude and 79◦30′ 00" E to 85◦00′ 00" E longitudewith a catchment area of 1,27,950 Km2 with 900 mm to 1400 mm annual precipitation.

Review

During rapid urbanization and industrialization in the catchment area of Ghaghara River theland use has been changed. The Ghaghara River is one of the largest tributaries of the GangaRiver by volume and it provides livelihood for several people in districts of the states of UttarPradesh and Bihar. The impact of this change has been observed with the help of remotesensing techniques and using Landsat-8 data on the vegetation, soil water content andchlorophyll content.

Major finding

The dynamic of these changes has been evaluated and comparison has also been made betweenyear 2014 and 2018. The result of the study reflects that from year 2014 to 2018 healthy anddense vegetation has decreased barren land area has increased. The water content in the regionhas also decreased and built-up area has increased over a period. The chlorophyll – aconcentration of the basin has also decreased from 2014 to 2018.

Keywords: Ghaghara River, LANDSAT- 8, Remote sensing technique.

References:

1. Mohan, R. (2018). Ghaghara River System—Its Current Status and Value to Society. In: Singh, D. (eds) The Indian Rivers. Springer Hydrogeology. Springer, Singapore. https://doi.org/10.1007/978-981-10-2984-4_12

PI: 208

Pharmaceutical compound distribution and impact on health and environment

Priti Kumari, Rupika Sinha, Joyabrata Mal
Department of Biotechnology, Motilal Nehru National Institute of Technology Allahabad,
Prayagraj 211004, India
*priti.2022bt07@mnit.ac.in

Background

The increasing concentration of pharmaceutical compounds (PhCs) in environment is a growing concern that has serious implications for both environmental and public health. The presence of PhCs in water bodies is primarily attributed to the discharge of untreated or inadequately treated wastewater from various sources, including pharmaceutical manufacturing units, hospitals, households, and agricultural runoff.It is evident that the harmful effects of medications on aquatic organisms because of their long-lasting, persistent, and bioaccumulative character, and nonaquatic habitat. The misuse of medications in people and pets has resulted in a number of noteworthy side effects, one of which is an increase in the resistance of microorganisms to various antibiotics.

Review

Various PhCs have been excessively used and released into the environment without any rule, causing significant negative effects on the environment and individual health systems. They are increasingly being identified as Contaminants of Emerging Concern. Over 600 APIs or their byproducts have been found in surface water, sewage effluent, ground water, and soil samples in more than 71 nations worldwide Li WC et.al(2014). To predict the effects of medications on biological systems and the environment, regulatory authorities recommend using in silico approaches such as QSAR to reduce time, cost, and animal use associated with toxicity prediction. Howard and Muir used QSAR models to examine the persistent and bioaccumulative (PB) characteristics of medications.

Major findings

Recently, 98 various PhCs were found in various water matrices (treated wastewater, surface water, and groundwater) in India sengaret al.(2016)Although, they were not found risk to human health due to low concentration, but 8% of them can cause high ecological risk. Importantly, PhCs have been found in different river streams as well including Cauvery, Yamuna, etc. and it also found to be meteorological dependent. For example, pre- and post-monsoon surface waters of the River Cauvery shown different concentration of PhCs with avegare concentrations were (ng/L): CBZ (205.62) > CAF (114.09) > DCF (28.51) >speaker
CIP (25.23) > ATL (18.86) > IPL (13.91) (). suggesting that the distribution of PhCs in rivers poses significant risks to both human health and the aquatic life. Although, the hazardous quotient of some PhCs present in the river samples showed no acute toxic effect to aquatic organisms due to low concentration, the same could lead into the chronic toxicity to the aquatic organisms and human health as the river water in India is used for major drinking water resource in various region which necessitate the for tighter regulation and development of suitable treatment system of PhCs-containing wastewater.

.

References:

1. Roy K, Kar S (2016) In silico models for ecotoxicity of pharmaceuticals.
2. Taylor D, Senac T (2014) Human pharmaceutical products in the environment – the “problem” in perspective.

Biochar – a sustainable approach to environmental applications

Prashant Yadav[a], Joyabrata Mal[a]
[a]Department of Biotechnology, Motilal Nehru National Institute of Allahabad- 211004, Teli-yarganj, Prayagraj, Uttar Pradesh

*prashant.2023rbt03@mnnit.ac.in

Background:

This review delves into the intricate world of biochar, a carbonaceous material produced from diverse organic waste like agricultural residues and municipal sewage sludge which plays a significant role in achieving resource recovery and sustainability. Recognizing its significant potential, it meticulously examines biochar's preparation, characterization, modification and multifaceted environmental applications through a comprehensive analysis of over 100 recent scientific publications (Amalina et al. 2023)

Review:

The physicochemical properties of biochar display significant heterogeneity, primarily driven by the nature of the feedstock employed. Common preparation techniques include pyrolysis, gasification, and hydrothermal carbonization, each yielding biochar with distinct characteristics (Jiao et al. 2021). To fine-tune biochar properties for specific environmental contexts, various modification techniques are implemented, such as acidification, alkali activation, and metal ion impregnation. These strategies enable targeted manipulation of surface area, porosity, and functional groups, ultimately influencing biochar's adsorption, catalysis, and ion exchange capacities.

Biochar presents remarkable potential for a range of environmental applications and sustainable development, including soil remediation and as biofertilizer, carbon sequestration, wastewater treatment, and also as catalystdue to its unique properties (Mona et al. 2021). In soil remediation, its ability to adsorb pollutants and enhance soil fertility is being explored with great interestfor sustainable agriculture. As a carbon sink, biochar also contributes to greenhouse gas mitigation by locking away atmospheric carbon in soil. In wastewater treatment, its porous structure and surface functionality facilitate the removal of organic and inorganic contaminants via adsorption. Additionally, biochar demonstrates promising catalytic activity for the degradation and removal of various toxic organic pollutants.

Major findings:

Despite these advancements, further research is crucial to elucidate the impact of biochar on soil microbial communities, particularly its potential disruption of delicate ecological balances. Mitigating potential environmental risks associated with biochar, such as heavy metal leaching, necessitates thorough investigation. Moreover, unraveling the intricate mechanisms underpinning biochar's catalytic properties is essential for optimizing its effectiveness in environmental remediation processes.

Keywords: Biochar, soil fertility, agriculture, waste management, sustainable development

References:

Amalina, F., Krishnan, S., Zularisam, A. W., &Nasrullah, M. (2023). Pristine and modified biochar applications as a multifunctional component towards a sustainable future: Recent advances and new insights. *Science of The Total Environment*, 169608.

Jiao, Y., Li, D., Wang, M., Gong, T., Sun, M., & Yang, T. (2021). A scientometric review of biochar preparation research from 2006 to 2019. *Biochar*, *3*(3), 283-298.

Mona, S., Malyan, S. K., Saini, N., Deepak, B., Pugazhendhi, A., & Kumar, S. S. (2021). Towards sustainable agriculture with carbon sequestration, and greenhouse gas mitigation using algal biochar. *Chemosphere*, *275*, 129856.

PI:210

Nano-perspective on the eco-nanotoxicity and cyto-nanotoxicity of microalgae: a review

Rajnandini Srivastava[a], Dr. R.C. Mishra[b], Dr. Chitranshu Srivastava[c]
[a,b]Mahakaushal University, Jabalpur, Madhya Pradesh, India 482001
[c]Senior Scientist Reliance Life Sciences, Mumbai, India
*r.srivastava2208@gmail.com

Algae, the primary in food chain, living in submarine terrain effectively sequesters carbon dioxide and produces 50 % of earth's oxygen, and are largely susceptible to nanoparticles (NP) which are discharged into submarine ecosystem by different human activities leading to its accumulation in food chains and dangerous consequences in submarine foliage and fauna. The toxin situations and impacts on numerous submarine species may vary from one NP to another. The commerce of algae with NP affects its morphological, physiological, biochemical, reproductive and inheritable character. Algae's capability to biosorb nano- essence and drop metallic ions makes it a better competitor for nanoparticles biosynthesis. This review has tried to epitomize the nano- perspective of the ecotoxicological and cytotoxicological impact of nanoparticle and chromatic factors like finagled nanoparticles (ENPs) in submarine terrain, natural organic matter (NOM), circumscribing agents etc. This review has also discussed toxic impacts of nanoparticles on algal blooms and their appearances acts as biomarkers. Further, on the base of response patterns, we tried seeking to some positive perceptivity regarding the recrimination of the nexus formed between nanoparticle and microalgae to develop sustainable nanotechnology in submarine terrain.

Keywords: Nano-Particle (NP), Micro algae, eco-nanotoxicity, cyto-nanotoxicity

Session-7

Biotechnological Intervention in Biomedical and Health

PI: 3

Therapeutic Potential of Rutin against Breast Cancer: An in vitro and in-silico study

Anchal Dubey[a], Bechan Sharma[a*]

[a]Department of Biochemistry, UniversityofAllahabad, Prayagraj, India

*dbanchal@gmail.com

Background

Breast cancer is the commonly diagnosed cancer in females. The treatment by the present chemotherapeutic drugs is accompanied by lots of adverse side effects. The role of phytochemicals as potential chemotherapeutic agent has been in investigation for a long time. Here property of one such beneficial phytochemical, rutin is explored as potent anti-breast cancer agent. Here in vitro anti- proliferative activity against breast cancer cell line is evaluated. This in-vitro study is followed by the in-sillico docking study of the rutin against the breast cancer proteins, estrogen receptor alpha (ER), cell division protein kinase 6 (CDK6) and protein kinase B (AKT1)

Review

According to World Health Organization, Breast Cancer is the most leading cancer in women all over the world (1). BC is generally a hormone dependent cancer, because of the involvement of sex steroid hormones such as estrogen and progesterone and also their respective nuclear receptors (NR) such as estrogen receptor (ER) and progesterone receptor (PR), which are the most important biomarkers for BC (2). The hyper production of estrogen is one of the leading causes for the development of breast cancer. Out of different protein kinases, overexpression of cyclin-dependent kinases (CDKs) is associated with the majority of cancer types, and thus, identification and establishment of CDKs targeted inhibitors become an attractive approach for cancer therapy (3).

Major findings

Effect of rutin on breast cancer cell line was found to be dose dependent. Rutin treated MCF-7 cells when observed under a phase contrast microscope demonstrated the cells to appear compact and shrunken which could be due to the nucleus shrinkage, chromatin condensation or blebbing. The IC50 of the rutin was observed at 51 µM. In sillico calculation of AKT1 was conducted by using two standard drugs Iptasertib and tamoxifen, both of which shows strong interaction with active site of protein. Rutin shows strongest interaction with the formation of several hydrogen bonds and glide score of -9.217 Kcal/mol.. The breast cancer protein estrogen receptor alpha was also docked with two standards Tamoxifen and Lasofoxifene which forms 1 and 3 hydrogen bonds respectively. Rutin again shows the strongest interaction with the ER protein with formation of 4 hydrogen bonds with a glide score of -

10.15 Kcal/mol. A similar pattern was observed in CDK6, where the strongest interaction with the protein was demonstrated by which forms 5 hydrogen bond with ASP 163, LYS 147, ASP 104, ASP 102 and GLU 99. The standard drug used here are Abemaciclib which forms 3 hydrogen bonds only. The result of this study demonstrates the anti-cancer potential of Rutin in treating MCF-7 breast cancer line, which is univasive and have functional estrogen receptor as well as EGF receptor. The in-sillico study also demonstrates the strong interaction between rutin and breast cancer proteins. Thus rutin can be potentially used as the novel drug against the estrogen receptor mediated breast cancer. Its efficacy can be examined further in an in vivo model.

Keywords: Breastcancer, Rutin, Molecular docking

References:

[1] Benson JR, I J (2012). The global breast cancer burden. Future Oncol, 8, 697-702

[2] Sever R, Glass CK (2013). Signaling by Nuclear Receptors. Cold Spring Harbor Perspectives Biol.

PI: 13

Methyl linolenate exhibit cathepsin B inhibition and anti-inflammatory activity by downregulating p65 expression in SW982 cells

Sabita Rangra[a], Prachi Agnihotri[b,c], Sagarika Biswas[b,c], Kamal Krishan Aggarwal[a]*
[a]University School of Biotechnology, Guru Gobind Singh Indraprastha University
Dwarka, Sector 16-C, New-Delhi-110078, India.
[b] Council of Scientific & Industrial Research (CSIR)-Institute of Genomics and Integrative Biology, Mall Road, Delhi University Campus, Delhi, India,110007
[c] Academy of Scientific and Innovative Research (AcSIR), Ghaziabad-201002, India
*kkaggarwal@ipu.ac.in

Abstract

Plant secondary metabolites have been characterized for their therapeutic relevance in diseases as arthritis, inflammation, cancer and many more. Therefore, they are suggested as an alternative in development of therapies to improve living quality of rheumatoid arthritis (RA) patients. Rheumatoid arthritis is associated with high expression of cathepsin B in joint synovial fluid and hence has been considered as target molecule to control RA. In the present study methyl linolenate identified from banana peel has been studied for its anti- cathepsin B and anti-inflammatory activity. The compound inhibited cathepsin B with an IC_{50} value of 282.9 nmoles in-vitro and turned out to be a mixed type inhibitor of cathepsin B as revealed by Line- weaver Burk plot. Inhibition constant (K_i) was calculated as 149.53 nmoles using Dixon plot. The effect of methyl linolenate on inflamed SW982 cell lines resulted in lower expression of p65 indicating it as a potential anti-inflammatory agent. These results support the anti-cathepsin B and anti-inflammatory effect of methyl linolenate and possibility of its therapeutic role in the treatment of RA.

Keywords: plant secondary metabolites, methyl linolenate, cathepsin B inhibition, anti-inflammatory

References

[1] Santiago, Luis Ângelo Macedo, et al. "Flavonoids, alkaloids and saponins: Are these plant-derived compounds an alternative to the treatment of rheumatoid arthritis? A literature review." *Clinical Phytoscience* 7.1 (2021): 1-10.

[2] Hashimoto, Yoko, et al. "Significance of cathepsin B accumulation in synovial fluid of rheumatoid arthritis." Biochemical and biophysical research communications 283.2 (2001): 334-339.

PI: 31

Exploring the Chemokine Landscape: Deciphering the Role of Chemokine and Chemokine Axis in Breast Cancer Progression

Amaresh Mishra[a], Vishwas Tripathi[a*]

[a]School of Biotechnology, [a]Gautam Buddha University, Greater Noida, India

*drvishwastripathi@gmail.com

Background

Breast cancer is a multifaceted disease with a complex microenvironment that significantly influences its progression. Chemokines, a family of small signalling proteins, play a crucial role in orchestrating cellular interactions within the tumor microenvironment. Understanding the intricate interplay between chemokines and breast cancer progression is essential for devising targeted therapeutic strategies. This review aims to provide a comprehensive overview of the current knowledge regarding the role of chemokines and chemokine axes in breast cancer pathogenesis.

Review

The review begins by elucidating the fundamental mechanisms underlying chemokine signalling and its impact on immune cell recruitment, angiogenesis, and metastasis in breast cancer. We delve into the diverse chemokine subtypes and their receptors, exploring how their dysregulation contributes to the initiation and progression of breast cancer. Additionally, we discuss the emerging evidence supporting the role of chemokine gradients in shaping the pre-metastatic niche and fostering a microenvironment conducive to tumour cell dissemination. The molecular crosstalk between chemokine signalling and various cellular components of the tumour microenvironment, including immune cells, fibroblasts, and endothelial cells, is dissected. Special emphasis is placed on the bidirectional communication between cancer cells and stromal elements, shedding light on how chemokine networks modulate the immunosuppressive milieu within the tumour.

Major findings

Identification of key chemokines and their receptors implicated in breast cancer progression. Insights into the impact of chemokine gradients on the establishment of the pre-metastatic niche. Understanding the intricate crosstalk between cancer cells and the tumour microenvironment mediated by chemokine signalling. Implications for potential therapeutic interventions targeting the chemokine axis in breast cancer.

Keywords: Chemokines, Breast Cancer, Tumor Microenvironment, Metastasis, Therapeutic Targets.

PI: 65

Comprehensive phytochemical screening and in vitro analysis of the antioxidant activity of *Curcuma caesia*Rox

Saima Sohrab and Sanjay Kumar Mishra
Department of Botany, Ewing Christian College, University of Allahabad (211003)

Background

Plants have long been esteemed for their role as natural repositories of therapeutic compounds, offering safe and economically viable alternatives due to their ability to produce potent secondary metabolites such as alkaloids, flavonoids, tannins, saponins, and terpenes which confer distinctive pharmacological implications [1]. Yet many medicinal plants, like *Curcuma caesia*Roxb. (black haldi), remain relatively overlooked and under-explored, lacking comprehensive information about their active components and underlying pharmacological mechanisms. Highlighting this rare species would captivate researchers' and conservationists' attention and foster a collective commitment to their conservation efforts. The present study aims to comprehensively analyze the phytochemical profile and antioxidant activity of both rhizomes and aerial parts of the plant using FT-IR and GC-MS methods and established in vitro techniques like DPPH methods respectively.

Review

Curcuma caesiaRoxb., a critically endangered perennial herb with bluish-black rhizomes is primarily found in the North-East part of India [2]. It has been traditionally employed for alleviating various ailments such as haemorrhoids, aphrodisiac, leprosy, asthma, fever, cancer, inflammation, wounds, vomiting, menstrual disorders, anthelmintic disorders, and gonorrhoea discharges [3]. Curcuma species are reported to have several bioactive secondary metabolites such as tannins, flavonoids, phenols, saponins and terpenes which impart antiviral, antitumor, antibacterial, antioxidant and antiparasitic activities [4].

Major findings

The current study highlights the major functional groups as well as bioactive components of Curcuma caesia. The phytochemical analyses revealed that the majority of the compounds belong to terpenes comprising monoterpenes and sesquiterpenes. Furthermore, compounds such as ar-turmerone, isoborneol, alloaromadendrene, carvacrol etc. are the major compounds reflected through GC-MS analysis are reported to have high antioxidant potential. The diverse array of phytochemicals identified in the plant underscores its therapeutic potential, suggesting avenues for exploration in both the pharmaceutical industry and traditional medicine. This research contributes to a deeper understanding of the chemical constituents and medicinal properties of Curcuma caesia, opening doors for its utilization in drug development and healthcare practices.

Keywords: *Curcuma caesia*, antioxidant activity, GC-MS, FTIR, secondary metabolites.

References

[1] Borah, A., Kumar, D., Paw, M., Begum, T., Lal, M. (2020). A review on ethnobotany and promising pharmacological aspects of an endangered medicinal plant, *Curcuma caesia*Roxb. Turk J Bot. 34, 205-213. doi:10.3906/bot-1910-33

[2] Devi, H.P., Mazumder, P.B., Devi, L.P. (2015). Antioxidant and Antimutagenic activity of *Curcuma caesia*Roxb. rhizome extracts. Toxicol. Rep. http://dx.doi.org/10.1016/j.toxrep.2014.12.018

PI: 67

Mycotoxin Deoxynivalenol assisted mitochondrial dysfunction and neurotoxicity

Sakshi Mishra[a], Divyansh Sharma[a], Sonam Kanchan[a], Gaurav Jha[a], Bhawana Tomar[a], Srikanta Kumar Rath[a*]
[a]Genotoxicity Laboratory, Division of Toxicology and Experimental Medicine
Central Drug Research Institute, (CSIR-CDRI), Sector 10, Jankipuram Extension, Sitapur Road Lucknow 226031, Uttar Pradesh, India
*drsakshimishra@gmail.com, *skrath@cdri.res.in

Background

Mycotoxins, notably Deoxynivalenol (DON), impact mitochondrial dynamics, posing health risks in food. Links to neurodegenerative disorders require further exploration, especially due to DON's prevalence and hazards. Investigating its role in neuronal cells aims to bridge the gap in understanding mycotoxins and neurodegenerative diseases.

Review

DON has been found to induce neurotoxicity. It can cross the blood-brain barrier and interfere with the homeostasis and functioning of the nervous system (Fæste et al., 2022). DON has been shown to induce apoptosis in neuronal cells through the mitochondrial apoptotic pathway (Cao et al., 2021). It also affects the viability and function of astrocytes and microglia in the brain. DON exposure leads to oxidative damage, altered neurotransmitter levels, and disruption of calcium signaling in the brain (Wang et al., 2020). Additionally, DON induces cytotoxicity in human brain endothelial cells through oxidative stress, which can be attenuated by the antioxidant Vitamin E (Shieh et al., 2021; Zhang et al., 2020). Findings suggest that DON causes neurotoxic effects through various mechanisms, including apoptosis, inflammation, and oxidative stress.

Major Findings

DON exposure to human SH-SY5Y cells showed dose-dependent cytotoxicity, increased ROS, and calcium levels. ATP and mitochondrial potential decreased with rising DON concentrations. Elevated expression of mitochondrial fission proteins and reduced fusion proteins activity led to increased autophagic markers, indicating augmented autophagic activity due to DON-induced mitochondrial damage. ROS initiated mitochondrial damage, emphasizing ROS and Ca2+-mediated pathways in DON-induced mitochondrial dynamics alterations. Specific inhibitors targeting these pathways could combat mycotoxin-induced neurodegenerative diseases.

Keywords: DON, SH-SY5Y, Mitochondrial fission, ROS, oxidative stress

PI: 74

Exploring the impact of Lead Acetate on vital organs of *Labeorohita*: An In-gel analysis of lactate dehydrogenase and antioxidant enzymes

Priya Agrawal[a] and Ajeet Kumar Singh[a]*

[a]Department of Zoology, CMP Degree College (A Constituent College of University of Allahabad), Prayagraj- 211002

* ajeet.bhuz@gmail.com

Background

Contamination of water bodies in wide range with a vast variety of pollutants has increased concern for aquatic organisms. Rapid urbanisation and industrialization is mainly responsible for the water pollution, because various pollutants and toxicants are released from industries such as pesticide, oils, fertilizers and heavy metals etc. Lead (Pb) is a toxic heavy metal, in 19th century, with the revolution of industrialisation consumption of lead has increased. Lead batteries, dyes and plumbing materials etc are the main sources of lead in water as industrial effluents, which possess a very serious threat to ecosystem and for human health (Li et al., 2019).

Review

Reactive oxygen species (ROS) play a major role in stress conditions. Living organisms possess multilevel and complicated antioxidant system to prevent ROS formation or to minimize its negative effects. Lactate dehydrogenase (LDH) regulates oxidative stress by balancing NAD/NADH ratio (Lin et al., 2022). It is observed that acute exposure of environmentally relevant concentration of lead exhibits neuro- behavioural alteration and hyperactivity in larval Zebra fish (Kataba et al., 2020), which may be correlated with altered activity of major antioxidant enzymes (Shaukat et al., 2018). Moreover, a significant increase in LDH activity was also observed in *Cyprinus caprio* after lead acetate exposure (Mirmazloomi et al., 2015). Therefore, present study is aimed to explore differential role of major antioxidant enzymes (Catalase, superoxide dismutase and glutathione peroxidase) and LDH in oxidative stress induced by different concentrations (3 mg/L, 6 mg/L and 12 mg/L) of lead acetate on vital organs of Indian major carp *Labeorohita*.

Major Finding

Dose dependent and tissue dependent changes in the activity of different antioxidant enzymes (CAT, SOD and GPx) on liver and gill were observed in exposed groups as compared to control, which reflects differential level of oxidative stress in liver and gill of the fish. Similarly, increased activity of LDH in both tissues reflects a robust response of this enzyme in varying level of oxidative stress induced by lead. These preliminary findings may pave a path to further understanding of stress physiology of fishes in response to heavy metal exposure.

Keywords: Heavy metal, Lead Acetate, Reactive oxygen species, Antioxidant enzymes,

References

[1] Kataba, A., Botha, T.L., Nakayama S. M. M., Ikenaka, Y., Wepener, V., Ishizuka, M. (2020). Acute exposure to environmentally relevant Pb levels induces oxidative stress and neurobehavioral alterations in larval zebrafish (Danio rerio). Aquat. Toxicol. 227, 105607.

PI:102

Effect of Thymolon Blood Brain Barrier disruption, Apoptotic Cell Death and Serum Cytokines Level in Cerebral ischemic stroke in Hyperglycemic Rats

Chetna Mishra[a*], Dinesh Tripathi[a], Sunita Tiwari[b], Sandeep Bhattacharya[a]
[a]Department of Physiology, King George's Medical University, Lucknow-226003, India
[b]Department of Physiology, Dr. Ram Manohar Lohia Institute of Medical Sciences, Lucknow - 226010, India

*chetnakgmu2016@gmail.com

Background

Oxidative stress and blood-brain barrier disruption are major causes of disability andmortality in stroke patients, and they have a considerable impact on diabetic-induced stroke progression. Thymol has been linked to both antioxidant and anti-inflammatory properties. The aim of this study wasto look into the therapeutic effects of thymol against ischemic stroke in hyperglycemic rats.

Methods

Streptozotocin (35 mg/kg) was administered intraperitoneally (i.p) to male Sprague Dawley (SD) rats to induce hyperglycemia and rats were subjected to middle cerebral artery occlusion (MCAO) for 1hour. Thymol was provided orally to rats both before and after ischemia induction. The lipid profile, blood glucose levels, neurological impairment, and oxidative stress markers (MDA and GSH) were also examined. The apoptosis ratio in the brain was evaluated using flow cytometry. Evans blue technique was used to determine blood-brain barrier breakdown. Serum IL-23 and IL-12 level was measured to assess the neuroprotection accordingly to manufacturer’s protocol.

Result

The results demonstrated that Thymol protects blood-brain barrier damage after ischemic injury compared to the MCAO group and dramatically reduces apoptotic cells at 24 hours after ischemic injury compared to the MCAO group. Thymol significantly attenuated the expression of serum IL-23 and IL-12 level in experimental model of cerebral ischemia.

Major findings

These results indicate that Thymol protects cells from apoptosis induced by oxidative stress by inhibiting free radical generation and promoting the antioxidant activity. This study also implies that the IL-23 and IL-12 pathways are promising therapeutic targets in stroke, and Thymol may be a better medication for stroke treatment.

Keywords: Apoptosis,CerebralIschemicinjury,Hyperglycemia,Inflammation,Thymol

References:

Peng T, Jiang Y, Farhan M, Lazarovici P, Chen L, Zheng W. Anti-inflammatory Effects of Traditional Chinese Medicines on Preclinical in vivo Models of Brain Ischemia-Reperfusion-Injury: Prospects for Neuroprotective Drug Discovery and Therapy. Front Pharmacol. 2019 Mar 7;10:204

Li TF, Ma J, Han XW, Jia YX, Yuan HF, Shui SF, Guo D, Yan L. Chrysin ameliorates cerebral ischemia/reperfusion (I/R) injury in rats by regulating the PI3K/Akt/mTOR pathway. Neurochemistry international. 2019 Oct 1;129:104496

Maleki SN, Aboutaleb N, Souri F. Berberine confers neuroprotection in coping with focal cerebral ischemia by targeting inflammatory cytokines. J Chem Neuroanat. 2018 Jan; 87:54-59.

Chen YF, Wu KJ, Huang WS, Hsieh YW, Wang YW, Tsai HY, Lee MM. Neuroprotection of Gueichih- Fuling-Wan on cerebral ischemia/reperfusion injury in streptozotocin-induced hyperglycemic rats via the inhibition of the cellular apoptosis pathway and neuroinflammation. Biomedicine. 2016 Dec; 6:1-9.

PI:104

Targeting GLUT1 for the treatment of both primary and drug-resistant oral cancer seems promising in animal cell culture but may present challenges when translating to a clinical setting

Anjali Kumari[a], Raja Kishore Mishra[a]*
[a]Department of Life Sciences, School of Natural Sciences, Central University of Jharkhand, Cheri-Manatu, Ranchi-835222, Jharkhand, India.
*rajakishore.mishra@cuj.ac.in

Background

Oral cancer, known for its formidable aggressiveness, poses a significant health challenge with substantial morbidity and mortality rates. Bioenergy metabolism intricately determines severity and therapy resistance. Tumor cells voraciously consume glucose from the bloodstream, increased by elevated GLUT1/3 expression. Inhibiting GLUT1/3 emerges as a promising therapeutic strategy.

Methods

We utilized 120 post-operated human tissue samples at different stages of oral cancer, including primary tumors, invasive tumors, recurrent chemoradiation-resistant tumors, and adjacent normal tissues.Additionally, parental and cisplatin-resistant cells were employed. Molecular biology techniques such as Western blot, immunohistochemistry, and reverse transcription-PCR were employed to analyze protein and mRNA expression levels.

Results

There was a progressive increase in GLUT1/3 expression in oral tumors. Notably, GLUT1 expression was significantly higher in therapy-resistant oral tumors and cisplatin-resistant cells. Furthermore, GLUT1 expression was positively correlated with tumor size and loco-regional invasiveness. The mRNA and protein levels of GLUT1/3 were positively linked to oncogenic transcription factors (HIF1α, AP1, NFκB), shedding light on their role in oral cancer severity and therapy resistance. The results also demonstrated that blocking GLUT1 receptors with BAY-876, enhanced cisplatin-induced cell death in cisplatin-resistant cells. This effect may be attributed to the induction of both apoptosis and autophagy.

Conclusion

In conclusion, our study elucidates the pivotal role of GLUT1/3 in driving oral cancer progression, invasion, and drug resistance through intricate transcriptional regulation. The identified transcription factors (c-Jun, HIF1α, NFκB, Fra-2, c-Fos) underscore potential therapeutic targets. These findings establish GLUT1/3 as severity markers, guiding future investigations for targeted therapeutic interventions in oral cancer.

Keywords: Oral Cancer, GLUT1/3 Expression, Therapy Resistance, Cisplatin Resistance, Targeted therapeutics

PI:114

Evaluating the therapeutic potential of SLC2 (GLUT) inhibitors in lung adenocarcinoma

Abhijeet Solomon Baptist[a] , Sameer Srivastava[a*], Shikha Kushwah[a]
[a]Department of biotechnology MNNIT allahabad UP 211004
*sameers@mnnit.ac.in

Background

One subtype of non-small cell carcinoma of the lung is lung adenocarcinoma (NSCLC) and which often forms in alveoli. It tends to grow more slowly than other lung cancers. Every cancer cell has an increased need for glucose. Glucose is essential for malignancies to generate energy effectively and to synthesize macromolecules. Certain glucose transporter proteins, such as the independent glucose transporters (GLUTs) family and the sodium-dependent glucose transporters (SGLTs) family, are responsible for delivering extracellular glucose into cancer cells.

Review

SLC2A1 and SLC2A3 are reported to be overexpressed in LUAD & can serve as potential targets for inhibition by natural compounds such as alkaloids, flavonoids, etc. Structure-based virtual screening (SBVS) predicts how ligands, which are often tiny, drug-like compounds, would interact with a target receptor's binding site, which is typically a protein structure, using a computer method known as molecular docking. Molecular docking and SBVS have proven successful in lead optimization and hit identification, making them popular tools in drug development attempts.

Major findings

From the alkaloid library of 716 compounds three compounds namely *Psychotridine, Tiliacorine&Atalanine* showed binding energy of -11.2, -10.5, and -10.0 with target protein. From the flavonoid library of 480 compounds two compounds namely *Hinokiflavone&Robustaflavone* showed binding energy of -12.2, and -11.6 with target protein (i.e.SLC2A1 & SLC2A3). The docked molecules shared common interactions and literature reported interactions like Phe291 suggest that these molecules can limit glucose uptake by the tumor in the advanced stage showing therapeutic potential and can be incorporated with traditional chemotherapies for lung cancer.

Keywords: GLUT, SGLT, SBVS

References

Jyotsana, Nidhi, Kenny T. Ta, and Kathleen E. DelGiorno. "The role of cystine/glutamate antiporter SLC7A11/xCT in the pathophysiology of cancer." *Frontiers in oncology* 12 (2022): 858462.

Xue, Qiao, et al. "Evaluation of the binding performance of flavonoids to estrogen receptor alpha by Autodock, Autodock Vina and Surflex-Dock." *Ecotoxicology and Environmental Safety* 233 (2022): 113323.

Li, Yan, et al. "The Effect of SLC2A3 Expression on Cisplatin Resistance of Colorectal Cancer Cells." *Iranian Journal of Public Health* 50.12 (2021): 2576.

Koppula, Pranavi, Li Zhuang, and Boyi Gan. "Cystine transporter SLC7A11/xCT in cancer: ferroptosis, nutrient dependency, and cancer therapy." ***Protein & cell*** **12.8 (2021): 599-620.**

PI:116

To study CHRDL1 gene as a candidate biomarkerfor Colorectal Cancer

Mubashra[a], Ankit Srivastava[a], Sameer Srivastava[a*]
[a]Department of Biotechnology, Motilal Nehru National institute of Technology Allahabad,
Prayagraj, Uttar Pradesh, India.

* sameers@mnnit.ac.in

Background

CHRDL1, also known as Chordin-like 1, is secreted protein that functions as a traffic controller in the body and act as bone morphogenetic protein (BMP) antagonist. BMP acts as an activator of a specific receptor known as BMP receptor II (BMPR II) that together promotes the transfer of extracellular signals into intracellular spaces which in turn aids in processes of cancer development. The binding of BMP to its receptor II leads to phosphorylation of Smad transcription, which alters the gene regulation pattern and induces a set of events occurring in tumors, including proliferation, migration, and invasion. CHRDL1 is released from the dorsal embryonic pole containing a unique type of domain termed as cysteine-rich von Willebrand factor type C (vWC) that helps bind to BMP4. This interaction between CHRDL1 and BMP4 prevents BMP from connecting to BMPRII and inhibits its role in cancer formation. Moreover, CHRDL1 has been identified as a biomarker for the prognosis of several cancers, including Gastric, Lung, Breast, and Thyroid cancer.

Review

Colorectal cancer (CRC) is a heterogeneous disease originating from the colon and rectum. However, CHRDL1 has recently been identified as a clinically valuable biomarker and reported that the initiation and progression of colorectal cancer (CRC) could be due to its altered epigenetic regulation. In case of gastric cancer (GC), it was reported that the expression of CHRDL1 gene was controlled by hsa-microRNA-204 and it is found to affect the proliferative and invasive property of gastric cancer cells. Similar results have been reported in case of thyroid cancer. Interestingly, in breast cancer it was observed that CHRDL1 could inhibit the migration and invasion of cells through inhibiting the BMP4 signaling. Moreover, in oral squamous cell carcinoma (OSCC) CHRDL1 exerts an inhibitory effect on tumors via the MAPK signaling pathway and concluded that CHRDL1 as a potential therapeutic target for OSCC therapy. From various experiments it was confirmed that CHRDL1 expression was directly correlated with proliferation, migration, and differentiation in various cancers. However, our literature review revealed that no experimental evidence in details are present pertaining to the role of CHRDL1 in CRC except in-silico study.

Major findings

From UALCAN tool we find that CHRDL1 gene is hypermethylated and downregulated in both COAD and READ samples of TCGA datasets. Transcription analysis and kinase analysis was done using X2K web tool. Further Bisulfite PCR optimization and restriction analysis was done for CHRDL1 which shows no methylation pattern were observed in all the tested tumor samples. Expression analysis was performed using qRT-PCR, and found that in most samples (6 tumor) CHRDL1 was downregulated out of total 10 samples tested.

Keywords: CHRDL1, CRC, Regulation, BMP

References

1. Pei, Y. F., Zhang, Y. J., Lei, Y., Wu, D. W., Ma, T. H., & Liu, X. Q. (2017). Hypermethylation of the CHRDL1 promoter induces proliferation and metastasis by activating Akt and Erk in gastric cancer. Oncotarget, 8(14), 23155.

Assessing the Toxicity of Erythrosine and Tartrazine on *Gymnocorymbusternetzi* (Black Widow) and *Poeciliasphenops* (Molly) Fish Species: An Investigation of Acute and Sub-Acute Effects

Divya Upadhyay[1], Kartikeya Shukla[1], Tanu Jindal[2], Manuj Bhardwaj[3], Arti Mishra[4,5,6] and Smriti Shukla[2*]

[1]Amity Institute of Environmental Sciences, Amity University Uttar Pradesh, Noida.

[2]Amity Institute of Toxicology, Safety and Management, Amity University Uttar Pradesh, Noida.

[3]Climate Scholar, United Nations Intergovernmental Panel Climate Change [IPCC], Geneva, Switzerland; Washington College of Law, American University, Washington, DC, USA and Advisor for India at The International Law Institute, Washington, DC, USA

[4]Department of Botany, Hansraj College, University of Delhi, India

[5]Chemistry and Biotechnology of Natural Products, CHEMBIOPRO, Universite de LA Reunion, Agroalimentaire, 15 Avenue René Cassin, CS 92003, CEDEX 9, F-97744, Saint-Denis, France

[6]Umeå Plant Science Center, Department of Plant Physiology, Umeå University, Umeå, Sweden

Background

Human activities in color-making, textile, and synthetic food color industries have led to significant water pollution, particularly in Pali city and Vapi CETP. The discharge of untreated wastewater and pollutants poses threats to aquatic habitats, groundwater quality, and river ecosystems.

Review

Efforts to achieve zero liquid effluent discharge in Vapi CETP require a comprehensive upgrade, emphasizing the removal of pollutants. Recent studies highlight the toxic effects of treated effluent on aquatic life, leading to significant fish mortality. The untreated industrial effluent in Vapi industrial cluster raises concerns for aquatic ecosystems. Aquaculture is suggested as a solution, emphasizing the need for controlling water pollution and choosing proper food colors (Deepali *et al*; 2010). Bioassays play a crucial role in understanding the impact of industrial effluents on fish populations (Makwana *et al*; 2020a, 2020b).

Major findings

Erythrosine (Red No. 3) and Tartrazine (Yellow No. 5) are two commonly used synthetic food additives and daily consumed by human. There high consumption is causing toxic effect and a major health concern. In this investigation, we have evaluated and contrasted the effects that vary with the dosage of Erythrosine (Red No. 3) and Tartrazine (Yellow No. 5) via the acute and sub-acute toxicity on two distinct fish species Gymnocorymbusternetzi (Black Widow) and Poeciliasphenops (Molly). Erythrosine was administered at concentrations of 0.0001 ppm, 0.0005 ppm, 0.001 ppm, 0.005 ppm, and 0.01 ppm, while Tartrazine was tested at concentrations of 0.005 ppm, 0.01 ppm, 0.05 ppm, 0.1 ppm and 0.5 ppm in both acute and sub-acute toxicity studies. For each colorant and fish species, five treatment groups were established, including one control group. Each group consisted of 20 fish. The study assessed the mortality rates at different time points, with acute toxicity observed on Day 14 and sub-acute toxicity on Day 28. Results revealed dependent on the concentration effects of Erythrosine and Tartrazine on both Black Widow and Molly fish. In general, the mortality rates increased with higher concentrations of the colorants, indicating a potential toxicity risk associated with their consumption.

Keywords: Erythrosine, tartrazine, acute, sub-acute, food colorants

PI: 172

Analysis of effects of drug induced hepatic damage on cardiac and gut electrophysiology of rats

Smriti Chandra[a*], KahakashanParween[a], Sugandha Jaiswal[a], Rakesh Kumar Sinha[a]
[a]Department of Bioengineering and Biotechnology
Birla Institute of Technology, Ranchi
*smriti.chandra12@gmail.com

Background

The aim of this study is to evaluate the effects of Streptozotocin (STZ) on liver and how the liver proteins and enzymes get altered. Simultaneously, the cardiac and gastric activities of the subjects can also be evaluated to understand and demonstrate the correlation between the electrophysiological signals and liver damaged condition.

Review

The liver is an essential organ used for nutrient metabolism. It also plays an important role in detoxifying harmful molecules. Any damage to liver has been reported to cause severe complications in the body [1]. STZ is well established chemical that severely affect the anatomy and physiology of vital organs and is also well known to induce both diabetes mellitus and liver damage [2]. Further, cardiac arrhythmias have also been reported to be associated with liver disease [3].

Major findings

This study was initiated by inducing liver damage by administering STZ (65 mg/kg b.w) in young male rats. The electrocardiogram (ECG) and Electrogastrogram (EGG) data were recorded digitally with the help of two channel bioamplifier (MP45, Biopac Inc, USA). The analysis of electrophysiological data revealed various abnormalities in morphological parameters of the recorded signals. The protein estimation was conducted to determine the changes in liver proteins. The specific liver enzyme was found to be elevated in STZ induced rats.

Keywords: Electrocardiogram; Electrogastrogram; Liver; Streptozotocin

References:

[1] Ozougwu, J. C. (2017). Physiology of the liver. International Journal of Research in Pharmacy and Biosciences, 4(8), 13-24.

[2] Rashmi, R., Magesh, S. B., Ramkumar, K. M., Suryanarayanan, S., and SubbaRao, M. V. (2018). Antioxidant potential of naringenin helps to protect liver tissue from streptozotocin-induced damage. Reports of biochemistry & molecular biology, 7(1), 76–84. PMID: 30324121; PMCID: PMC6175592.

[3] Toma, L., Stanciu, A.M., Zgura, A., Bacalbasa, N., Diaconu, C. and Iliescu, L. (2020). Electrocardiographic Changes in Liver Cirrhosis—Clues for Cirrhotic Cardiomyopathy. Medicina, 56, 68. https://doi.org/10.3390/medicina56020068.

PI:182

Dysregulated miRNAs in Progression and Pathogenesis of Alzheimer's Disease

Tania Arora, Jyoti Parkash
Central University of Punjab,Bathinda

Abstract

Alzheimer’s disease (AD) is a progressive degeneration of neurons due to the accumulation of amyloid-β peptide (Aβ) and hyper-phosphorylation of tau protein in the neuronal milieu leading to increased oxidative stress and apoptosis. Numerous factors contribute towards the progression of AD, including miRNA, which are 22–24 nucleotides long sequence which acts as critical regulators of cellular processes by binding to 3′ UTR of mRNA, regulating its expression post-transcriptionally. This review aims to determine the miRNA with the most significant dysregulation in the brain and cerebrospinal fluid (CSF) of human patients. A systemized inclusion/exclusion criterion has been utilized based on selected keywords followed by screening of those articles to conclude a list of 8 highly dysregulated miRNAs based on the fold change of AD vs control patients, which could be used in clinical testing as these miRNAs play central role in the pathophysiology of AD. Furthermore, a network study of highly dysregulated miRNA estimated the association of these miRNA in the mediation of Aβ generation and aggregation, inhibition of autophagy, reduction of Aβ clearance, microglial and astrocytic activation, neuro-inflammation, tau hyper-phosphorylation, and synaptic loss.

Screening and quantitative analysis of the Plant Growth Promoting Rhizobacteria armed with ACC deaminase activity

Megha Baghel[a], *Shivesh Sharma [a] [a]Department of Biotechnology, Motilal Nehru National Institute of Technology, Allahabad, 211004, Uttar Pradesh, India

***shiveshs@mnnit.ac.in**

Background

The rhizospheric zone of plants is home to helpful bacteria known as plant growth-promoting rhizobacteria (PGPR), which promote symbiotic partnerships for improved plant growth and development. They enhance plant growth, improve stress tolerance, and serve as eco-friendly alternatives to chemical fertilizers. PGPR provide nutrients to plants through various mechanisms such as, phosphorus solubilization, indole acetic acid production, ammonia production & siderophore production. (Nagargade, Tyagi, & Singh, 2018). Under stress conditions, plants produce a large amount of ethylene, which negatively affects their growth. PGPR uses 1-aminocyclopropane-1-carboxylic acid (ACC) deaminase activity to lower the amount of ethylene and provides plants stress tolerance. (Gupta & Pandey, 2019).

Review

Plants undergo several types biotic and abiotic stresses that significantly affect their growth and development (Chandwani&Amaresan, 2022). Certain PGPR contains ACC deaminase, which can hydrolyze ACC into α-keto butyrate & ammonia, resulting in the reduction of ACC & subsequently preventing the production of ethylene (Gupta & Pandey, 2019). It is one of the crucial mechanisms of stress tolerance in plants. In the present investigation, fourteen distinct bacterial strains were extracted from the rhizosphere of rice and mustard plants, and their ACC deaminase activity was assessed in response to a range of environmental factors, including temperature, pH, and ACC concentration. In addition, estimates were made for additional PGPR features.

Major findings

It was discovered that eight of the fourteen isolates had ACC deaminase activity, which varied from 400 - 600 nmol α-keto butyrate/mg protein/hour. Under 5 mM ACC concentration, pH-7, and 30˚C, strains K9 and A21 showed the highest ACC deaminase activity, with values of 595.181 nmol α-keto butyrate/mg protein/hour and 581.912 nmol α-keto butyrate/mg protein/h, respectively. Additionally, these rhizobacteria were also exhibiting other PGPR activities such as ammonia production, IAA production, siderophore, and phosphorus solubilization. The findings indicate that these bacterial isolates could be used as potential biofertilizers, providing stress tolerance to plants.

Keywords: ACC deaminase, PGPR, biofertilizer, indole acetic acid, siderophore production, phosphorus solubilization

References

1. Chandwani, S., &Amaresan, N. (2022). Role of ACC deaminase producing bacteria for abiotic stress management and sustainable agriculture production. *Environmental Science and Pollution Research*, *29*(16), 22843–22859. doi:10.1007/s11356-022-18745-7
2. Gupta, S., & Pandey, S. (2019). ACC deaminase producing bacteria with multifarious plantgrowth promoting traits alleviates salinity stress in French bean (phaseolus vulgaris) plants. *Frontiers in Microbiology*, *10*. doi:10.3389/fmicb.2019.01506

PI:198

Exploring Algal Diversity: A comparative study on extracellular polysaccharides (EPS) production across various species.

Vishal Sonkar [a], ***Anjana Pandey*** [a*]
[a] *Department of Biotechnology, MNNITA Prayagraj-211004*
[a*]*Department of Biotechnology, MNNITA Prayagraj-211004*
*anjanap@mnnit.ac.in

Background:

Microalgal biotechnology is gaining a lot of attention due to the rising need for sustainable alternatives. Extracellular polysaccharides (EPS) are a valuable resource with a broad spectrum of potential applications, including pharmaceuticals, wastewater treatment and biofuel generation. It is crucial to understand the factors affecting EPS generation in various algae species in order to optimally utilise their bioeconomic potential.

Review:

This comprehensive review delves into the comparative analysis of various algal species, focusing on their capability for EPS production. Key factors such as growth conditions, nutrient availability, and cultivation strategies are systematically examined to provide insights into the distinctive features influencing EPS yield, composition, and structural characteristics among different algae. The review also explores recent advancements in cultivation technologies, including open pond systems, photobioreactors, and hybrid approaches, aimed at enhancing EPS production efficiency(Babiak & Krzemińska, 2021; Narala et al., 2016).

Major Findings:

A review of the data that is currently available shows that different algae species produce EPS at exceptionally varying rates. Significant findings shed light on the unique properties and possible disadvantages of different algae, offering a more complex picture of their appropriateness for EPS generation. The review also emphasises how crucial scalability and environmental sustainability are to enhancing EPS production. The main conclusions help to shape future research paths by highlighting knowledge gaps. They also provide insightful information for scientists, biotechnologists, and officials involved in using the bioeconomic potential of algae-derived EPS for a sustainable future.

Keywords: Algae, Extracellular polysaccharide (EPS), Open Pond system, Photobioreactor.

References:

1. Narala, R. R., Garg, S., Sharma, K. K., Thomas-Hall, S. R., Deme, M., Li, Y., & Schenk, P. M. (2016). Comparison of Microalgae Cultivation in Photobioreactor, Open Raceway Pond, and a Two-Stage Hybrid System. Frontiers in Energy Research, 4. https://doi.org/10.3389/fenrg.2016.00029
2. Babiak, W., & Krzemińska, I. (2021). Extracellular Polymeric Substances (EPS) as Microalgal Bioproducts: A Review of Factors Affecting EPS Synthesis and Application in Flocculation Processes. Energies, 14(13), 4007. https://doi.org/10.3390/en14134007

PI: 202

Neurotensin agonist PD149163 modulation of endotoxemia induced immunotoxicity in lipopolysaccharide challenged swiss albino mice

Swarnima Mishraa, Sonia Srivastavaa, Gyan Babu and Banalata Mohantya*
Department of Zoology, University of Allahabad, Prayagraj, Uttar Pradesh, India-211002

*banalata.mohanty@gmail.com

Background

NTS, a tridecapeptide present throughout the central nervous system, gastro-intestinal tract and in other peripheral organs. NTS has been implicated in the modulation of inflammation through its cognate receptor, NTS1. The present investigation evaluated the efficacy of NTS1 agonist PD149163 in LPS-induced inflammation in the spleen, thymus and kidney.

Review

The immune system encompasses immune organs and a variety of immune cells such as lymphocytes, macrophages, basophils, neutrophils which constitutes a complex interactive network, helps in defense, monitoring and regulation of host immune status thereby establishing the homeostatic and physiological balance in the internal environment. Impairment in the immunological response eventually culminates into multiple organs dysfunction such as spleen, thymus and kidney resulting in immunotoxicity.

Major Findings

PD149163 treatment was effective in preventing the LPS-induced inflammation by reducing the pro-inflammatory cytokines (TNF-α, IL-6), elevating the IL-10 and attenuating the effect of oxidative stress in spleen, thymus and kidney; also reflected in the improved histoarchitecture of the kidney. The oxidative stress was also reduced, indicated by significant decrease of lipid peroxide and increase of antioxidant defense enzymes (Superoxide dismutase, Catalase). The plasma level of corticosterone was restored. The anti-inflammatory and anti-oxidative properties of the PD149163 might have effective role in modulation of the renal functions and any kind of immune stress effect on major immune organs in mice.

Keywords: Lipopolysaccharide; Inflammation; Immune organs; kidney; Neurotensin Agonist PD149163

References:

[1] D. Xue, J. Wei, W. Lu, B. Xia, S. Li, D. Liu, N. Liu, X.Wang, G. Lin (2022). BDE-47 disturbs the immune response of lymphocytes to LPS by downregulating NF-κB pathway, Chemosphere, 308(Pt 3), 136562. https://doi.org/10.1016/j.chemosphere.2022.136562.

[2] R. Carraway, S. E Leeman, The isolation of a new hypotensive peptide, neurotensin, from bovine hypothalami. J Biol Chem. 248(19) (1973) 6854–6861. https://doi.org/10.1016/S0021-9258(19)43429-7

PI: 203

Neurotensin receptor-1 agonist PD149163 modulates the lipopolysaccharide induced adrenal toxicity in swiss albino mice

Asheesh Kumar Tiwari[a], Gyan Babu and Banalata Mohanty[a]*
Department of Zoology, University of Allahabad, Prayagraj-211002, India

* banalata.mohanty@gmail.com

Background

Endotoxemia, the elevated plasma level of the Lipopolysaccharide (LPS) resulting from gut microbiota imbalance, promotes increase of pro-inflammatory cytokines which crossing through blood brain barrier elicits activation of the hypothalamic–pituitary–adrenal (HPA) axis. Neurotensin (NTS), a tridecapeptide originally isolated from bovine hypothalamus, is a major peptide of the gastrointestinal tract (GIT) and is also localized in the adrenal gland which is linked to modulation of inflammation. This study evaluated the efficacy of the PD149163, neurotensin receptor 1 agonist (NTSR1), in modulation of endotoxemia induced impairment of the HPA axis. PD149163, reported to have anti-inflammatory and anti-oxidative properties.

Review

The response of an organism to stress is characterized by the activation of neuroendocrine-hypothalamic-pituitary-adrenal axis (HPA), constituting sympathetic nerves as well as neuropeptides and hormones. LPS is gram negative bacterial endotoxin, considered as a systemic immunological stressor, elicits prolonged activation of the HPA axis. NTSR1 agonist PD149163 a non-peptide analog of NTS (8-13), is brain penetrant evaluated for its pro-cognitive, antipsychotic, anxiolytic and antidepressant effect. Anti-psychotic effect of PD149163 has been suggested through central anti-inflammatory role. NTS anti-inflammatory and anti-oxidative role in gut and liver of LPS challenged mice have been elucidated using the non peptideanalog PD149163 in mice.

Major Finding

In only LPS-exposed mice, the plasma levels of IL-6, TNF-α were significantly increased, while IL-10 was significantly decreased. Significant increase in the plasma corticosterone (CORT) indicated HPA axis activation. Adrenal oxidative stress was revealed from elevated TBARS and reduced SOD and CAT. Distorted cellular arrangement, cytoplasmic vacuolization and fragmented nuclei displayed distinct histopathology. PD149163 supplementation decreased plasma levels of TNF-α, IL-6 and increased IL-10, normalized plasma CORT level, reduced oxidative stress and adrenal histopathology. The NTSR1, agonist PD149163 thus has efficacy in amelioration of the endotoxemia induced adrenal toxicity by suppressing inflammatory response and oxidative stress. Further research would explore the potential of NTSR1 analogs as a possible pharmacological agent in modulation of inflammation.

Keywords: HPA-axis; Lipopolysaccharide; Endotoxemia; Inflammation; PD149163

Reference:

[1] Mueller B, Figueroa A, Robinson-Papp J (2022) Structural and functional connections between the autonomic nervous system, hypothalamic–pituitary–adrenal axis, and the immune system: a context and time dependent stress response network. Neurol Sci pp.1-10.https://doi.org/10.1007/s10072-021-05810-1.

PI: 204

Comparative binding analytics on inhibitors of Shikimate pathway enzymes from Plasmodium falciparum

Shruti Shukla[a], Dr. Ashutosh Mani[a *]
[a] Department of Biotechnology, Motilal Nehru National Institute of Technology Allahabad, Prayagraj, Uttar Pradesh, 211004, India.
*amani@mnnit.ac.in

Background

Malaria is a fatal parasite infection that is most common in Sub-Saharan Africa, some parts of Asia, and South America. In 2023 The World Health Organization (WHO) reported 249 million cases of malaria worldwide, a rise of five million from 2021. A resistance has emerged in Plasmodium falciparum to the majority of currently used medicines. To stop the parasite from growing without altering the metabolism of the host, a route specific to the parasite will be a good target. For Plasmodium falciparum to thrive, the shikimate biosynthesis pathway must be operational. The common aromatic precursor chorismite is produced by a group of seven enzymes known as the shikimate pathway. Mammals lack the shikimate pathway, making it a prime candidate for the creation of novel chemotherapy drugs.

Review

This study expands the earlier research on inhibitors of shikimate pathway by targeting its key enzyme5-enolpyruvylshikimate 3-phosphate synthaselike glyphosate, sulfadiazine, pyrimethamine, and atovaquone. After obtaining binding data for inhibitors, a comparison study is conducted to evaluate each inhibitor's affinity, kinetics, and thermodynamics of binding.

Major findings

Interaction study shows that among the inhibitors glyphosate, sulfadiazine, pyrimethamine, and atovaquone, Atovaquone is the most effective inhibitor which show best binding affinity against 5-enolpyruvylshikimate 3-phosphate (EPSP) synthase.

Keywords: *Plasmodium falciparum*, Shikimate pathway, Chorismate

References

[1] McRobert, L., Jiang, S., Stead, A., & McConkey, G. A. (2005). Plasmodium falciparum: interaction of shikimate analogues with antimalarial drugs. *Experimental parasitology*, *111*(3), 178–181. https://doi.org/10.1016/j.exppara.2005.07.002.

PI: 205

Applicable approach of nanomaterials in the field of biomedicine and therapeutics

Vaishali Chaudhary[a], Monika Prakash Rai[a*]
Department of Biotechnology,
Motilal Nehru National Institute of Technology Allahabad, Prayagraj, India- 211004
*mprai@mnnit.ac.in

Background

Nanobiotechnology has emerged as a promising technology in healthcare and medicine. In the last few years, nanotechnology has developed into a collaborative field that encompasses the creation of different systems, devices, and structures along with their characterization and their application at the nanoscale. Nanobiotechnology has brought revolutionary advancement in the fields of wound healing, tissue engineering, gene therapy, development of nanobiosensors, efficient bioimaging and more prominently in the domain drug delivery (Abid Haleem *et al.*, 2023).

Review

There are different categories of nanomaterials based on their size, shape, and type of material. The study reviews the application of nanotechnology-assisted techniques has led to improvement of the sensitivity, cost, and accessibility of diagnosis and therapeutics in medical biotechnology. This has the potential to aid in the advancement of cancer immunotherapy, providing focused and efficient therapeutic alternatives and offers new opportunities to design scaffolds encouraging optimal tissue regeneration. Development of biosensor and bioimaging techniques with the help of nanostructured materials, including metal nanoparticles, semiconductors, and carbon materials has also seen a significant advancement.

Major findings

Modified metallic silver (Ag) and gold (Au) nanoparticles effectively studied for the treatment of skin cancer, epithelial cancer and breast cancer. Studies showed that the bimetallic Fe–Pt nanoparticles are proven as an efficient therapeutic agent for brain cancer and breast cancer. TiO_2 is the metallic oxide widely researched as a therapeutic agent for MDR breast cancer (Gava *et al.*, 2021). Nanoparticles, owing to their small dimensions, effectively allow for the localized release of bioactive agents and drugs, enhancing the therapeutic potential of wound dressings and gene therapy. The metallic Fe-Pt nanoparticles show promise in enhancing the imaging capabilities not only for CT, MRI but also for fluorescence imaging. The nanoparticles offer versatility in detecting biomolecules and integrating them using microfluidic technologies with nanopatterning for molecular diagnostics (Nikta*et al.*, 2022).

Keywords: Nanobiotechnology, targeted drug delivery, cancer therapy, bioimaging, nanobiosensors

References

[1] Haleem, A., Javaid, M., Singh, R. P., Rab, S., & Suman, R. (2023). Applications of Nanotechnology in Medical field. *Global Health Journal*.

Session-8

Biotechnological Intervention in Resource recovery and circular economy

Evaluation of Chlorine Dioxide Induced Damage and Recovery in Marine Phytoplankton

Shubhangi Parishwadkar[1,3], D. Inbakandan[3*], S. Venkatnarayanan[1],
T.V. Krishna Mohan[1,2], Y.V. Nancharaiah[1, 2], P. Sriyutha Murthy[1, 2,*]
[1]Water & Steam Chemistry Division, Bhabha Atomic Research Center, Kalpakkam 603 102,
[2]Homi Bhabha National Institute, Anushaktinagar, Mumbai 400 094, India.
[3]Centre for Ocean Research, Sathyabama Institute of Science and Technology, Chennai - 600 119, India.
* sriyuthamurthy@yahoo.in

Background:

Coastal power stations abstract large quantities of seawater for condenser cooling, wherein phytoplankton species are entrained briefly in the cooling water system (CWS) and are subjected to different stress factors including biocides, elevated temperature and hydrodynamic forces. In tropical countries, power plant discharges are regulated with respect to biocides and temperature. Passive entrainment in CWS and discharges can impact the phytoplankton community in the vicinity of coastal power stations. Hence, the effect of common oxidizing biocide (e.g., chlorine dioxide) used in power stations was evaluated on the dominant phytoplankton groups to ascertain tolerance, susceptibility and recovery.

Review:

Many coastal power stations are switching over to chlorine dioxide from chlorine due to advantages including higher efficacy, environmental compatibility and absence of dis-infection byproducts. In the present study, acute (20 min) exposure to chlorine dioxide (0.1 and 0.2 mg/l), was evaluated on different classes of phytoplankton viz: Chlorophyceae (Chlorella sp.,); Bacillariophyceae (Centric diatom – Chaetoceros sp., Skeletonema sp., Pennate diatomAmphora sp.) and Haptophyceae (Isochrysisgalbana). Cell viability was measured using SYTOX® green staining and correlated with chlorophyll a levels and cell counts.. In addition, total reactive oxygen species (ROS) generation was measured in control and treated population. Exposure to 0.1 mg/l for 20 min revealed highest susceptibility by Chlorella sp.,>Isochrysisgalbana.,>Amphora sp.,>Chaetoceros sp.,>Skeletonema sp. Treatment with 0.2 mg/l revealed highest susceptibility by Isochrysisgalbana,>Chlorella sp.,>Amphora sp.,>Skeletonema sp.,>Chaetoceros sp. Significant increase in total ROS was observed in almost all the phytoplankton species exposed to chloride dioxide.

Major findings:

Results reveal that Chlorophycean member of Chlorella sp., is a highly susceptible organism to both the tested concentrations of chlorine dioxide. Bacillariophycean member exhibit reduced susceptibility as compared to Chlorophycean and Haptophycean members. Among the Bacillariophycean members., Pennate diatoms were found to be more susceptible than centric diatoms to chlorine dioxide. It is evident that the different classes of phytoplankton can respond to biocide different and can be clearly demarcated as highly succeptible, succeptible and tolerant. The data providedan insight on the response of phytoplankton and their abundance in the vicinity of outfall areas of power stations.

Keywords: Chlorine dioxide, phytoplankton, Haptophyceae, Chlorophyceae, Bacillariophyceae

PI: 08

New insights of Naproxen Adsorption onto Magnesium Oxide-Modified Castor Wood Biochar: A Holistic Investigation of Optimization, Isotherm, Kinetic, and Thermodynamic Profiles

Amreen Bano[a], Kumar Suranjit Prasad[a,*]
[a]Centre of Environmental Studies, Institute of Inter-Disciplinary Studies, University of Allahabad, Prayagraj, Uttar Pradesh, 211002

ksuranjit@allduniv.ac.in

Background

Pharmaceutical residues emerge as pervasive micropollutants in aquatic environments, ranging from surface to ground waters. Classified as emerging pollutants, these micro-pollutants warrant vigilant monitoring and effective removal strategies to safeguard the integrity of water sources.

Review

To address this environmental challenge, various methods, including zonation, electrochemical oxidation, photocatalytic reactors, and adsorption, have been employed to remove naproxen until now. Among these methods, the adsorption technique has garnered significant attention from researchers due to its straightforward operation, feasibility, environmentally friendly procedures, easy recovery, and applicability on an industrial scale.

Major findings

In this current investigation, the thermal conversion of castor wood into biochar and its subsequent utilization for the adsorptive removal of naproxen from aqueous solutions was explored. SEM–EDX and LIBS analyses illuminated the surface composition, revealing the presence of magnesium (Mg) incorporated into the adsorbent material. FTIR spectra unveiled the participation of various functional groups in the adsorption of naproxen. The batch study was enhanced by employing optimization tools such as response surface methodology (RSM). Batch adsorption experiments unveiled that magnesium oxide-modified biochar significantly enhanced the naproxen binding capacity of the adsorbent. Equilibrium data from adsorption experiments demonstrated the superiority of the Langmuir model over the Freundlich and Temkin models, yielding a maximum adsorption capacity of 95.61 mg g^{-1} for nMgO@CWBC (modified biochar) and 72 .46 % for pCWBC (pristine biochar). The kinetic second-order model emerged as the most fitting, presenting a high R^2 value of 0.983 and the lowest root mean square error and chi-square ($\chi 2$) values, effectively elucidating the naproxen adsorption process. Our findings suggested that the chemisorption or ion exchange processes, as described by the PSO model, aptly captured the mechanism of naproxen adsorption onto both adsorbents. The thermodynamic analysis, including $\Delta G°$ values, indicated the spontaneous nature of naproxen adsorption on pCWBC and nMgO@CWBC. Thus, the prepared magnesium oxide-modified adsorbent shows promise to tackle the menace of naproxen contamination.

Keywords: naproxen, biochar, response surface methodology, adsorption

References

[1] Huynh, N. C., Nguyen, T. T. T., Nguyen, D. T. C., & Tran, T. Van. (2023). Occurrence, toxicity, impact and removal of selected non-steroidal anti-inflammatory drugs (NSAIDs): A review. *Science of The Total Environment*, *898*, 165317. https://doi.org/10.1016/J.SCITOTENV.2023.165317

[2] Mohammadi Nodeh, M. K., Kanani, N., Beirak Abadi, E., Sereshti, H., Barghi, A., Rezania, S., & Nabi bidhendi, G. (2021). Equilibrium and kinetics studies of naproxen adsorption onto novel magnetic graphene oxide functionalized with hybrid glycidoxy-amino propyl silane. *Environmental Challenges*, *4*(February), 100106. https://doi.org/10.1016/j.envc.2021.100106

[3] Rout, P. R., Zhang, T. C., Bhunia, P., &Surampalli, R. Y. (2021). Treatment technologies for emerging contaminants in wastewater treatment plants: A review. *Science of the Total Environment*, *753*, 141990. https://doi.org/10.1016/j.scitotenv.2020.141990

Exploring the UV-Protective Capacities of *Oscillatoria* sp. Malviya-1: Potential forBio-BasedSunscreens

Rinkesh Gupta, Pankaj Kumar Maurya, Priyul Pandey, Sapna Tiwari, Anjali Gupta, Deepa Pandey, Shailendra Pratap Singh*
Centre of Advanced Study in Botany, Institute of Science, Banaras Hindu University, Varanasi-221005,India

*spsingh@bhu.ac.in

Background

Cyanobacteria, recognized as Gram-negative, widespread, and capable of oxygen-evolving photosynthesis, are notably known for synthesizing diverse UV-protective compounds. Among these compounds, mycosporine-like amino acids (MAAs), known for their colorless, water-soluble, and lightweight properties, are synthesized by range of organisms, including cyanobacteria. However, scytonemins exclusively accumulate in the extracellular sheaths of cyanobacteria as a response to ultraviolet radiation (UVR). The synthesis of MAAs and scytonemins in cyanobacteria holds significance due to their ability to offer protection against UV radiation, act as osmoprotectants, and scavenge free radicals. Our focus has been on investigating Oscillatoria sp. Malviya-1, a cyanobacterium forming dark soil crusts, to unravel its capacity for producing these essential UV shielding compounds.

Review

Society faces a concern regarding the increasing levels of ultraviolet radiation (UVR) reaching Earth surface, primarily due to ozone layer depletion. The rise in damaging UV-B radiation, particularly harmful to the skin, emphasizes the need for effective protection. The synthetic sunscreens rely on organic filters like oxybenzone and inorganic metal oxide particles such as ZnO and TiO2 to counteract UV radiation. Therefore, there is a need to find bio-based sunscreen chemicals which are effective, safe, durable and prevent damage caused by UV radiation and increases the effectiveness of natural sunscreens. Characteristics of MAAs offer a chance in the search for an alternative natural product source of sunscreen chemical.

Major findings

We found that Oscillatoria sp. Malviya-1 possesses a remarkable capability to thrive under various light conditions, including blue, green, and red light, alongside white light. Notably, it synthesizes UV- protective compounds crucial for bio-based sunscreens while adapting to this diverse light spectrum.

Keywords: Bio-based sunscreen, Mycosporine-like amino acids, Scytonemins, Ultraviolet radiation, UV-absorbingcompound

Reference

[1] Maurya,P.K.,Kumar,V.,Mondal,S.,&Singh,S.P.(2023).Photoautotrophicblack-coloredcyanobacterial soil crust biosynthesizes photoprotective compounds and is capable of using blue, green,and red wavelengths of light for its growth. Environmental Science and Pollution Research, 30(6), 16756-16769

PI: 62

Comparative study of phytochemical profile andradical scavenging activity of *Hyptissuaveolens*(L.) Poit growing in different locations

Pratibha Mishra[a*]and Sanjay Kumar Mishra[b]

[a,b]Department of Botany, Ewing Christian College (University of Allahabad), Prayagraj, Uttar Pradesh, 211003, India.

*pratibhaprakashmishra512@gmail.com

Background

To protect themselves from naturally occurring diseases and environmental stressors plants produce a range of secondary metabolite such as flavonoids, saponins, alkaloids, terpenes, and tannins [1]. Medicinally aromatic plants when grown in different habitats with different environmental conditions leads to variations in the quantity and quality of chemical compounds and any modification in secondary metabolite profile enhance the therapeutic potential of the medicinal plants significantly [2] [3]. Thus, in the current study, our main objective is to establish the phytochemical and pharmacological properties of the under-explored invasive weed *Hyptissuaveolens* (L.) Poit and investigate the diverse and changing responses of various plant secondary metabolites of plants growing in two different locations (L1 & L2). Sophisticated analytical techniques, including FTIR paired with GC/MS were used for the characterization of the metabolite profiles and DPPH assay was performed to determine the antioxidant activity of the plant.

Review

Hyptissuaveolens (family Lamiaceae) is a valuable medicinal plant that has been used to cure a variety of diseases in conventional healers. Pharmaceutically important secondary metabolites with antioxidant, anti-microbial, anti-inflammatory, antiviral, anti-colic, anti-rheumatic, and anti-fertility activities are found in the leaves of this plant [4].

Major findings

From the results of GC-MS analysis, we found that most of the compounds identified in the leaf and root extract of this plant belong to the terpene and fatty acid groups. The increased synthesis of fatty acids and terpenes in the plants may be due to a change in the expression of the enzymatic genes that are involved in their metabolic biosynthetic pathways. Environmental stressors may also trigger the expression of specific genes, influencing the synthesis and activity of antioxidant enzymes. The plants growing in L1 showed higher radical scavenging activity than L2, which can be evidently correlated with the GC-MS results of extracts from both locations, as it was found that methanolic and petroleum ether extracts of leaf and root from L1 showed a greater number of antioxidant compounds than L2. The compounds identified from GC-MS analysis such as squalene, cis-lanceol, n-hexadecanoic acid, and methyl 4, 7, 10, 13-hexadecatetraenoate are reported to have well-established antioxidant activity. Furthermore, the current phytochemical and radical scavenging activity revealed considerable phytochemical variations and consecutive antioxidant activity in two different locations, which strongly suggests that these might be chemotypes of *Hyptissuaveolens*. However, more extensive research is needed in this direction, and this is the matter of further investigation.

Keywords: *Hyptissuaveolens*, Secondary metabolites, FTIR, GC-MS, Antioxidant activity

References

[1] Ebel, J. (1986). Phytoalexin synthesis: the biochemical analysis of the induction process. Annual Review of Phyto-pathology 24(1):235-264

[2] Parekh, J., Chanda, S. (2007). In vitro antimicrobial activity and phytochemical analysis of some Indian medicinal plants. Turkish Journal of biology 31:53-58

[3] Pant, P., Pandey, S., Dall'Acqua, S. (2021). The Influence of Environmental Conditions on Secondary Metabolites in Medicinal Plants: A Literature Review, Chem. Biodiversity 18, e2100345

PI: 93

Dairy wastewater treatment with microalgae for edible oil production: Circular bioeconomy approach

Anamika Singh[a], Sumer Singh Meena[a], Anee Mohanty[a*]
[a]Department of Biotechnology (Dr B R Ambedkar National Institute of Technology
Jalandhar – 144008 Punjab)

*mohantya@nitj.ac.in

Background

Dairy industry wastewater is characterized by high organic load, wide pH range thus requiring special treatment strategies before their discharge into the environment. Microalgae have ability to grow rapidly by absorbing nutrients efficiently from dairy wastewater and while doing so can accumulate high level of lipids.

Review

Dairy wastewater treatment with microalgae for edible oil production is a promising approach that can address both environmental and economic challenges. In this study the isolation of algal biomass was done from the wastewater pond of dairy industry and they were grown using the nutrient present in wastewater for production of algal biomass. Wastewater from different stages of treatment (primary treatment pond, secondary treatment effluent etc.) were taken and change in COD, pH, DO of the wastewater along with the growth of microalgae were monitored at regular intervals. The algal biomass was harvested through filtration and can be valorized for edible oil production. Further, algal de-oiled cake can be used as animal feed, biofertilizers, or biogas production.

Major findings

In this circular bioeconomy approach we can recycle nutrients, produce microalgal biomass and accumulate lipids. Estimation of nitrate, ammonia, reducing sugars, DO, COD and other parameters were done. COD was observed to be decreased by 54% and the lipid extracted was 9.1%.

Keywords: Dairy wastewater, Edible oil, Microalgae, Waste valorisation, Circular bioeconomy

References

[1]Biswas, T., Bhushan, S., Prajapati, S. K., & Ray Chaudhuri, S. (2021). An eco-friendly strategy for dairy wastewater remediation with high lipid microalgae-bacterial biomass production. *Journal of Environmental Management*, *286*. 10.1016/j.jenvman.2021.112196.
[2] Acién Fernández, Francisco Gabriel; Gómez-Serrano, Cintia; Fernández-Sevilla, José María (2018). Recovery of Nutrients From Wastewaters Using Microalgae. *Frontiers in Sustainable Food Systems, 2(), 59–*. doi:10.3389/fsufs.2018.00059

PI:94

Physicochemical and structural characteristics of starch after physical modification

Anam Tanveer, Ayushi Singh, Parul Katiyar and Harinder Singh*
Dept of Chemical Engineering, MNNIT Allahabad
*hsingh@mnnit.ac.in

Physical modification of starches is environment friendly, feasible and more conducive for health as these do not entail the addition of chemicals to change the physicochemical and structural characteristics of starches. The process of physical modification of starch can be tweaked to obtain desired change in the particle size variation, structural properties, water and oil solubility pasting and gelation ability of starch. These may require more detailed research than chemical modification of starch because the changes in starch characteristics are not proportional as in chemical modification. The downstream processing involved in treating water after starch modification is also minimal. However, there may be involvement of energy in modifying the starches in these processes e.g. in heat moisture treatment, pulse electric field, ultraviolent radiation, freeze-thaw, high pressure modification, superheating, irradiation, and cold plasma modification. The food industry is increasingly looking for clean label starches to be sold as ingredients or use them in food products as texturing agent, stabilizer in dairy, bakery products to name a few and physically modified starches can serve as alternatives. This poster summarizes and compares various physical modifications of starches for easy understanding of the reader and for increasing awareness among consumers.

Nutrient recovery from sewage sludge - A review

Kajal Singh[a], Kanika Saxena[b]
Department of Civil Engineering, (Motilal Nehru National Institute of Technology - Allahabad, Prayagraj-211004, Uttar Pradesh, India)
* Kanika@mnnit.ac.in

Background

Sewage sludge is a tarry black by-product which is generated by sewage treatment plants. Currently sludge is disposed in sludge drying beds or landfills which require ample amount of land area. Despite the hazards posed by sewage sludge, it is rich in phosphorus and nitrogen.

Review

The objective of this review is to deal with the issue of sludge management and promote sustainability by focusing on environment friendly methods that recover important nutrients from sewage sludge, especially phosphorus and nitrogen. This work analyzes several approaches, such as chemical extractions, biological processes, and thermal processes, and evaluates how effective they are for extracting nutrients while considering their potential impact on the environment and economic viability. The review shows achievements in nitrogen and phosphorus recovery from sewage sludge by carefully examining current studies and practical applications. It highlights how crucial it is to reduce environmental damage while optimizing the possibility of nutrient reuse. The recovery of nitrogen and phosphorus in the form of struvite or other compounds help in enhancing soil fertility for crop growth ensuring that we use and recycle these nutrients in a way that minimizes harm to the environment.

Major findings

The major finding of this work is studying potential environment friendly techniques to recover nutrients from sewage sludge in a sustainable manner. resource efficiency can be increased, and environmental impact can be decreased through the effective application of these strategies. Struvite precipitation and calcium phosphate procedures are used to recover nutrients from sewage sludge. Struvite precipitation produces magnesium ammonium phosphate crystals, while calcium phosphate processes precipitate calcium phosphate compounds. The comparison indicates that both approaches effectively recover phosphorus, but struvite precipitation may be more energy-efficient and cost-effective in certain situations.

Keywords: Nutrient Recovery, Sewage Sludge Management, Phosphorous recovery

References

[1] Fengmei, Yang. (2023). Recent Advancement in Commercial and Other Sustainable Techniques for Energy and Material Recovery from Sewage Sludge. Water, 15(5):948-948. doi: 10.3390/w15050948

PI:125

Sustainable treatment of domestic sewage along with bioelectricity generation using an integrated constructed wetland- Microbial Fuel Cell (CW-MFC)

Sneha Gupta, Sangita Karmakar, Radha Rani[1]*
Department of Biotechnology, Motilal Nehru National Institute of Technology, Prayagraj, India

* radharani@mnnit.ac.in; raadharaani1982@gmail.com

Background

The global race for developing technologies that could solve major problems including harvesting energy from renewable sources, wastewater management and pollution have never been more demanding than the present. With the goal to cleanse wastewater and produce bioenergy, constructed wetland coupled microbial fuel cell (CW-MFC) systems combine an aerobic and anaerobic zone.

Review

Acrylic glass with a thickness of 1.8 cm was used to manufacture symmetrical pilot-scale built constructed wetland- microbial fuel cells (CW-MFC), with a total volumetric capacity of around 228 liters. Two sample sites are included in the design of the CW-MFC system: one is located 4 cm from the bottom in the anode zone and the other is located 17 cm from the bottom in the cathode region. Electrode layer was stack between the electrode collectors (charcoal). The distances between the cathode and anode 1 were 75 cm, anode 2 and cathode 42 cm, and anode 3 and cathode 36 cm respectively. Macrophytes *Pistia stratiotes* and *Lemna minor Arales* (duckweed) were planted after waste water was poured into the CW-MFC. In order to complete the external circuit, copper wire with a 0.75 mm thickness was used to connect all three anodes (A1, A2, and A3). Using a digital multimeter, the voltage output of the CW-MFC was measured and recorded.

Major findings

Open circuit voltage (OCV), polarization curve measurements, was used to study the performance of CW-MFC. After 12 days of operation, the maximum OCV was 520 mV, at which point it was nearly steady. The highest power density was 2226mW/m^3 and the corresponding current density of the CW-MFC system was 6.4 mA/m^3. COD was performed through chemical (closed reflux) method to analyze the oxygen demand of wastewater before and after the 5 days of operation. After 5 days of operation, the COD of the water sample, which was 928 mg/l on day 0, was found to be 754 mg/l. It was observed after 5th day that the COD removal percentage was 19.28%.

Keywords: **CW-MFC, artificial wetland, macrophytes.**

Reference:

[1] Abdulwahab, Y. D., Mohammed, A., & Abbas, T. (2021). Improving the performance of constructed wetland microbial fuel cell (CW-MFC) for wastewater treatment and electricity generation. *Baghdad Science Journal*, *18*(1), 0007-0007.

Dioecious plant diversity and their conservation status in the allahabad district, Uttar pradesh, india

Ankita Verma* and Deepak Kumar Gond
Chaudhary Mahadeo Prasad Degree College, Department of Botany (A Constituent PG College of University of Allahabad), Mahatma Gandhi Marg, George Town, Prayagraj- 211002, Uttar Pradesh, India
***ankita2596ver@gmail.com**

Background

Dioecy is a condition where staminate and pistillate flowers are present on separate individuals. These plants are prevalent among angiosperms and it is evaluated that only 6% of angiosperms show dioecy nature (Renner 2014; Seethapathy et al. 2018). These plants exhibit pure dioecy, androdioecy, gynodioecy and more commonly found among woody species than herbs (Baker 1959; Freeman 1977). In different sexual system of these plants different phytochemicals are found and their pharmacological effects also vary.

Review

Evolution of dioecy is considered as an example of irrevocable evolution or dioecy follows Dollo's law i.e., incompetent for the retrieval of latest ancestral state (Barrett 2021). There are several ecological factors, genetic factors and evolutionary pathways which facilitate expansion of these plants in hermaphrodite population and lead to dioecy (Senarath 2008; Barrett 2021). Distribution of these flora are uneven throughout the world and the exact statistical data are still not known.

Major findings

Present study gives an account of the dioecious plant diversity of the Allahabad district as well as their conservation status according to the IUCN red list. About 51 species (24 trees, 18 climbers, 7 herbs, and 2 shrubs) belonging to 20 different families and 41genera are reported in this field survey. Menispermaceae is the largest family having 9 species followed by Euphorbiaceae (6 species) and Moraceae (6 species). The dominating genera of dioecious flora belong to two medium sized woody trees i.e., Diospyros (3 species) and Morus (4 species) and one woody climber i.e., Tinospora (2 species). The result indicates that dioecy is more common among woody plants with fleshy fruits in comparison to the herbs, shrubs and climbers. These plants contribute very low to the species richness of a plant community of the district. Only 7.1% of the flora of the district of Allahabad is occupied by dioecious plants of Angiosperms. According to the IUCN data out of 51 species 16 species (31.3%) are Least Concern (LC), 34 species (66.6%) are Not Evaluated (NE), and 1 species (1.9%) is Data Deficient (DD).

Key words: dioecious; diversity; flora; IUCN

References

1. Barrett, S.C. (2021). Plant sex: Best to be bisexual when mates are scarce. Current Biology, 31(6), pp. R298-R300.
2. Renner, S.S. (2014). The relative and absolute frequencies of angiosperm sexual systems: dioecy, monoecy, gynodioecy, and an updated online database. American Journal of botany, 101(10), pp.1588-1596.
3. Senarath, W.T.P.S.K. (2008). Dioecy and monoecy in the flora of Sri Lanka and their evolutionary correlations to endemism, growth form, fruit type, seed number and flower size. Bangladesh Journal of Plant Taxonomy, 15(1), pp.13-19.

PI: 140

An innovative sustainable process development for nanolignin production from natural fiber

Raj lakshmi[a], Rintu Banerjee[a, *]
[a]Microbial Biotechnology and Downstream Processing Laboratory,
Agricultural and Food Engineering Department, Indian Institute of Technology
Kharagpur, Kharagpur-721302, India

*rb@iitkgp.ac.in,rintuin@gmail.com.

Background

Lignocellulosic biomass is recognized for its potential in the production of various products including biomaterials, biofuels, chemicals etc. Lignin, the second most abundant natural polymer after cellulose comprises 10–25% of total lignocellulosic biomass is a crucial component that provides a structural support to the plants. Lignin is a complex, three- dimensional, extremely cross-linked macromolecule formed through the enzymatic polymerization of three types of substituted phenols: sinapyl, coniferyl and p-coumaryl alcohols. This process results in the generation of numerous functional groups and linkages within the lignin structure.

Review:

Various sources contribute to the availability of lignin, including jute, coconut coir, hemp, cotton, wood pulp etc. As a result, the physical and chemical characteristics of lignin vary depending on the original source and the extraction method employed. Understanding these differences is essential for tailoring lignin to specific applications in the production of efficient product. Thus, the objective of this work is to utilize the lignin obtained from the liquor post processing of natural fibre (jute) for the formation of lignin nanoparticle. These nanoparticles show promising applications in functional surface coatings, composites formation, drug delivery and other products.

Major findings

1. The nanoparticles exhibited a consistent size distribution and maintained excellent stability across different aqueous pH conditions.

2. Characterization study (SEM, FTIR) were performed to confirm the lignin nanoparticle formation.
3. According to the study, the stability of the lignin nanoparticle dispersion persisted for over two months in pure water at room temperature.

Keywords: Waste valorization, Lignin,naturalfibre,Nanocomposites

References

[1] Lam,H.Q.,LeBigot,Y.,&Delmas,M.(2001).Formicacidpulpingofricestraw.*IndustrialCropsandProducts*,*14*(1),65-71.
[2] Lievonen,M.,Valle-Delgado,J.J.,Mattinen,M.L.,Hult,E.L.,Lintinen,K.,Kostiainen,M.A.,& Österberg, M. (2016). A simple process for lignin nanoparticle preparation. *GreenChemistry*,*18*(5),1416-1422.

A major challenge and threat on lignocellulosic biofuel production: a concept of circular economy

Anusha[a], Subhodeep Banerjee[b, c], SubharaDey[c], Rintu Banerjee[a,b,c]*
[a] Agricultural and Food Engineering Department, Indian Institute of Technology Kharagpur, Kharagpur, India
[b]Advanced Technology Development Centre, Indian Institute of Technology Kharagpur
[c]PK Sinha Center for Bioenergy and Renewables, Indian Institute of Technology Kharagpur

*rintuin@gmail.com

Background

Bamboo, a versatile and abundant natural resource, holds immense significance in various facets of human life, particularly in India. Its fast growth, renewability, and versatility make it an essential component of traditional practices, construction, and handicrafts. In the emerging bioeconomy, bamboo's potential extends to the realm of sustainable energy and biochemical production. In this context, the exploration of *Bambusabambos* as a substrate gains significance due to its widespread availability, economic relevance, rapid growth and renewability, holds immense potential in the Indian economy for bioenergy production.

Experimental study

The increasing demand for sustainable biofuel and biochemical sources has spurred interest in refining pretreatment strategies to maximize sugar yields from lignocellulosic materials. Leveraging a central composite design within response surface methodology, this study systematically investigates the intricate parameters including ultrasound intensity, treatment duration, solid loading, temperature, pH and enzyme concentration, that govern the synergistic effects of ultrasound and enzymatic pretreatment on *Bambusabambos*.

Major findings

(1) Through CCD based RSM studies, an increase in 4 and 6-fold enhanced reducing sugar release was observed when a chronological impact of ultrasound along with enzyme were employed.
(2) The enhanced release profile of the reducing sugar has been scientifically validated by XRD, FTIR and SEM studies.

Conclusion

The results not only highlight significant improvements in reducing sugar yields but also pinpoint optimal conditions crucial for the efficient enzymatic hydrolysis of this particular bamboo species. This research not only contributes to the evolving field of biomass conversion but also provides a nuanced understanding of the potential applications of sequential ultrasound and enzymatic pretreatment in enhancing the value proposition of *Bambusabambos* for sustainable biorefinery processes.

Keywords: Bamboo, Ultrasound pretreatment, enzymatic pretreatment, Response surface methodology

References

[1] Calcio Gaudino, E., Grillo, G., Tabasso, S., Stevanato, L., Cravotto, G., Marjamaa, K., Pihlajaniemi, V., Koivula, A., Aro, N., Uusitalo, J., Ropponen, J., Kuutti, L., Kivinen, P., Kanerva, H., Arshanitsa, A., Jashina, L., Jurkjane, V., Andersone, A., Dreyer, T., & Schories, G. (2022). Optimization of ultrasound pretreatment and enzymatic hydrolysis of wheat straw: From lab to semi-industrial scale. *Journal of Cleaner Production*, *380*, 134897.

[2] Naveena, B., Armshaw, P., & Tony Pembroke, J. (2015). Ultrasonic intensification as a tool for enhanced microbial biofuel yields. *Biotechnology for Biofuels*, *8*(1), 140. https://doi.org/10.1186/s13068-015-0321-0.

Immobilization of cellulase on green synthesized magnetite nanoparticles for effective recovery towards sustainable biocatalysis

GaddalaVijaykumar[a], Anusha, Rintu Banerjee[a]*
Agricultural and Food Engineering Department, Indian Institute of Technology Kharagpur, Kharagpur, India

*rintuin@gmail.com

Background

Enzyme immobilization is pivotal for enhancing the efficiency and sustainability of biocatalytic processes, particularly in biofuel production where cellulase plays a crucial role in cellulose hydrolysis. However, challenges in enzyme recovery and reuse necessitate innovative approaches. This study explores the immobilization of cellulase on magnetically responsive nanoparticles synthesized through a green approach, addressing both the technical and environmental aspects of sustainable biocatalysis.

Experimental Study

Green synthesis of magnetite nanoparticles is achieved using neem leaf extract, aligning with green chemistry principles. The synthesized nanoparticles are characterized through SEM, XRD and FTIR to elucidate morphology, crystalline structure, and surface functionality. Cellulase immobilization parameters, including enzyme loading, nanoparticle concentration, and reaction conditions, are systematically studied. The immobilized cellulase's stability, reusability, and catalytic activity are assessed and compared to its free enzyme counterparts.

Major Findings

(1) The successful synthesis of magnetite nanoparticles was validated by Fourier transform infrared spectral analysis, which revealed a significant peak between 400-600 cm^{-1}. The XRD pattern revealed the crystal structure of magnetite nanoparticles free of impurities.

(2) Immobilized cellulase exhibits enhanced stability over a pH range of 5-7 and temperatures of 40-70°C.

(3) The magnetic recovery facilitates easy separation and enables sustainable biocatalysis by promoting enzyme reuse. The immobilized cellulase retained 40% of its initial activity after 8 cycles.

This study provides a significant advancement in sustainable bioprocessing for biofuel production, highlighting the potential of green-synthesized magnetic nanoparticles as a promising platform for effective cellulase recovery and reuse.

References

[1] Ashwini John, J., Samuel, M. S., &Selvarajan, E. (2023). Immobilized cellulase on Fe3O4/GO/CS nanocomposite as a magnetically recyclable catalyst for biofuel application. *Fuel*, *333*. https://doi.org/10.1016/j.fuel.2022.126364

[2] Zambri, N. D. S., Taib, N. I., Latif, F. A., & Mohamed, Z. (2019). Utilization of neem leaf extract on biosynthesis of iron oxide nanoparticles. *Molecules*, *24*(20). https://doi.org/10.3390/molecules24203803

[3] Khoshnevisan, K., Bordbar, A. K., Zare, D., Davoodi, D., Noruzi, M., Barkhi, M., & Tabatabaei, M. (2011). Immobilization of cellulase enzyme on superparamagnetic nanoparticles and determination of its activity and stability. *Chemical Engineering Journal*, *171*(2), 669–673. https://doi.org/10.1016/j.cej.2011.04.039

PI: 146

A novel mutualistic consortium of oleaginous microbes for biodiesel production

Sarveshwaran Saravanabhupathy[a], Rintu Banerjee[a*]
[a]Agricultural and Food Engineering Department, Indian Institute of Technology Kharagpur,
Kharagpur-721302, India
*rb@iitkgp.ac.in

Background

The increasing need for sustainable energy sources has led to the emergence of biodiesel as a potential alternative to conventional fossil fuels. Microbial biodiesel, categorised as a third-generation fuel, has garnered major attention due to its prominence as a potential renewable energy resource. Biofuels derived from microbial sources provide a viable and sustainable solution to the world's energy issues, which has recently gained significant attention.

Review

Microbial consortia are assemblages of diverse microorganisms that exhibit a broad spectrum of uses in several biotechnology fields, including the synthesis of organic compounds, the purification of wastewater, and the elimination of harmful contaminants. An experiment was conducted to explore the potential of algae-fungi co-cultivation in enhancing the production of biomass and lipids utilizing chlorella and aspergillus species (Dash & Banerjee, 2017). In a different research, municipal wastewater was treated together with the generation of lipids using algae (Chlorella sp.) and bacteria (Kluyvera sp.) (Zhou et al., 2020).

Major findings

To enhance the microbial lipid synthesis in this investigation, a microbial mixed-culture system made up of bacteria, fungus, and algae was constructed. Chlorella sp. in the mixed culture serves as a source of oxygen emission, ensuring a continuous oxygen supply and pH regulation, resulting in increased biomass and lipid synthesis. Rhodococcus sp. consumes oxygen and releases CO_2 into the medium, which algae then use for photosynthesis to create biomass. Aspergillus sp. functions as a bioflocculant, aiding in the increase of biomass and the accumulation of lipids in the developed mixed culture. Various culture supplements were evaluated to enhance the growth and lipid storage in the axenic cultures, with the intention of subsequently employing them for growing in a mixed culture. Glycerol, a cost-effective by-product of the biodiesel industry, had optimal results among the evaluated supplements. Notably, the fatty acid content analysed though GC-MS analysis resulted in a considerable alteration in FAMEs produced through axenic and mixed culture systems.

Keywords: Lipids, Mixed culture, Symbiosis, Glycerol, Gas chromatography.

Reference:

[1] Zhou, X., Jin, W., Wang, Q., Guo, S., Tu, R., Han, S.F., Chen, C., Xie, G., Qu, F., & Wang, Q. (2020). Enhancement of productivity of Chlorella pyrenoidosa lipids for biodiesel using co-culture with ammonia-oxidizing bacteria in municipal wastewater. *Renewable Energy*, *151*, 598-603.

[2] Dash, A., & Banerjee, R. (2017). Enhanced biodiesel production through phyco-myco co-cultivation of Chlorella minutissima and Aspergillus awamori: an integrated approach. *Bioresource technology*, *238*, 502-509.

Use of crumb tyre rubber waste affecting environment in alluvial soil

Shivendra Singh Chauhan [a], Kumar Venkatesh [a], Prashant Kumar [a*]
[a]Department of Civil Engineering, Motilal Nehru National Institute of Technology
Allahabad, Prayagraj-211004, UP, India

*prashant.2023rce06@mnnit.ac.in

Background

Crumb tyre rubber includes a variety of organic pollutants and heavy metals, which can become volatile and spew poisons into the atmospheric environment. To avoid the harmful consequences of dumping worn out rubber tyres which *pose serious health issues, one has to imply this waste*. This can be achieved by incorporating crumb tyre rubber (CTR) in clayey alluvial soil which in turn results in enhanced properties of soils.

Review

Scrap tyres present a problem for recycling and disposal due to their thickness and the inclusion of numerous components. The tyre sector in India is developing at a 12% annual rate, resulting in increased waste volume. This article examines laboratory studies done on CTR in clayey soil.

Major findings

A series of trials were conducted by increasing the proportion of CTR from 2% to 8%, with each increment being 2%. The results showed that the unconfined compressive strength (UCS) of clayey soil improved, and the ideal amount of CTR was 4%.

Keywords: Clayey soil, Crumb tyre rubber, Unconfined compressive strength

References

[1] Yadav A K, Gaurav K, Kishor R and Suman S K 2017 Stabilization of alluvial soil for subgrade using rice husk ash, sugarcane bagasse ash and cow dung ash for rural roads *International Journal of Pavement Research and Technology***10** 254–261

[2] Owino A O, Nahar N, Hossain Z and Tamaki N 2022. Dimensional influence of basalt fiber reinforcements on the consolidation behaviour of rice husk ash stabilized soils *Construction and Building Materials***339** 127686

Optimization of process parameters for enhanced production and extraction of squalene from the yeast *Saccharomyces cerevisiae*

Adhithya Balaji[a], Suparna Sen[a], Kannan Pakshirajan[a]*
Department of Biosciences and Bioengineering, Indian Institute of Technology Guwahati, Assam, India – 781039
*pakshi@iitg.ac.in

Background

Squalene, a linear polyunsaturated triterpenoid, is used in different sectors, such as pharmaceuticals, and cosmetics, and as a nutritional supplement. Squalene is conventionally obtained from shark liver oil, which raises significant ethical and environmental concerns. In recent years, efforts have been directed towards exploring alternative natural sources such as plants (e.g., olives or amaranth) and microorganisms. Among the microbial sources, the yeast *Saccharomyces cerevisiae*, is promising for squalene production, owing to its easy cultivation under ambient room temperature conditions. Moreover, it is considered a GRAS microorganism (generally regarded as safe) and exhibits high tolerance to various stress conditions, including low pH, osmotic stress, and phage attack.

Review

In contrast to the traditional method of obtaining squalene from animal sources, microbial fermentation is significant in terms of sustainability and increased environmental friendliness [1]. Amyris, Inc., a biotechnology firm, has achieved successful commercial production of squalene by utilizing a modified yeast strain [2]. The extraction of squalene has been extensively documented in S. cerevisiae [3-5].

Major findings

This study aimed to examine and optimize different parameters that affect the production of squalene in S. cerevisiae BY4742. The results indicated a significant increase in squalene yield after 24 hours of incubation in mineral salts – based media containing 1% glucose as the carbon source, surpassing the yield obtained with conventional Yeast Extract, Peptone, and Dextrose (YPD) media. The squalene produced was extracted by employing three cell disruption techniques – homogenization, sonication, and saponification, and quantified through reverse phase high – performance liquid chromatography (RP-HPLC). Homogenization (0.1916g/L) was found to be the most effective extraction method, outperforming sonication (0.07381g/L) and saponification (0.04993g/L). Furthermore, the addition of an optimum concentration (0.02g/L) of the antifungal agent terbinafine hydrochloride in the medium enhanced the squalene titer (6.4125g/L), due to the inhibition of squalene epoxidase (ERG1), compared to that without terbinafine addition (0.1916g/L).

Keywords: Squalene,*S. cerevisiae*, extraction,production,optimization.

References

[1] Kim,etal.(2019).MetaolicEngineering,56,50–59,doi:10.1016/j.ymben.2019.08.013
[2] Fisheretal.(2013)UnitedStatesU.S.Patent8,586,814B2.
[3] Garaiováetal.(2014).FEMSyeastresearch14.2,310-323,doi:10.1111/1567-1364.12107

PI: 155

Encapsulation of Auxin into sodium alginate and chitosan matrix

Kavita Tiwari [a], Sneha Tripathi [a], Shivani Mahra [a], *Shivesh Sharma [a]
[a] Department of Biotechnology, Motilal Nehru National Institute of Technology, Allahabad, 211004, Uttar Pradesh, India

*shiveshs@mnnit.ac.in

Background

Since the dawn of modern civilization, the agriculture industry has consistently benefited from technological advancements. The importance of food production in meeting the demands of the world's expanding population is implied by the agricultural sector's emphasis in implementing technological advancements (Carpenter et al., 2011). The increasing need for biological products in agriculture fuels research on the formulation methods. (Do et al., 2021). In the world of plants, growth and development have their own conductors—tiny compounds called phytohormones. Consequently, phytohormones play a crucial role in moderating the plant's response to abiotic stress. (Skirycz and Inzé et al.,2010). The primary issue is that PGRs easily break down in the presence of environmental elements like light and temperature, which causes them to lose activity. These phytohormones can be shielded from deterioration and environmental variables by being encapsulated in agricultural areas (De et al 2021).

Review

The new formulation presented in this work enhances the effectiveness and durability of plant growth regulators in challenging environmental conditions. In this work, plant growth regulators were encapsulated using an ionic gelation-biopolymer method by combining alginate and chitosan. In addition to lowering the concentrations needed and making the products safer for the environment, encapsulation can enhance the physicochemical characteristics of the products and lessen issues like sorption and leaching. With regulated release and enhanced solubility, this study sought to encapsulate plant growth regulators.

Findings

99.6% and 96.12% Encapsulation efficiency were by mixing 600 mg of sodium alginate with 120 mg and 90 mg of chitosan. In both the formulation 108 mg and 103 mg of IAA were added.

References

[1] Carpenter, S. R., Cole, J. J., Pace, M. L., Batt, R., Brock, W. A., Cline, T., ... & Weidel, B. (2011). Early warnings of regime shifts: a whole-ecosystem experiment. *Science*, *332*(6033), 1079-1082.

[2] Do Nascimento Junior, D. R., Tabernero, A., Cabral Albuquerque, E. C. D. M., & Vieira de Melo, S. A. B. (2021). biopesticide encapsulation using supercritical CO2: A comprehensive

PI:157

Biosurfactants as pioneering agents in medical applications for enhanced therapeutics and diagnostics

Utpreksha Thapliyal[a] and Sangeeta Negi[a]
[a]*Department of Biotechnology, Motilal Nehru National Institute of Technology Allahabad, Prayagraj, Uttar Pradesh, 211004, India.*
**sn5@mnnit.ac.in*

Background:

The pharmaceutical industry is one of the major consumer catering industries for biosurfactants, accounting for a significant share of the market. The demand for biosurfactants in the pharmaceutical industry is driven by the need for eco-friendly, biocompatible, and sustainable solutions. In addition to this, biosurfactants offer several advantages over synthetic ones, such as low toxicity and high biodegradability, and remain active at extreme pH and salinity. In the pharmaceutical industry these compounds are used either individually or in combination with other bioactive compounds as drug delivering agent, anti-microbial agent, and anti-cancer agent. Their anti-adhesive, antibiotic, immunomodulatory and sperm-immobilizing activity have paved way for the exemplary research in pharma industry.

Review:

Biosurfactants such assaponins have been found to be a potential candidate for drug delivery system [1]. Further studies have shown that the drugs when combined with saponins have improved solubility and bioavailability. Similarly, another biosurfactant rhamnolipid have proven to regulate both humoral and cell-mediated immune responses. They also possess hemolytic, cytotoxic, antimicrobial, antibiofilm and anti- adhesive properties [2]. Lipopeptide biosurfactant such as surfactin have shown immunomodulatory properties by inhibition of CD40, CD80, CD54 and MHC-II which are present on the surface of macrophage [3].

Conclusion:

Although biosurfactants have proven to be very beneficial in medical and pharmaceutical industry but their high production cost and the lack of standardization in the industry are some of the key challenges faced by these industries. However, with the increasing demand for sustainable solutions, the market is expected to grow in the coming years. This review provides detailed knowledge about the application of biosurfactants in pharmaceutical industry along with the insights of their role in biomedical industry.

Keywords: **Drug delivery; immunomodulatory agent; sustainable; anti-adhesive**.

References

[1] Bottcher, S., Drusch, S., (2017). Saponins — Self-assembly and behaviour at aqueous interfaces. Advances in Colloid & Interface Science 105–113.

[2] A.M. Abdel-Mawgoud, F. Lepine, E. Deziel, Rhamnolipids: diversity of structures, microbial origins and roles, Appl. Microbiology. Biotechnology. 86 (2010) 1323–1336.

[3] Y. Kameda, S. Oira, K. Matsui, S. Kanatomo, T. Hase, Antitumor activity of Bacillus natto. V. Isolation and characterization of surfactin in the culture medium of Bacillus natto KMD 2311, Chem. Pharm. Bull. (Tokyo). 22 (1974) 938–944.

PI: 158

Enzymatic scouring of Cotton and Jute fiber using blend of pectinase and xylanase produced under solid state fermentation

Priya Kaithvar[a]Sangeeta Negi[a]*
Department of Biotechnology, Motilal Nehru National Institute of Technology, Allahabad, Prayagraj, 211004, India

*sn5@mnnit.ac.in

Background

Bio scouring is a process that used enzymes to remove non-cellulosic impurities from natural fibers such as cotton, wool, and jute.This process is eco-friendly and sustainable, as it reduces the need of harsh chemicals and minimizes wastewater pollution. Pectinase is one of the enzymes commonly used in bio scouring, as it breaks down pectin, a major non-cellulosic impurity in natural fibers. This method is more environmentally friendly and sustainable, which does not cause the release of hazardous substances in the environment as compare to the traditional scouring techniques used in the textile industry.

Methodology

Herein, the production process of pectinase enzyme we used strain i.e. Phenarochaete *chrysosporium*, the fungus was grown on substrates wheat bran in solid state fermentation. Optimal growth conditions were maintained to enhance enzyme yield. In enzymatic scouring of cotton fibers, the enzyme or enzyme blend was used in under the controlled conditions, followed by washing and drying for effective scouring, providing an ecofriendly alternative to hazardous chemicals.

Major findings

The crude extract of pectinase and xylanase enzymes displayed significant activity levels, measuring at 9.42 U/gds and respectively. Enzymatic scouring of cotton and jute fibers utilized different concentrations (4%, 8%, and 12%) of enzymatic blends. Bio scouring efficacy was assessed based on weight loss, impacting the initial cotton thread weight (68.1 mg). The highest post-scouring weight recorded was 67.8 mg for the 4% concentration, with the highest weight loss at 2.3% for 12% pectinase. Observations revealed a correlation between enzyme concentration and capillary action, with chemically scoured fibers exhibiting higher capillary action compared to enzymatically scoured ones. Additionally, as enzyme strength increased, capillary action followed suit, albeit to a lesser extent in jute fibers due to their higher weight loss and reduced material.

Keywords: Textile industry; Pectinase enzyme; Fiber; Bio scouring;

References

[1]Rocky, A. M. K. B. P. (2012). Comparison of effectiveness between conventional scouring & and bio-scouring on cotton fabrics. *Int. J. Sci. Eng. Res.*, *3*(8), 1-5.

[2] Madhu, A., & Chakraborty, J. N. (2017). Developments in the application of enzymes for textile processing. *Journal of cleaner production*, *145*, 114-133.

PI: 177

Characterization of deep eutectic solvents through computational approach and demonstration of interaction between the DES and residual catalyst from biodiesel

Sumaiya Zafar[a*], Dr. Padmini Padmanabhan[a]
[a]Department of Bioengineering and Biotechnology
Birla Institute of Technology, Ranchi

*sumaiyazk01@gmail.com

Background

Biodiesel is produced by alkali-catalyzed (eg: KOH) transesterification. Low content of catalyst is essential for biodiesel for its utilization as an alternative fuel. The international biofuel standard ASTM D6751 and EN 14214 suggests quantity of residual alkali metal to be less than 5mg/kg [1].

Review

Deep eutectic solvents (DES) are employed to remove residual catalyst (KOH) from biodiesel [2]. DES are biodegradable, low cost, non-toxic and ideal alternative solvents with respect to organic solvents. Classical molecular dynamic simulation based on OPLS force field are used for characterization of DES and its interaction with the catalyst. [3]

Major findings

DES is synthesized using hydrogen bond donor (choline chloride) and hydrogen bond acceptor (ethylene glycol). The molecular ratio of 1:1, 1:2, 1:3 of HBD:HBA is investigated for maximum efficiency. The molecules are packed using PackMol to pack the molecules and prepare the system. Spatial and radial distribution function (SDF and RDF) along with hydrogen bonding is investigated. RDF and H bonding are calculated by VMD (Visual Molecular Dynamics) whereas SDF is determined using TRAVIS program. Hydrogen bond interaction of Cl atom of ChCl and H atom of OH in catalyst showed essential interaction for its binding and separation. Present results open further prospects for utilization of DES for removal of residual catalyst from biodiesel system.

Keywords: Biodiesel, alkali catalyst, DES, Molecular Dynamic Simulation

References

[1] Bateni, H., Saraeian, A., & Able, C. (2017). A comprehensive review on biodiesel purification and upgrading. *Biofuel Research Journal*, *4*(3), 668-690.

[2] Shahbaz, K., Mjalli, F. S., Hashim, M. A., &AlNashef, I. M. (2011). Removal of residual KOH from palm oil based biodiesel using deep eutectic solvents. 1-12.

[3] Tolmachev, D., Lukasheva, N., Ramazanov, R., Nazarychev, V., Borzdun, N., Volgin, I., ... & Karttunen, M. (2022). Computer simulations of deep eutectic solvents: Challenges, solutions, and perspectives. *International journal of molecular sciences*, *23*(2), 645.

Valorisation of agro-industrial waste for high- titre production of lipopeptide biosurfactant to augment circular economy

Utpreksha Thapliyal[a] and Sangeeta Negi[a]*
Department of Biotechnology, Motilal Nehru National Institute of Technology Allahabad, Prayagraj, Uttar Pradesh, 211004, India.

*sn5@mnnit.ac.in

Background

Waste generation's detrimental impact on our ecosystem and the health of the population is an issue that demands prompt actions. Application of the waste as a feedstock for producing value-added products such as enzymes, proteins, biosurfactants etc. has given rise to exciting possibilities for environmental sustainability. Using waste such as wheat bran, mustard cake, soybean meal and waste cooking oil as a substrate, microorganisms have been used to produce biosurfactants as secondary metabolites. This has considerably reduced the overall process cost.

Methodology

In this research, the media was screened and the incubation time was optimized by using one variable at a time (OVAT) strategy. The solid substrate fermentation was used and *Aspergillus niger* was grown on waste material such as wheat bran (C1), soybean meal (C2), molasses (C3), cassava flour (C4) and rice husk (C5) in combination with mustard cake to produce lipopeptide biosurfactant. The incubation time taken were 2 (T1), 3 (T2) and 4 (T3) days respectively. The downstream processing of the biosurfactant was carried out and qualitative tests such as thin layer chromatography, oil displacement assay and drop collapse assay were carried out to ascertain the presence of biosurfactant. Further quantitative tests were also performed such as emulsification index, protein concentration and free fatty acid percentage to quantify the amount.

Result and Discussion

The emulsification index of C5 was found to be maximum 53.3% followed by C1 which was 50% at T3 respectively. The oil displacement assay was found to be maximum for C4 i.e. 8cm. The protein concentration was found maximum when using C3 i.e. 0.3118 mg/ml. The FFA% was 11% when using C1 as a substrate which was found to be maximum.

Keywords: Valorisation; emulsification index; lipopeptide; thin layer chromatography.

References:

1. Market research report 2022. The global biosurfactants market is projected to grow from $4.18 billion in 2022 to $6.04 billion by 2029, at a CAGR of 5.4% in forecast period, 2022-2029. https://www.fortunebusinessinsights.com/biosurfactants-market-102761.
2. Subramaniam, M.D.; Venkatesan, D.; Iyer, M.; Subbarayan, S.; Govindasami, V.; Roy, A.; Narayanasamy, A.; Kamalakannan, S.;Gopalakrishnan, A.V.; Thangarasu, R.; et al. Biosurfactants and anti-inflammatory activity: A potential new approach towards COVID-19. Curr. Opin. Environ. Sci. Health 2020, 17, 72–81.

Session-9

Young Scientist Award

Fungal-pectinases mediated retting of *sesbania aculeata* for extraction of sustainable natural fibers

Shruti Dwivediaa,*, Ankur Singha, and Dinesh Yadava
Department of Biotechnology, Deen Dayal Upadhyaya Gorakhpur University
Gorakhpur-273009, U.P. India
*dwivedishruti.727@ gmail.com

Background

The soil of different fruit orchards from Gorakhpur Uttar Pradesh was collected and used for soil fungi isolation and elucidation of their biotechnological application potential like retting of natural fibers, fruit juice clarification, and formations of calcium pectate gel sheets. These soil fungi were enzymatically characterized for pectinases (PG, PNL, and PME), and the effect of pH and temperature was studied on them. Among the 22 indigenous isolates, four Soil fungi identified as A. albamensis MTCC 13291, A. foveolatus MTCC 13310, F. falciforme MTCC 13298 and F. irregulare MTCC 13296 showed alkaline behavior on pH and were showed promising retting of fibers of Crotalaria and Cannabis. Pectinases of these isolates were used in the present study for pectinase-mediated retting of fibers of S. aculeata.

Review

The pectin-rich fiber, which is primarily located near the middle lamella, has a high degree of elasticity. Filamentous fungi being the natural sources of pectinases are often employed due to their shorter shelf life and mass production of enzymes. *Sesbania* is a legume frequently grown as a green manure crop to enrich the soil with organic matter and nitrogen. This plant produces fibers that are robust, long-lasting, and have a high tensile strength. Retting is a biological procedure that eliminates non-cellulosic substances that have been enzymatically linked to the fiber bundle, leaving only the detachable cellulosic fibers. Water retting is the most common method but requires submerging fibers for a long duration preferably months and yields low-quality fibers. Compared to fibers produced using conventional retting techniques, pectinase-retted fibers can have increased strength. Fibers may become less harmed and more breakage-resistant due to the regulated enzymatic breakdown of pectins. The composite performance was said to be improved by using the best pectinolytic retting formulation.

Major findings

1. Among all four screened isolates *F. irregulare* MTCC 13296 was found most promising isolate.
2. The water retting yielded total fiber in 15 days, water with calcium sequestering agent EDTA reduced time to 10 days.
3. Pectinase-mediated retting using indigenous soil fungi *F. irregulare* MTCC 13296 successfully showed 75% fiber extraction in 48 hours in water.

Keywords: soil fungi, pectinase-mediated retting, natural fibers

References:

1. Yadav, S., Maurya, S. K., Anand, G., Dwivedi, R., & Yadav, D. (2017). Purification, characterization and retting of Crotolariajunceafibres by an alkaline pectin lyase from Fusarium oxysporum MTCC 1755. *3 Biotech*, *7*, 1-9.
2. Dwivedi, S., Yadav, K., Gupta, S., Tanveer, A., Yadav, S., & Yadav, D. (2023). Fungal pectinases: an insight into production, innovations and applications. *World Journal of Microbiology and Biotechnology*, *39*(11), 305.
3. Monika, N., Anita, R., & Anupriya, S. (2017). Effect of retting methods on properties of Dhainchafibres. *Asian Journal of Home Science*, *12*(2), 395-401.

Ecological assessment of Sharda river by application of diatom indices

Saleha Naz[a*], Prateek Srivastava[a]
[a]Department of Botany, University of Allahabad, Prayagraj, India

*saleha_phd2020@allduniv.ac.in

Background

Rivers are among the most diverse and threatened ecosystems on Earth (Sabater et al., 2013). Biological communities of rivers reflect the overall ecological integrity by unifying various stressors, thus providing a broad measure of their synergistic impacts. Diatoms have been extensively used in rivers for bioassessment purposes throughout the world (Hughes et al., 2012). The Sharda River is a tributary of the River Ghaghara which originates from Kalapani in the Lesser Himalayas and flows along the international boundary of India and Nepal. The Sharda River is proposed to be linked to Yamuna in the National River Interlinking Project.

Review

The European Commission had passed a legislation mandating the use of different organism groups to monitor the integrity of inland waters and coastal regions (The Water Framework Directive 2000/60/EC (WFD). Many diatom indices were developed in the last decade of twentieth century, which were based on multiple taxa (genus or species). They are determined either in terms of presence/absence of key indicator species (e.g. Palmers index) or are based on the weighted average equation of Zelinka and Marvan (1961). Although the taxonomy of diatom flora has been well documented (Sarode & Kamat, 1984; Gandhi, 1957 – 1998; Nautiyal & Nautiyal, 1999; Karthick & Kociolek, 2011;) studies of the ecology and application of diatom assemblages in assessment of water quality have been dismally neglected.

Major findings

In the present study, water and diatom samples were collected from 17 sites in November 2022. PCA revealed three groups of sites, exhibiting moderate pollution (MP), Low pollution (LP) and Pristine conditions (PR). A high diversity of diatoms belonging to 40 genera were identified. CCA was employed to investigate the correlation between the composition of diatom assemblies and environmental factors. Using data from the diatom assembly, seventeen distinct diatom indices were computed in OMNIDIA software. Studies were also conducted into the association between index scores and measured water quality metrics which exhibited strong correlations with water quality variables. SPI and TDI were found to be most efficient and ascertaining in water quality assessment. Water quality maps for the Sharda River were hence prepared in accordance with these two indices. The results showed that Sharda River is a slight to medium polluted, oligotrophic-mesotrophic; quality ranging from moderate to good.

Keywords: Biomonitoring, Water quality, OMNIDIA, Diatom indices, Sharda River

References:

1. Gandhi, H. P., 1998. Freshwater Diatoms of Central Gujarat. Bishen Singh Mahendra Pal Singh. Dehra Dun.
2. Hering, D., Johnson & R. K., Kramm, S. (2006). Assessment of European streams with diatoms, macrophytes, macroinvertebrates and fish: a comparative metric-based analysis of organism response due to stress. Freshwater Biology, 51, 1757–85.

Melatonin and gamma-aminobutyric acid modulate cadmium toxicity in the paddy field cyanobacteria *Anabaena* sp. and *Nostoc muscorum*

Sakshi Pandey and Sheo Mohan Prasad*
Ranjan Plant Physiology and Biochemistry Laboratory, Department of Botany, University of Allahabad, Prayagraj-211002, India
sakshipandey02610@gmail.com
*****profsmprasad@gmail.com

Abstract:

In recent years, the rising population is putting pressure on the supply of food commodities, while another side severe alteration in the environment particularly in soil and water due to enhanced anthropogenic activities is negatively impacting the productivity of crops. Paddy is one of the prime staple foods that supports the growth and development of humans in several developing countries. Cyanobacteria are the important inhabitants of paddy fields and contribute as a source of carbon and nitrogen as they can convert atmospheric nitrogen to ammonia and fix carbon dioxide to organics. Hence, they are considered as biofertilizers since time immemorial. Increasing contamination by toxic chemicals such as heavy metals and pesticides of soil and water is directly affecting the crops and also the beneficial microbes, causing a great loss to crop productivity. To minimize such losses, in recent years several attempts have been made by scientists, governments, and agriculturists by applications of molecular manipulations, and exogenous applications of phytohormones and signaling agents. In present investigation, an attempt has been made by exogenous application of signaling molecules such as melatonin (MT) and gamma-aminobutyric acid (GABA) to alleviate the toxicity induced by cadmium (Cd) in two paddy field cyanobacteria *Nostoc muscorum* and *Ananaena* sp. Cadmium caused damaging effects on growth, photosynthetic pigments, PS II photochemistry, and photosynthetic oxygen evolution by accumulating Cd which resulted into excessive generation/accumulation of oxidative biomarkers: H_2O_2, superoxide radicals, and MDA equivalents contents despite of upregulation in enzymatic antioxidants: SOD, POD, and CAT. The exogenously applied MT and GABA considerably alleviated toxicity induced by Cd on these parameters by down-regulating the oxidative biomarkers and further elevating the antioxidant defense system.

Keywords:,Heavy metal, photosynthetic pigments, PS II photochemistry

Mycotoxin Deoxynivalenol assisted mitochondrial dysfunction and neurotoxicity

Sakshi Mishra[a], Divyansh Sharma[a], Sonam Kanchan[a], Gaurav Jha[a], Bhawana Tomar[a], Srikanta Kumar Rath[a*]
[a]Genotoxicity Laboratory, Division of Toxicology and Experimental Medicine
Central Drug Research Institute, (CSIR-CDRI), Sector 10, Jankipuram Extension, Sitapur Road Lucknow 226031, Uttar Pradesh, India

drsakshimishra@gmail.com, *skrath@cdri.res.in

Background

Mycotoxins, notably Deoxynivalenol (DON), impact mitochondrial dynamics, posing health risks in food. Links to neurodegenerative disorders require further exploration, especially due to DON's prevalence and hazards. Investigating its role in neuronal cells aims to bridge the gap in understanding mycotoxins and neurodegenerative diseases.

Review

DON has been found to induce neurotoxicity. It can cross the blood-brain barrier and interfere with the homeostasis and functioning of the nervous system (Fæste et al., 2022). DON has been shown to induce apoptosis in neuronal cells through the mitochondrial apoptotic pathway (Cao et al., 2021). It also affects the viability and function of astrocytes and microglia in the brain. DON exposure leads to oxidative damage, altered neurotransmitter levels, and disruption of calcium signaling in the brain (Wang et al., 2020). Additionally, DON induces cytotoxicity in human brain endothelial cells through oxidative stress, which can be attenuated by the antioxidant Vitamin E (Shieh et al., 2021; Zhang et al., 2020). Findings suggest that DON causes neurotoxic effects through various mechanisms, including apoptosis, inflammation, and oxidative stress.

Major Findings

DON exposure to human SH-SY5Y cells showed dose-dependent cytotoxicity, increased ROS, and calcium levels. ATP and mitochondrial potential decreased with rising DON concentrations. Elevated expression of mitochondrial fission proteins and reduced fusion proteins activity led to increased autophagic markers, indicating augmented autophagic activity due to DON-induced mitochondrial damage. ROS initiated mitochondrial damage, emphasizing ROS and Ca2+-mediated pathways in DON-induced mitochondrial dynamics alterations. Specific inhibitors targeting these pathways could combat mycotoxin-induced neurodegenerative diseases.

Keywords: DON, SH-SY5Y, Mitochondrial fission, ROS, oxidative stress

References:

Cao, L., et al., 2021. Deoxynivalenol Induces Caspase-8-Mediated Apoptosis through the Mitochondrial Pathway in Hippocampal Nerve Cells of Piglet. Toxins (Basel). 13, 73.

Fæste, C. K., et al., 2022. Neurotoxic Potential of Deoxynivalenol in Murine Brain Cell Lines and Primary Hippocampal Cultures. Toxins (Basel). 14.

Shieh, P., et al., 2021. Mechanisms underlying protective effects of vitamin E against mycotoxin deoxynivalenol-induced oxidative stress and its related cytotoxicity in primary human brain endothelial cells. Environ Toxicol. 36, 1375-1388.

Wang, X., et al., 2020. Mechanism of deoxynivalenol-induced neurotoxicity in weaned piglets is linked to lipid peroxidation, dampened neurotransmitter levels, and interference with calcium signaling. Ecotoxicol Environ Saf. 194, 110382.

Zhang, J., et al., 2020. The neurotoxicity of trichothecenes T-2 toxin and deoxynivalenol (DON): Current status and future perspectives. Food Chem Toxicol. 145, 111676.

PI: 137

Combined ultrasound enhanced enzymatic pretreatment and saccharification of corn stalk for generation of monomeric sugar for 2G biofuel generation

Subhodeep Banerjee[a,b], SubharaDey[b], Anusha[d], Tapas Kumar Bandhyopadhyay[c], Rintu Banerjee[a,b,d*]
[1] Advanced Technology Development Centre, Indian Institute of Technology Kharagpur
[2] PK Sinha Center for Bioenergy and Renewables, Indian Institute of Technology Kharagpur
[3] Department of Metallurgical and Materials Engineering, Indian Institute of Technology Kharagpur
[4] Department of Agricultural and Food Engineering, Indian Institute of Technology Kharagpur

[*]rb@agfe.iitkgp.ac.in; banerjeesubhodeep9@gmail.com

Background:

The global interest in biobased processes is increasing, and significant efforts are being made to create efficient technologies for the utilisation of bioresources.. Maize cultivation allows farmers to conserve 90% of water and 70% of power in comparison to Paddy cultivation. This contributes to an annual production of about 21 MT, makes corn stalk an ideal lignocellulosic waste as 2G biofuel feedstock.

Review:

Corn stalks primarily consist of leaves and stems, with the stems being formed of cortex and pith. The untreated Corn Stalk had hemicellulose, cellulose, and lignin levels of 33.6%, 38.7%, and 18.9% correspondingly, that needs to be converted into monomeric sugars for biofuel generation. Ultrasound exposure in a liquid medium produces highly reactive free radicals, which stimulate localised turbulence and microcirculation in the liquid, hence increasing the rates of mass transfer. The integration of laccase and ultrasound techniques results in decreased utilisation of chemicals, energy, and water. These methods show great potential in minimising the environmental footprint and operational expenses associated with traditional industrial processes. If lignocellulosic biomass is effectively saccharified, it has the potential to serve as an excellent raw material for the generation of biofuels.

Major findings:

The reduction of lignin polymers in biomass had been reduced to 80.43% which enables greater sachharification efficiency with reducing sugar yield after hydrolysis to 83% of holocellulose being converted to reducing sugars. CCD-RSM based optimization of combined enzymatic pretreatment and saccharification of biomass resulted in efficient removal of lignin, and production of monomeric sugars for fermentation to 2G biofuels like ethanol, butanol and biohydrogen.

Keywords: corn stalk, enzyme, biofuel, ultraosund

References:

1. Rajak, R. C., & Banerjee, R. (2016). Enzyme mediated biomass pretreatment and hydrolysis: a biotechnological venture towards bioethanol production. Rsc Advances, 6(66), 61301-61311.
2. Gonçalves, I., Silva, C., & Cavaco-Paulo, A. (2015). Ultrasound enhanced laccase applications. Green Chemistry, 17(3), 1362-1374.
3. Adekunle, A. E., Rabeya, T., Jehadin, F., Asad, M. A., Ayodele, O. O., & Islam, M. S. (2021). Compositional and microstructural changes in compressed hot water pretreated corn stalk. Current Research in Green and Sustainable Chemistry, 4, 100057.
4. Sherpa, K. C., Kundu, D., Banerjee, S., Ghangrekar, M. M., & Banerjee, R. (2022). An integrated biorefinery approach for bioethanol production from sugarcane tops. Journal of Cleaner Production, 352, 131451.

Invitro digestibility studies and physicochemical, structural evaluation of resistant starch from giant taro

Sayantan Santra, Mohan Das, Rintu Banerjee*
Microbial Biotechnology and Downstream Processing Laboratory, Agricultural and Food Engineering Department, Indian Institute of Technology Kharagpur, Kharagpur, India-721302
*rintuin@gmail.com

Abstract

Background: A sedentary lifestyle and unbalanced dietary habits contribute to a range of metabolic disorders. The significance of nutrition and diet is gaining prominence in cutting-edge research known as foodomics. Consumer demand for tailor-made food products with functional health-promoting properties has propelled rapid developments in modern food processing technologies (Sajilata et al., 2006). Several metabolic diseases are becoming prevalent now a days for example, India is the epicenter of diabetes due to inactive life style. Among the crucial factors which are responsible for worst pathophysiology of the Type II diabetes is consumption of carbohydrate rich foods which increases the blood glucose level

Review

Starch is a major component of any food and on the basis of extent of digestibility starch can be classified as rapidly digestible starch, slowly digestible starch and resistant starch. Recent research on resistant starch has demonstrated its ability to reduce blood glucose level and promote growth of beneficial gut microbiome (Das et al., 2022). Therefore, resistant starch is a potential raw material for formulating food specifically for patients suffering from diabetes and obesity

Major findings

The present research emphasizes on ultrasound assisted enzymatic biotransformation of giant taro (Alocasia macrorrhiza) for improving the resistant starch content followed by food formulation for therapeutic application. At optimized condition, ultrasound-assisted enzymatic treatment has improved the resistant starch content from 5.64% to 49.58 %. It was observed that enzymatic treatment has modulated several functional properties like water absorption capacity, oil absorption capacity and swelling power. The surface morphology of the enzymatically modified giant taro starch became compact and crystalline percentage also improved by 6.02%.

Keywords: Gianttaro, resistant starch, enzymatic processing, ultrasound treatment, prebiotic

Reference:

Sajilata, M. G., Singhal, R. S., & Kulkarni, P. R. (2006). Resistant starch–a review. Comprehensive reviews in food science and food safety, 5(1), 1-17. https://doi.org/10.1111/j.1541-4337.2006.tb00076.x

Das, M., Rajan, N., Biswas, P., & Banerjee, R. (2022). A novel approach for resistant starch production-fromgreen banana flour using amylopullulanase. LWT, 153, 112391. https://doi.org/10.1016/j.lwt.2021.112391

PI: 146

A novel mutualistic consortium of oleaginous microbes for biodiesel production

Sarveshwaran Saravanabhupathy[a], Rintu Banerjee[a*]

[a]Agricultural and Food Engineering Department, Indian Institute of Technology Kharagpur,
Kharagpur-721302, India

*rb@iitkgp.ac.in

Background

The increasing need for sustainable energy sources has led to the emergence of biodiesel as a potential alternative to conventional fossil fuels. Microbial biodiesel, categorised as a third-generation fuel, has garnered major attention due to its prominence as a potential renewable energy resource. Biofuels derived from microbial sources provide a viable and sustainable solution to the world's energy issues, which has recently gained significant attention.

Review

Microbial consortia are assemblages of diverse microorganisms that exhibit a broad spectrum of uses in several biotechnology fields, including the synthesis of organic compounds, the purification of wastewater, and the elimination of harmful contaminants. An experiment was conducted to explore the potential of algae-fungi co-cultivation in enhancing the production of biomass and lipids utilizing chlorella and aspergillus species (Dash & Banerjee, 2017). In a different research, municipal wastewater was treated together with the generation of lipids using algae (Chlorella sp.) and bacteria (Kluyvera sp.) (Zhou et al., 2020).

Major findings

To enhance the microbial lipid synthesis in this investigation, a microbial mixed-culture system made up of bacteria, fungus, and algae was constructed. Chlorella sp. in the mixed culture serves as a source of oxygen emission, ensuring a continuous oxygen supply and pH regulation, resulting in increased biomass and lipid synthesis. Rhodococcus sp. consumes oxygen and releases CO_2 into the medium, which algae then use for photosynthesis to create biomass. Aspergillus sp. functions as a bioflocculant, aiding in the increase of biomass and the accumulation of lipids in the developed mixed culture. Various culture supplements were evaluated to enhance the growth and lipid storage in the axenic cultures, with the intention of subsequently employing them for growing in a mixed culture. Glycerol, a cost-effective by-product of the biodiesel industry, had optimal results among the evaluated supplements. Notably, the fatty acid content analysed though GC-MS analysis resulted in a considerable alteration in FAMEs produced through axenic and mixed culture systems.

Keywords: Lipids, Mixed culture, Symbiosis, Glycerol, Gas chromatography.

Reference:

[1] Zhou, X., Jin, W., Wang, Q., Guo, S., Tu, R., Han, S.F., Chen, C., Xie, G., Qu, F., & Wang, Q. (2020). Enhancement of productivity of Chlorella pyrenoidosa lipids for biodiesel using co-culture with ammonia-oxidizing bacteria in municipal wastewater. *Renewable Energy, 151*, 598-603.

[2] Dash, A., & Banerjee, R. (2017). Enhanced biodiesel production through phyco-myco co-cultivation of Chlorella minutissima and Aspergillus awamori: an integrated approach. *Bioresource technology, 238*, 502-509.

PI:206

Exploring citrate synthase of *Leishmania donovani* for potential drugs against Leishmaniasis

Preeti Ranjan[a], Vikash Kumar Dubey[a]*
School of Biochemical Engineering, Indian Institute of Technology (BHU), Varanasi-221005

*vkdubey.bce@iitbhu.ac.in

Abstract

Globally, infectious diseases have been considered as the third leading cause of the death, and many of them fall under the category of neglected diseases. As per the World Health Organization, leishmaniasis ranks second among the major tropical illnesses after malaria, with an annual global mortality toll of 20,000–30,000 and 700000–1 million new cases. Since there are currently no commercially accessible vaccines to prevent this illness, chemotherapy is the only option for treatment. These medications also have a number of drawbacks, such as drug toxicity and parasite resistance, which make it necessary to investigate vital parasitic pathways that may serve as therapeutic targets and identify some promising antileishmanial compounds that may be targeted to combat this disease.

In this study, five compounds were selected using an *in-silico* drug repurposing approach. These compounds complied with Lipinski's five rules. Additionally, the *Leishmania donovani* citrate synthase gene was cloned and expressed in a bacterial system. Following affinity chromatography purification, these enzymes show more affinity towards acetyl-CoA compared to oxaloacetic acid in enzyme kinetics studies, and in inhibition studies, these selected compounds exhibit competitive behavior towards acetyl-CoA with ki values between 2 to 3 µM. Further, in vitro studies were conducted to investigate cytotoxicity and antileishmanial effects. With IC_{50} values of 0.92 ± 0.02, 0.65 ± 0.09, and 6.1 ± 0.91 against *Leishmania donovani* promastigote and EC_{50} values of 1.52 ± 0.37, 2.11 ± 0.38, and 10.4 ± 1.27 against intra-macrophagic amastigote without causing significant harm to macrophage cells, the three compounds—Abemaciclib, Bazedoxifene, and Vorapaxar—showed efficacious anti-leishmanial activities.Altogether, the present study identifies the potential FDA-approved compounds that might emerge as a lead to treat leishmaniasis.

Keywords: Leishmaniasis, TCA cycle, citrate synthase, enzyme kinetics, FDA-approved compound

References

[1] Saleem Yousuf Bhat and Insaf Ahmed Qureshi* (2021), Structural and Functional Basis of Potent Inhibition of Leishmanial Leucine Aminopeptidase by Peptidomimetics. ACS Omega, 6, 19076−19085.doi: 10.1021/acsomega.1c02386.

[2] Kartikeya Tiwari, Ritesh Kumar, Vikash Kumar Dubey*(2016). Biochemical characterization of dihydroorotase of Leishmania donovani: Understanding pyrimidine metabolism through its inhibition. Biochimie 131, 45-53.doi: 10.1016/j.biochi.2016.09.009.

PI: 207

Metamorphosis of hemocytometry: a paradigm shifts towards expedited bloodcellquantificationthroughautomation

D. S. Vohra[1]
[1]Research Scholar, Indian Institute of Technology (IIT) Roorkee, India
[1]ds_vohra@ce.iitr.ac.in(correspondingauthor)

Abstract

Purpose. The established procedure for quantifying red blood cells, white blood cells, and platelets through the methodology of hemocytometry is characterized by its substantial time demand. Nonetheless, a transformative alteration is projected via comparatively underexplored mechanisms of automation. This manuscript centralizes its focus on a particular automated modality designed to re-define the process of enumerating blood cells. It is imperative to recognize that the initial acquisition of a blood sample stands as the pivotal stride in the identification of medical conditions. The aspiration of this endeavour is the enhancement of the time-consuming nature inherent to the conventional blood cell quantification technique reliant on traditional hemocytometry. This objective aligns with the potential harboured by emerging automated methodologies in their infancy within this investigative domain.

Methods.
This article accentuates an emergent methodological pathway that promises to reshape the established framework governing the enumeration of blood cells. It remains pertinent to underscore that the primary phase of ailment diagnosis involves the procurement of a minute blood specimen. The methodology expounded upon in this paper orbits around the automation technique known as 'You Only Look Once' (YOLO), facilitating the prompt enumeration of blood cells from a minute micrometric droplet.

Results.
This arena remains relatively uncharted, sparking curiosity within investigative realms. Empirical outcomes accentuate the proficiency of the automated approach in discerning diverse blood cell morphologies within the testing dataset. Achieving accuracy levels surpassing 95% in discriminating erythrocytes, leukocytes, and platelets is realized within a fraction of the temporal investment demanded by hemocytometry.

Conclusions.
The outlined methodology can potentially empower medical practice with accelerated and precise quantifying of blood cells derived from diminutive specimens. This expeditious pace can accelerate the diagnostic process spanning various pathological conditions.

Keywords: Red Blood Cells, White Blood Cells, Platelets, Neubauer Counting Chamber, and YouOnly Look Once version 8(YOLOv8) Deep LearningModel

EFFICIENT PREDICTION OF BIOCHAR YIELD FROM PYROLYSIS OF AGRO-RESIDUES USING ENSEMBLE LEARNING WITH DECISION TREES

Saurav Kandpal, Ashish N. Sawarkar*
Department of Chemical Engineering
Motilal Nehru National Institute of Technology Allahabad
Prayagraj, Uttar Pradesh, INDIA

*Corresponding author email id: ansawarkar@mnnit.ac.in

Background

Pyrolysis is a prevalent technology used to convert biomass into pyro-gas, pyro-oil, and biochar under anoxic (low-oxygen) conditions. Biochar is a carbon-rich substance with a porous structure and large surface area, making it highly attractive for various scientific applications. The yield of biochar depends on both, the type of biomass used and the operating conditions of the pyrolysis process (Cao et al., 2016). To efficiently produce biochar, it is crucial to assess and optimize the pyrolysis conditions.

Review

To make pyrolysis a commercially viable energy production process, its efficiency under various operating conditions needs to be assessed. It is both expensive and time-consuming to determine the optimum conditions for efficient pyrolysis through experimental tests alone. Therefore, efficient machine learning methods can be employed to design models that accurately predict the yield of biochar based on the proximate and ultimate analysis of biomass, as well as the operating conditions of the reactor (Haq et al., 2022, Pathy et al., 2020).

Major findings

To evaluate the intricate relationship between biochar yield, biomass properties, and operating conditions, ensemble machine learning methods utilizing decision trees as the base class has been employed in the present investigation. Ensemble learning aids in enhancing the prediction accuracy of individual weak machine learning models. In this study, three ensemble learning methods—Random Forest, AdaBoost, and Xtreme Gradient Boosting algorithm—were utilized, resulting in low root mean square error (RMSE) and high R-squared (R^2) values for the prediction of biochar yield.

Keywords: Machine learning, Ensemble Learning, Decision Trees, Pyrolysis, Biochar yield

References

1. Cao, H., Xin, Y., Yuan, Q. (2016). Prediction of biochar yield from cattle manure pyrolysis via least squares support vector machine intelligent approach. Bioresource Technology 202, 158–164. doi:10.1016/j.biortech.2015.12.024
2. Pathy, A., Meher, S., P, B. (2020). Predicting algal biochar yield using eXtreme Gradient Boosting (XGB) algorithm of machine learning methods. Algal Research 50, 102006. doi:10.1016/j.algal.2020.102006
3. Haq, Z.U., Ullah, H., Khan, M.N.A., Raza Naqvi, S., Ahad, A., Amin, N.A.S. (2022). Comparative study of machine learning methods integrated with genetic algorithm and particle swarm optimization for bio-char yield prediction. Bioresource Technology 363, 128008. doi:10.1016/j.biortech.2022.128008

Organized by
Department of Biotechnology
Motilal Nehru National Institute of Technology
Allahabad, Prayagraj-21004, India

ISBN : 978-81-963268-9-0

9 788196 326890

MOHAN ENTERPRISES
Publisher and Printer (C/o Belvedere Press)
56C/13, Motilal Nehru Road, Prayagraj - 211001
7651834175