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ICABB-2024

THEME: FOOD & MICROBIAL BIOTECHNOLOGY

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and
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Jaypee Institute of Information Technology
(Declared Deemed to be University u/s 3 of the UGC Act)

MANOJ GAUR
Chancellor

January 10, 2024

MESSAGE

I am happy to know that the **Department of Biotechnology, Jaypee Institute of Information Technology, Noida**, is organizing the **’International Conference on Advances in Biosciences and Biotechnology (ICABB-2024)**’ from 31st January — 2nd February 2024, with its theme as **“Food & Microbial Biotechnology: Insights and Innovations”.**

The food and beverages market have gained tremendous importance after the Covid-19 outbreak and subsequent focus on health, and more importantly, food as the main source to combat many health issue. A strong focus on the food sector, where there is considerable emphasis and need for innovations is expected to contribute to the **Decade of Innovations,** also a significant theme in JIIT. There is an urgent need to develop linkages between budding researchers, scientists and entrepreneurs using biotechnological tools.

This conference will provide an excellent opportunity to all participants to share available knowledge base in the main theme as well as other important areas of biotechnology. Discussions and deliberations during the conference will encourage students, researchers and scientists, motivating them to develop interest in the entire chain of events from lab to market.

I am sure that the conference will be a great success.

With best wishes,

(Manoj Gaur)

Jaypee Institute of Information Technology
(Declared Deemed to be University u/s 3 of the UGC Act)

Prof. S.C. Saxena
Pro-Chancellor

January 10, 2024

MESSAGE

Our visionary founder, Shri Jaiprakash Gaur ji's dream of using technology for economic growth has resulted in establishment of institutes of higher education with excellent infrastructurefacilities, offering technical, undergraduate, post-graduate and doctoral programmes. Jaypee Institute of Information Technology, Noida has gained a reputation for high academic standards, along with excellent research infrastructure. The university aims to develop a human resource pool with sound technical skills and with the ability to fit into the global industrial environment effortlessly.

It brings me great joy to announce the upcoming **"International Conference on Advances in Bioscience and Biotechnology (ICABB-2024)"** organized by the **Department of Biotechnology at Jaypee Institute of Information Technology, Noida.** This is the 7th edition unfolding from January 31 to February 2, 2024, focusing on the theme **"Food and Microbial Biotechnology: Insights and Innovations."**

Conferences hold a special place in the scientific community, serving as crucial platforms for scholars, scientists, professionals, and researchers to converge, establish connections, and share their wealth of knowledge and expertise. In the spirit of fostering multidisciplinary collaboration, I am confident that ICABB-2024 will prove to be an exceptional forum, creating new avenues for research across various domains of Food and Microbial Biotechnology, as wellas in the broad biotechnology domain. Your presence and contributions are integral to the success of this conference, and I am optimistic that the insights shared and collaborations formed during these days will immensely benefit each participant.

I would like to extend my sincere appreciation to the organizers for their dedicated efforts in orchestrating this event. Their commitment and hard work are instrumental in ensuring that ICABB-2024 will be a resounding success.

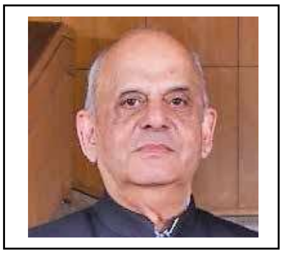
With best wishes,

(S.C. Saxena)

Jaypee Institute of Information Technology
(Declared Deemed to be University u/s 3 of the UGC Act)

Prof. B.R. Mehta
Vice-Chancellor

January 10, 2024



MESSAGE

The Department of Biotechnology has been very active in organizing international conferences for the past several years, each providing a vibrant platform for the exchange of ideas, and fostering collaborations. This edition, the 7th in the series, from January 31st to February 2nd, 2024, has a specific focus on the theme "Food and Microbial Biotechnology: Insights and Innovations."

As we enter the 'Decade of Innovation', from 2021-2030, initiated by Hon'ble Chancellor Sh. Manoj Gaur ji, it is imperative that we understand the true spirit of innovations, starting from lab to market scale, wherein student-led innovations are expected to play a major role, leading ultimately to self-sufficiency. JIIT has been making strides in fostering the innovation culture by establishing dedicated incubator facilities and digital technology-led education.

The food sector is especially an exciting one and developing into a crucial aspect of our economy. The theme of the conference fits in very well with India's current economic status. As we delve into discussions and presentations, I extend a warm welcome to all the esteemed delegates who will be participating in ICABB-2024. Through a diverse range of sessions and presentations, we anticipate uncovering novel strategies and breakthroughs that will shape the future of these critical disciplines.

This gathering is an opportunity to not only stay current with the latest developments but also to contribute to the ongoing dialogue that propels these fields forward. We believe that your expertise and contributions are invaluable.

With best wishes for a very successful conference

(Prof. B.R. Mehta)

Jaypee Institute of Information Technology

(Declared Deemed to be University u/s 3 of the UGC Act)

Message from the Organizers

It is with great anticipation and excitement that we extend our warmest welcome to each of you for the 7th "International Conference on Advances in Bioscience and Biotechnology (ICABB- 2024)" hosted by the Department of Biotechnology at Jaypee Institute of Information Technology, Noida.

We invite each of you to engage in thoughtful discussions, collaborative sessions, and the exchange of ideas during the conference. Let us collectively explore new frontiers in Food and Microbial Biotechnology, and fostering interdisciplinary collaborations that have the potential to shape the future of these fields.

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

We thank all the speakers and delegates who have kindly responded to our invitation and shown keen interest. Our Advisory Committee members have guided us throughout and we acknowledge the same. We give our heartfelt thanks to our enthusiastic organizing team, comprising our faculty members and students whose efforts in the meticulous planning and execution have contributed in making this event possible. The support received from oursponsors Department of Biotechnology, Govt. of India and Council of Science and Technology, Uttar Pradesh (UPCST), and our industry and publishing partners is gratefully acknowledged.

We sincerely believe that you will benefit from participating in the conference, meeting leading scientists in the field and interacting with budding scientists. We apologize for any shortcomings and look forward to your continued support for this and subsequent events in the coming years.

Thank you all once again.

Prof. Pammi Gauba
Chairperson

Prof. Indira P. Sarethy
Organizer

Smriti Gaur

Dr. Smriti Gaur
Organizer

SPEAKERS

Dr. Neerja Hajela

Dr. Neerja Hajela has done her Ph. D in Biotechnology and has a special interest in probiotics. She is currently the Head of Science and Regulatory Affairs at Yakult Danone India Pvt. Ltd. She has over 16 years of experience and has worked in organizations like Ranbaxy Laboratories Pvt. Ltd. and Biotech Consortium India Limited (Department of Biotechnology).

She is involved in the development, planning, and implementation of scientific programs including clinical trials for the company. She handles all the regulatory issues and ensures compliance related to the category and individual product. She works closely with health care professionals and scientists to advance the science, promote evidence-based clinical use, and improve consumer understanding of probiotics. She is associated with the Asian Federation of Societies for Lactic Acid Bacteria (AFSLAB).

She is a member of the Gut Microbiota and Probiotic Science Foundation (India) that aims to establish credibility for the science of intestinal microbiota and probiotics in the country. She is a member of the scientific committee of the Probiotic Association of India. She is also a member of the Governing Council for ILSI-India Knowledge Center for Functional Foods, Gut Health, and Immunity (IKFHI). She has presented at International and National conferences and has several publications in peer-reviewed journals.

Dr. Michael Sagner

Dr. Michael Sagner, a clinician and researcher, focuses on sports medicine and preventive medicine. He holds a certification as a nutritionist. He earned his MD from Technical University, Munich. He has specialised in sports medicine, endocrinology, and preventive medicine and has been affiliated with the College of Applied Health Sciences at the University of Illinois, Chicago. Dr. Sagner is the Founding Director of the European Society of Preventive Medicine, and partner of the European Innovation Partnership on Active and Healthy Aging. He was a member of the European Union Platform for Action on Diet, Physical Activity and Health, and the UK All-Parliamentary Group for Longevity. As a clinician he has spearheaded interventions in the field of endocrinology and cardiometabolic prevention such as the use of GLP1 agonists in Europe. His focus is on interdisciplinary approaches, looking at the systems of the human body as part of an integrated whole, incorporating biochemical, physiological, and environment interactions and translating these systems biology principles into clinical practice. He works on the convergence of systems biology and consumer-driven healthcare to transform medicine from its current reactive approach to an approach that is predictive, preventive, personalized and participatory. As a public health expert, he has spearheaded several international initiatives in the field of systems biology driven preventive medicine working with governments and NGOs. One of his interests is closing the gap between clinical practice and public health to promote more effective and patient-oriented care and preventive interventions for which he has collaborated with many NGOs such as the World Heart Federation (WHF), the World Obesity Federation and the World Health Organization (WHO).

Dr. Michael Danquah

Dr. Michael Danquah, Professor & Director, Chemical Engineering, at The University of Tennessee at Chattanooga, US, is a dynamic and innovative research leader specializing in the application of bioprocess and biomolecular engineering principles. Currently serving as the Tickle College of Engineering (TCE) Associate Dean for Academic and Student Affairs, Professor Danquah has found his faculty home within the Department of Chemical and Biomolecular Engineering. Dr. Danquah's expertise extends across diverse domains such as biopharmaceuticals, biosensing, environmental bioremediation, and biofuels.

Holding a bachelor's degree from Kwame Nkrumah University of Science and Technology in Ghana and a doctorate from Monash University in Australia, both in chemical engineering, Dr. Danquah is recognized as a Fellow of both the Institution of Chemical Engineers and the Royal Society of Chemistry.

With over a decade of active research, product development, and production-scale operations experience, Dr. Danquah has excelled in bioprocess engineering, process optimization, and technical consulting. His leadership style emphasizes practical outcomes, fostering diverse, multi-disciplinary research teams that balance imagination with modern management practices.

Dr. Danquah's key areas of expertise and consultancy encompass biomanufacturing, bioenergy, environmental remediation, cell culture, sustainable processing, and biopharmaceuticals. His impactful contributions are evident through more than 300 research publications and over 17,000 citations, particularly in biosensing, targeted delivery, and bioremediation.

Dr. Karuppiah Kannan

Dr. Karuppiah Kannan, Chief Development Officer, Wells Therapeutics Inc., US pursued his education from Madurai Kamaraj University, Madurai.

He has an extensive background in the biopharmaceutical and research sectors. Currently, he serves as the Chief Development Officer (CDO) at Wells Therapeutics Inc. Before this role, he dedicated over a decade to Takeda, where he held various leadership positions, including Executive Director - Global Program Leader, Senior Director, and Director. His tenure at Takeda was marked by his commitment to leading global programs, especially for clinical assets.

Mr. Yatee Gupta

Mr. Yatee Gupta is the Founder & CEO, Fabiosys Innovations, a Healthcare company based in IIT Delhi. The Fabiosys Team consists of graduates from IIT Delhi. and has mentors from IIT Delhi, AIIMS Delhi & Industry experts from the Indian Healthcare ecosystem. They have in-house prototyping and testing capabilities for the products being developed using their patented technology. Fabiosys has been supported by Dept. of Biotechnology, IIT Delhi, Pfizer & private funding for R&D, product development & commercialization.

Dr. Arockiasamy Arulandu

Dr. Arockiasamy Arulandu completed his BSc in the field of chemistry from St. Josephs College, Tamil Nadu, India. He further went on to pursue his Masters and PhD from Madurai Kamaraj University.

He is the Group Leader, Membrane Protein Biology at International Centre for Genetic Engineering and Biotechnology. His main research focus is on structure-based drug discovery for cancer and atherosclerosis therapy, targeting Vitamin-C recycling soluble human Chloride Intracellular Channels (hCLICs) and proatherogenic oxidized low-density lipoprotein (ox-LDL) receptor LOX-1, respectively. He also has various publications to his name. He is also a distinguished member of the Indian Biophysical Society.

Dr. Apurba Kumar Sau

Dr. Apurba Kumar Sau completed his master's degree in chemistry at the University of Calcutta in the year 1992. He later enrolled in the Ph.D. programme at the Tata Institute of Fundamental Research (TIFR), Mumbai, where he collaborated with Prof. Samaresh Mitra on the study of metalloprotein kinetic and spectroscopic research, which he finished in 1999. For his postdoctoral study, he relocated to the University of Texas at Austin in the United States. There, he focused on integrase and tyrosine family site-specific recombinases for almost two years. After that, he relocated to Yale University School of Medicine in the United States, where he worked for almost four years on target enzymes that are antibacterial and antimicrobial and are essential for the development of novel inhibitors. In 2004, he joined as a faculty at the National Institute of Immunology in New Delhi. He's currently holding a position of Scientist VII. His main research interest is Molecular mechanism of regulatory processes, Structural Biochemistry, Antibacterial and antimicrobial target enzymes and their functions and Drug-design. His group has published papers in leading journals such as J. Mol. Biol, J. Biol. Chem, Biochemistry, Biophysical Journal and Biochemical Journal.

Dr. Kar Muthumani

Dr. Kar Muthumani is currently Chief Scientific Officer at GeneOne Life Science, Inc., US. He is an experienced executive in vaccine development for infectious diseases and cancer with demonstrated history of pharma and academic collaborations. Skilled in design and testing of nucleic acid-based vaccines and immunotherapies. Strong R&D experience at top-tier research institutions. He has developed, evaluated, and demonstrated efficacy of vaccine immunogens for human immunodeficiency virus (HIV), chikungunya virus (CHIKV), middle east respiratory syndrome (MERS), Zika virus (ZIKA), Mayaro virus (MAYV), Nipah (NiV) and SARS-CoV2. He has also isolated a new strain of chikungunya virus, identified host cellular targets and host interactions of viral genes, and developed and characterized a novel, vector-based delivery for immunomodulatory antibodies (DMAbs) as a novel prophylactic or immunotherapeutic approach against viral pathogens, including HIV, CHIKV, Dengue, ZIKV, MAYV, and several cancer targets. In DMAbs, IgG genes are cloned into enhanced synthetic DNA expression vectors to provide an artificial source of antibody production in vivo. He has led and/or participated in multi-investigator research projects bringing together basic science/translational and preclinical scientists to evaluate synthetic nucleic-acid vaccines.

He has received several awards for his research including the (i) Young Scientist Award at the Nobel Symposium on Global HIV Therapeutics-HIV Vaccines in Stockholm (2001) (ii) the International Cytokine Society Young Investigator Award (2005), and many more.

Mr. Rohan Seth

Mr. Rohan Seth completed his engineering course from Jaypee Institute of Information Technology and further higher studies from New York University specialized in Biotechnology & environmental sciences. He has a total experience of 7+ years working with start-ups, as Business and ops head, focused on sustainable growth in new techs like UAVs, Solar, EVs and energy management at Energime, Anektos Energy, Raphe mPhibr Pvt Ltd and Vyom Power Pvt Ltd. He is passionate about preventing climate change and is constantly encouraging and promoting new & improved sustainable technologies. He co-founded the Anektos group which uses globally acclaimed technologies used in factory made building construction.

Mr. Abhishek Tyagi

Mr. Abhishek Tyagi completed his bachelor's degree in engineering in the field of Biotechnology from Jaypee Institute of Information Technology. He has an experience of more than 5 years in consulting for food safety systems, social audits, industrial set up. He does management consulting for EMS, QMS, OHSAS, BRCGS Food & Packaging, FSSC, FSQF, IFS, US FDA, FSSAI, Labelling development for domestic & international markets, Sedex, FSC COC, SA 8000, CTPAT, ESG , Costco COC.

Dr. Anukriti Verma

Dr. Anukriti Verma Founder of Simulacrum AI, Noida, Uttar Pradesh Dr. Anukriti Verma did research on predictive models in healthcare during her PhD and Post-Doc. She wanted to apply it at larger scale with intent to provide ore predictive models to more healthcare bodies with wider range of applications and faster improvement in the welfare of patients. Hence, she came up with the idea of forming Simulacrum AI.

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SESSION - ONE

Food
and
Agri-Biotechnology

ICABB_F_1

Investigating the Beneficial Effects of Mono Sodium Glutamate (MSG)

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ABSTRACT

Monosodium glutamate (MSG), also known as Ajinomoto, is a key component in the taste perception and personal well-being of individuals. Umami, a term first introduced by Ikeda in 1909, refers to the unique savory flavor found in various foods and beverages. It can reduce salt and fat intake and increase food consumption among older individuals. MSG, a component of the fifth fundamental taste, contributes to this sensation. The taste buds in the tongue have three types of cells, with Type II cells possessing G protein-coupled receptors that enable them to perceive sweetness, bitterness, or umami. When a ligand attaches to a receptor, intracellular heterotrimeric G proteins trigger a series of reactions, leading to the activation of sensory nerve fibers responsible for processing taste signals in the brain. MSG is often used in processed foods and Asian cuisine to enhance low-sodium dishes without compromising consumer approval. Research by Yamaguchi has shown that pure glutamate does not significantly impact food aroma. MSG can be introduced in its pure form or concealed within ingredients like yeast extracts or hydrolyzed proteins. This review aims to dispel myths and negative associations surrounding MSG while highlighting its positive attributes.

Keywords: Umami, Ajinomoto, MSG, Culinary Application, Sensory Perception, Health Effects.

ICABB_F_2

An Approach to Disrupt and Characterise Stable Bee Pollen Structure Using Ultrasonication

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ABSTRACT

Bee pollen, an API- product, is a potential source of various therapeutic activities such as antioxidant, anti-inflammatory, anti-bacterial etc. However, nutrient availability is restricted due to rigid exine and intine layers. In order to overcome the hindrances caused, the implementation of ultrasonication processing to bee pollen brings about notable positive changes in morphology, proximate, antioxidant, and functional properties of disrupted bee pollen. Scanning electron microscopy (SEM) micrographs reveal proficient segregation of the bee pollen cell wall into fragments, facilitating the efficient release of nutrients from the pollen grains. Proximate analysis reflects a substantial increase in fat and protein content by 31.6% and 49.3%, respectively. Antioxidant and TPC values exhibit a noteworthy concentration increase of nearly 13.9 and 83.94% along with significant improvement in techno-functional properties such as solubility (81.8%), OHC (98.5%), FA (61.4%), EA (61.2%). Processing treatment reflects that 4 hours of ultrasonication is sufficient to break the cell wall effectively and subsequently releases nutrients. Therefore, the application of ultrasonication emerges as the optimal technique for disrupting and maximising the utilisation of bee pollen superfood, which is currently under-exploited. The use of cell wall breaks bee pollen in various food and pharmaceutical products makes this under-utilised food source a high-performance food ingredient for better functionality and applicability.

Keywords: Bee Pollen, Ultrasonication, Superfood, Therapeutics.

ICABB_F_3

Edible Insects: A Novel Culinary Attraction for Tourists

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ABSTRACT

The present research aims to explore the world of entomophagy, specifically focusing on various edible insects and their potential as enticing attractions in the realm of culinary tourism. As the global interest in sustainable and exotic gastronomic experiences continues to rise, this study seeks to explore the nutritional value, cultural significance, and culinary versatility of different edible insect species. By investigating the incorporation of entomophagy into culinary practices, the research aims to shed light on the potential of edible insects as distinctive attractions for culinary tourists. Arunachal Pradesh, renowned for its tourism potential and biodiversity with rich flora and fauna, serves as a unique context. The indigenous tribes in the region consume edible insects, presenting a potential culinary attraction for tourists. The study focuses on various edible insect species found in Lower Subansiri and examines their potential as food attractions for tourists in the area. The findings contribute to our understanding of entomophagy's role in culinary tourism and offer practical implications for sustainable gastronomic practices within the local community.

Keywords: Edible Insects, Entomophagy, Culinary Tourism, Lower Subansiri, Arunachal Pradesh.

ICABB_F_4

Asparagus Adsendens Ameliorative Effect on 5-Fluorouracil Induced Gastrointestinal Mucositis in Wistar Rats

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ABSTRACT

Twenty-four five-week old male Wistar rats weighing 100-200 g were acquired from the Indian Institute of Integrated Medicine (IIIM), Jammu and acclimatized for 2 weeks before start of experiment in the Division of Pharmacology and Toxicology, SKUAST-Jammu. The animals were housed in a controlled environment (23°C, relative humidity of 50-55%, with a 12 hour light/dark cycle) with access to ad libitum food and water. The animals were randomly divided into four groups of six rats each, viz. Group-I as negative control receiving oral saline, Group-II receiving 5-FU, Group-III receiving 5-FU and *Asparagus adscendens* extract, and lastly Group-IV receiving *Asparagus adscendens* ethanolic root extract (AREE) alone. Parameters monitored were body weight, diarrhoea, histological scoring, survival. Gastrointestinal mucositis score (OMS) was recorded daily. Histological changes of the chemotherapeutic agent (5 FU) administered intestine were assessed by hematoxylin and eosin staining. Experiments were conducted following the injection of 5-FU. Significant weight loss resulted from repeated 5-FU dosing. Modifications in the diarrhoea score after administering 5 FU shots. With 5-FU, the diarrhoea-score dramatically rose. The mean ± S.D. of six mice is shown by each point. P value is shown to be $p<0.05$ compared to the control (saline) between each group.

Keywords: Chemotherapy, Wistar Rats, 5 FU, *Asparagus Adscendens*, Diarrhoea.

ICABB_F_5

Antioxidant Activity of Green Synthesized Ag-Ni-Mn-Zn Nanoparticles

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ABSTRACT

Nanotechnology enables the creation of new, innovative materials, gadgets, and technologies with special qualities and functions, nanotechnology has the potential to transform several fields, including materials science, energy, electronics, and medicine. Nanotechnology can also modify matter at the nanoscale. This study outlines an environmentally acceptable process for producing Ag-Ni-Mn-Zn quadmetallic nanoparticles from industrial and household waste i.e., *Citrullus lanatus* (watermelon) peel extract, which serves as a reducing and stabilizing agent. UV-Vis spectroscopy was used for the initial characterization of the nanoparticles. Further synthesized nanoparticles were used to evaluate the antioxidant activity i.e., DPPH scavenging activity. Results exhibited enhanced antioxidant activity by the Ag-Ni-Mn-Zn quadmetallic nanoparticles. The quadmetallic nanoparticles Ag–Ni–Mn–Zn showed a greater scavenging activity of 75.62% at 500 µg/ml and 89.94% at 1000 µg/ml, which is similar to the well-known antioxidant ascorbic acid. As a result, watermelon peel-derived Ag-Ni-Mn-Zn quadmetallic nanoparticles may have new uses as antioxidants.

Keywords: *Citrullus Lanatus*, Nanoparticles, Antioxidants, Quadmetallic, Spectroscopy.

ICABB_F_6

Developing Hydrocolloid-Infused Honey Fillings for Cookies: A Comparative Study against Commercially Available Fat-Based Alternatives

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ABSTRACT

This study aimed to develop honey fillings for cookies using a variety of hydrocolloids, including xanthan gum (XG), guar gum (GG), and gelatin. The optimization of hydrocolloids concentration in honey for developing honey fillings was successfully achieved through a Box-Behnken design, involving three independent variables: XG (5-10% w/w), GG (0.1-1.5% w/w), and gelatin (8-12% w/w). The effects of these variables were assessed in terms of the honey filling's baking stability, antioxidant capacity, firmness, and water activity. The ideal concentrations for the honey filling were identified as 5.23% XG, 1.4% GG, and 10.46% gelatin. The physicochemical, antioxidant, and rheological characteristics of the optimized honey filling (OHF) were analyzed and compared to a commercial chocolate filling (CCF) as a reference. OHF displayed slightly superior viscoelastic properties and maintained structural stability across all frequencies, while CCF exhibited liquid-like behavior at higher frequencies, indicating weaker structural strength. OHF also demonstrated higher total phenolic content (TPC), enhanced antioxidant activity, and negligible fat content. Subsequently, OHF was employed as a filling ingredient in cookies and compared to non-filled cookies and CCF-based cookies. The OHF-based cookie exhibited similar textural attributes and sensory appeal to the CCF-based cookie, along with improved TPC and antioxidant activity, and substantially lower fat content compared to both non-filled and CCF-based cookies.

Keywords: Hydrocolloids, Box-behnken Design, Antioxidants, Cookies.

ICABB_F_7

Development of Cake Pre-Mix by Replacing the Fat by Addition of Quince Mucilage

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ABSTRACT

The fast-paced nature of today's hectic lifestyle, characterized by limited time for cooking, has driven the food industry to prioritize the production of quickly prepared, more convenient, and nutritionally improved foods. As a reflection of this trend, this study sought to create a ready-made cake mix that utilizes dry quince mucilage as a substitute for fat and only necessitates the addition of water in the preparation process. The premix was formulated with wheat flour, sugar, powdered milk, dehydrated whole milk, dehydrated whole egg, baking powder, and dry quince mucilage. Furthermore, these formulations were compared to a commercial cake mix based on their proximal composition and technological and physical characteristics. The cake mix developed with quince mucilage proved to be easier and faster to prepare than the other recipes, primarily because it didn't require the addition of extra ingredients. Additionally, the new mix formulations exhibited lower lipid content than the commercial product, with particular attention given to the pre-made mix that incorporated quince mucilage. Moreover, the new ready-made cake mix had a less dense texture (6.75N) than the alternatives (9.58N), making it more palatable. In summary, this cake premix was developed to offer superior nutritional properties and easy preparation.

Keywords: Cake mix, Quince Mucilage, Ready-to-Cook, Fat Replacement.

ICABB_F_8

Exploring the Multifaceted Roles of Lactic Acid Bacteria in Managing Irritable Bowel Syndrome

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ABSTRACT

In the exploration of the close relationship between microbes and human health, the focus on beneficial bacteria residing in the gut, especially *Lactobacillus* and *Bifidobacterium*, has gained a great attention in recent years. These bacteria are often classified as probiotics and commonly found in fermented foods, contributing significantly to human health by producing diverse metabolites and bioactive components. Their crucial role in gastrointestinal health is increasingly recognized, resulting in evaluation of their potential therapeutic applications. A prevalent gastrointestinal disorder, namely Irritable Bowel Syndrome (IBS) has been largely managed without utilizing established pharmacological treatments. However, recent advances in research have utilized the efficacy of lactic acid bacteria, in managing IBS symptoms. This review aims to elucidate and discuss existing literature studies focusing on beneficial properties of probiotics as well as exploring their suitability as an alternative biological approach for treating IBS. This review also comprehensively explores the mechanisms of actions, which could possibly contribute to filling the therapeutic gaps and offer novel perspectives on addressing the complexities of IBS through the harnessing these beneficial bacteria.

Keywords: Lactic Acid Bacteria, Probiotics, IBS, Fermented Food, Therapeutics.

ICABB_F_10

T-2 Toxin: A Silent Killer of the Heart

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ABSTRACT

Mycotoxins are naturally produced fungal secondary metabolites which grow on a variety of foods, including cereals, nuts, dried fruits, and spices. Trichothecenes-2 (T-2) toxin, one of the most toxic mycotoxins, is known to have adverse effects on the immune system, neurological system, cardiovascular system, and reproductive system.

Importantly, cardiovascular diseases are recently reported to be associated with T-2 toxin and its metabolized forms. Increased capillary permeability, necrosis of cardiomyocytes, and the infiltration of inflammatory cells in the heart are the hallmarks of T-2 toxin-induced cardiac toxicity and death. Mechanistically, T-2 toxins are believed to exert cardiac stress by Reactive Oxygen Species (ROS), Mitochondrial Malfunction, Endoplasmic Reticulum Stress, Peroxisome Proliferator-Activated Receptor-Gamma (PPAR-γ) signaling pathway modulation, autophagy, and inflammatory responses. In order to fully comprehend the systemic toxicity of T-2 toxins and to inform strategies to reduce the cardiovascular risks associated with mycotoxin exposure, research on T-2 toxins and the cardiovascular system is essential.

Keywords: Mycotoxins, Trichothecenes-2, Reactive Oxygen Species, Cardiovascular Diseases.

ICABB_F_11

Characterization of genes and Phylogenetic Analysis of Protein Sequence Data in Indigenous Cattle Mitochondrial Genome

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ABSTRACT

India prevails to be a reservoir of magnificent and diverse germplasm of cattle genetic resources. In order to explore the mitochondrial protein sequence information of 45 distinct breeds and with the aim of indigenous cattle conservation strategy and improvement, we annotated the mitochondrial genome of 341 cattle animals. The bovine mitochondrial genome with a length of 16,339 bp and base composition of 33.4% A, 27.1% T, 13.4% G and 26% C, contains 37 genes coding for 13 polypeptides, 22 tRNA, 2 rRNA and a control region as well. Out of 64 codons, the most frequently used codons were Leucine (CUA), Valine (GUA), Serine (UCU), Proline (CCU), Threonine (ACA), Alanine (GCC), Arginine (CGA) and Glycine (GGA). We also analysed the 13 nucleotide coding genes finding variations in them and estimate the amino acid substitution observing that none of the variation causes any deleterious effect on protein functioning. These variations were observed in 18 animals belonging to 12 breeds supporting *Bos taurus* while the rest of the 323 animals were supporting *Bos indicus*. The maximum likelihood method was utilized for phylogenetic analysis of 45 breeds which confirms two different clades, Clade 1 indicating *Bos taurus* whereas Clade 2 suggest *Bos indicus* species. While evaluating the Codon based Z test of evaluation, we observed the value equals to < 1 (-25.52) which indicates a purifying selection in our populations. The study will pave the path in development of conservation policies and initiating more research on the indigenous cattle.

Keywords: Mycotoxins Coding genes, Variations, Nucleotide.

ICABB_F_12

Recovery of Mycelial Biomass of *Agaricus bisporus*, *Pleurotus ostreatus*, *Ganoderma lucidum*, *Hieracium erinaceus*: A Comparative Study

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ABSTRACT

Mushrooms are the spore-bearing fruiting body of fungi. They are typically made of hyphae, the tiniest threads which comprises most fungi. Mycelia are tiny thread like structure which help in making vegetative part of fungus. In this study, the growth of mycelia from four mushroom species *Agaricus bisporus*, *Pleurotus ostreatus*, *Ganoderma lucidum*, *Hieracium erinaceus* in PDA and PDB was compared. We report morphological characteristics of the mycelia on the basis of colour, texture, growth time requirement. There was a significant difference in yield of mycelial biomass in the PDA and PDB. We could recover 0.260 gm of *Pleurotus ostreatus* mycelia, 1.760 gm of *Agaricus Bisporus* mycelia, 0.038gm of *Ganoderma lucidum* and 0.427 gm *Hieracium Erinaceus* mycelial biomass after 15 days of culturing on PDA agar plates. recovery of mycelial biomass on PDA was better than PDB The culturing of fungal mycelia on PDA is a good way to produce fungal biomass. The utilization of fungal biomass can prove to be helpful in different areas such as medicine, nutrition, agriculture, and sustainability of environment.

Keywords: Mycelial Growth, PDA, PDB, Species *Agaricus bisporus*, *Pleurotus ostreatus*, *Ganoderma lucidum*, Mane *Hieracium erinaceus*.

ICABB_F_13

Optimizing Fermentation Conditions for Enhanced Production of ACE Inhibitory Peptides from Cow Milk

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ABSTRACT

Angiotensin I-converting enzyme (ACE) plays a crucial role in blood pressure regulation, specifically in managing hypertension. During the fermentation of milk, lactic acid bacteria (LAB) can produce ACE-inhibitory peptides through the breakdown of milk proteins. This study aimed to determine the optimal conditions for producing ACE inhibitory peptides through lactic acid bacteria (LAB) fermentation in both Desi and American cow milk. Different parameters, including the impact of temperature (25°C, 30°C, 35°C, 40°C, 45°C), inoculum amount (1%, 3%, 5%, 7% and 9%), and incubation period (Day 1, Day 2, Day 3, Day 4, Day 5) on ACE inhibition rate were studied. Other parameters, including pH, titration acidity %, and proteolytic activity were also studied. The results suggest that the fermentation of milk with a 1% inoculum of bacteria at 37°C for two days was the most favorable fermentation conditions. Under these conditions, ACE inhibition rates reached their maximum at 89.59% for American cow milk and 89.5% for Desi cow milk.

Keywords: Cow Milk, ACE, LAB Fermentation, Hypertension.

ICABB_F_14

Inhibition of Quorum Sensing to Mitigate the Risks of Membrane Biofouling in Biological Wastewater Treatment

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ABSTRACT

Membrane-based systems play a pivotal role in various applications, providing efficient separation, purification, and filtration processes across diverse industries such as reverse osmosis, nanofiltration, ultrafiltration, and microfiltration. Membrane biofouling poses a persistent challenge in various water treatment processes, particularly in membrane-based systems, impacting the efficiency and sustainability of such systems. Quorum sensing (QS), a communication mechanism among microorganisms, plays a crucial role in the formation of biofilms on membrane surfaces. This article gives a comprehensive review of Quorum sensing (QS) regulation, biofilm formation, and role of QS inhibition: Quorum quenching, Quorum sensing inhibitor in preventing membrane biofouling. This article delves into the potential of disrupting quorum sensing pathways to prevent or reduce biofilm formation, thereby enhancing the performance and longevity of membranes in wastewater treatment. At last, knowledge gaps present in current researches and challenges are also proposed.

Keywords: Membrane Biofouling, Quorum Sensing, Quorum Sensing Inhibition, Waste Water Treatment.

ICABB_F_15

Quality Evaluation of Prebiotic Cookies Utilizing a Sensor Based Electronic Nose System

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ABSTRACT

Human nose fails to sense and quantify all the released gases in the form of volatile compounds from spoiled food due to several environmental reasons. Hence, there is a need to find an alternative to the human nose which could detect the spoilage of food products in a more precise and accurate way. Considering the need, research interests have sparked the development of an electronic nose which operates similar to the human nose and provides values of gases released during spoilage of any food product. Nowadays, electronic noses have been widely used for determining shelf life of food products. This study focusses on development of Arduino Uno-R3 microprocessor based electronic nose system which is equipped with different MQ sensors, namely MQ3, MQ4, MQ5 and MQ9. The developed E- nose system was further used in evaluating the freshness of different prebiotic cookies during 5 months of storage. During analysis odor intensity values were recorded, compared and positively correlated with physical, microbiological and FTIR parameters in determining the overall quality. Findings from this research study will further contribute in advancing the development of electronic nose systems, enabling their versatile application across the food industry.

Keywords: Shelf- life, Prebiotic, Cookies, E-nose, Sensors, Quality.

ICABB_F_17

Contribution, Limitations and Future of Plant Growth Promoting Consortium in Sustainable Agricultural

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ABSTRACT

Present agricultural practices depend heavily upon chemical fertilizers, pesticides and other crop chemicals for plant growth promotion and pathogen control with an intention to increase crop yield. Chemical residues left in soil after cropping decrease soil fertility by gradually altering its chemical composition and rendering it non-fertile. The highrisk conditions associated with these agricultural chemicals such as bioaccumulation, chemical toxicity and development of resistance in pathogens is leading to increased awareness and acceptance of sustainable agricultural practices promoting usage of microbial alternatives as plant growth promoting microbes.

Modern agricultural practices prefer to use biological agents for plant growth promotion and biocontrol with aim for sustainable soil management, as these are cost effective and eco-friendly. Widely popularized and scientifically explored plant growth promoting microbes promise great solutions to increase crop productivity while providing an alternative to agricultural chemicals. Many such commercial biofertilizers and bio pesticides are available in market, which are cost effective and eco-friendly too. Despite these qualities, market penetration and acceptability of these bioinoculants are limited.

The study explores major limitations of existing bioinoculants, major hurdles affecting formulation quality, gap between potential market demand and production, concepts of consortia to produce synergistic effects, challenges in consortia-based formulation development. The study also presents solutions to overcome these bottlenecks so that these bio-products can help to reduce the toxic chemical load in soils augmenting the soil health, and prove to be a valuable and better acceptable option for sustainable agriculture.

Keywords: Consortia, Bioformulations, Biopesticides, Biofertilisers, Bioinoculants, Plant Growth Promotion and Biocontrol, Sustainable Agriculture.

ICABB_F_18

Scope and Veracity of Synthetic Biology and its Potential Contribution to Meet National Food Security Goals

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ABSTRACT

The projected global population statistic of 9 billion by 2050, is sending serious signals to all concerned and pushing the expectations on Agriculture research to an all-time high. The future of the agriculture sector depends upon how researchers address the food security crisis and attempt to plug-in crop productivity losses due to abiotic and biotic stress factors. By now, plant-microbial relationships and plant-microbiome are well studied schools of research. Most recently, strong research evidence is emerging, where use of plant-microbiome through synthetic biology approaches and attempting to address different stress conditions is being identified as the primary option to attain sustainable agriculture development. Synthetic biology is opening new opportunities for modern agricultural practices.

Different countries like the UK, USA, China, Australia have established different synthetic biology centers to promote the evolutionary development of bioengineering. Synthetic biology works on targeted engineering of beneficial microbiomes. Taking cue from advances in synthetic biology research, certain international companies have come up with microbiome-based fertilizers too. The study presents an overview of national agriculture policy and its approach to attain food security. The study presents a calculated insight on how various advances in synthetic biology can help in design strategies that are aimed to improve agriculture dynamics both at national and internal levels.

Keywords: Synthetic Biology, Plant Growth Promoting Rhizobacteria (PGPR), PGPM, Plant Microbiome.

ICABB_F_19

Plant Growth and Response in Microgravity

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ABSTRACT

In our pursuit of sustainable human space exploration, we have delved into the pivotal realm of plant space biology. This review highlights the interdisciplinary nature of plant biology in space, encompassing aspects of biology, engineering, and psychology. Here we present an overview of the factors influencing plant growth in space and the experimental conditions designed to simulate extraterrestrial environments on Earth. A brief overview of the effect of microgravity/hypogravity - altered growth patterns, affecting root orientation and shoot development is presented. Molecular and physiological changes in gene expression related to growth, development, and stress response are analyzed to comprehend the impact of microgravity on plants. Further, optimization of nutrient delivery methods i.e. hydroponic and aeroponic methods, are investigated to optimize plant nutrition in the absence of traditional soil-based agriculture. In addition to this simulation of light conditions to compensate for the absence of sunlight in space, with an emphasis on providing optimal conditions for photosynthesis is discussed. Further challenges due to radiation exposure in space affecting plant DNA, growth, and reproduction is also reviewed in terms of transcriptomic analysis. The knowledge gained from these investigations not only addresses the challenges of space exploration but also contributes to advancements in terrestrial agriculture and ecological sustainability.

Keywords: Microgravity, Hypogravity, Sustainable Agricultural Ecosystems, Transcriptomic Analyses.

ICABB_F_20

Fermented Functional Foods for Regulation of Scalp Microbiome and Alopecia

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ABSTRACT

Fermented plant extracts can be used as functional foods, formed by the fermentation of fresh plants by microorganisms, mainly bacteria or fungi. The structural breakdown of plant cell walls and hydrolysis activity of the bacteria/fungi during fermentation increases plant derived secondary metabolites (polyphenol, alkaloids, terpenes) and also increases the bioavailable phyto-molecules' content, which have been potentially shown to have cosmetic properties, especially in hair improvement. Several studies report the effectiveness of these fermented plant extract metabolites on human hair follicle dermal papilla cells (HDP), a specialised fibroblast in hair bulb, that plays a role in controlling hair growth. The fermented plant extracts are reported bring about activation of various signalling pathways that improves HDP cell proliferation. These fermented plant derived bioactives are emerging as promising agent for innovative therapeutic approach towards alopecia areata, a dermatological autoimmune disorder, characterised by non-scarring hair loss or body skin, with the focus on modulating skin and gut microbiome. The present review reports the diverse studies that have shed light on the role of gut microbiome and metabolome having a central role in determining the hair/skin conditions, and interventions based on fermented plant extracts that have shown efficacy in favourably modulating the microbiota residing on the scalp skin and hair shaft. These studies pave the way for pioneering next-generation probiotic-based cosmetics.

Keywords: Microbiome, Fermented Extracts, Bioactives, Metabolites, Probiotics.

ICABB_F_21

Current Industrial Applications of Members of *Zingiberaceae* Family

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ABSTRACT

The medicinal properties of plant species have made an outstanding contribution in the origin and evolution of many traditional herbal therapies. The use of medicinal plants has become more widespread as people's confidence in herbal medicine has grown due to its less side effects and cost-effective nature. The traditional medicinal systems have been documented in various mythological texts in India and was been in use since the Indus Valley civilisation. India being a rich source of medicinal plants, has a potency to meet the global demand of various natural plant-products. The *Zingiberaceae* family is a great example of the same as few members of this family are a rich source of diverse bioactive phytochemicals and others are in research. This family comprises about 52 genera and 1300 species of aromatic flowering perennial herbs with characteristic creeping horizontal or tuberous rhizomes. Notable members of this family include ginger (*Zingiber officinale* Roscoe), turmeric (*Curcuma longa* L.), Javanese ginger (*Curcuma zanthorrhiza* Roxb.), and Thai ginger (*Alpinia galanga* L.). This review focuses on the major bioactive compounds present in the members of *Zingiberaceae* family and their therapeutic properties. In addition, this review presents an overview of the knowledge of current industrial applications of some members of the *Zingiberaceae* family.

Keywords: Herbal Medicine, Bioactive Compounds, Industrial Application, *Zingiberaceae*, India.

ICABB_F_22

Extension of Chronological Lifespan Assay in Yeast by Indian Dietary Spices: A Preliminary Screening Study

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ABSTRACT

Aging is a perennial phenomenon in living organisms responsible for deteriorating and compromising the biochemical, molecular and physiological composition/functioning of the individual cell and organism. It is an escalating factor for geriatric diseases on a global scale. Anti-ageing interventions based on herbals/plant extracts are a part of traditional medicine and purified phytocompounds or combinations thereof are emerging in research and are also commercialized after clinical trials. The present study is a preliminary screening to identify anti-ageing activity of selected traditionally used Indian dietary spices. Aqueous extracts of five dietary spices(carom seeds, cumin seeds, fenugreek seeds, fennel seeds and black cumin seeds) were analyzed for qualitative phytochemical profile, antioxidant activity (DPPH and FRAP) and *in vitro* anti-inflammatory activity (denaturation of egg albumin) in a dose response curve. The most potent dose of each of the extracts were additionally explored for their ability to extend the chronological life span assay in yeast strain BY4741. The phytochemical constituents identified were phenols, glycosides, terpenoids, steroids, tannins, flavonoids, alkaloids and saponins being the most abundant. The aqueous extract of fennel seeds shows highest anti–ageing activity amongst all the selected spices with the dose of 500 µg/mL against BY4741, in comparison to reference anti-ageing intervention metformin.

Keywords: Chronological Lifespan Extension, Yeast, Anti-Ageing, Plant Extract, Anti-Oxidant, Anti-Inflammatory.

ICABB_F_24

Pharmacological and Medicinal Attributes of *Clitorea ternatea* as an Immunomodulatory Herb for the Management of Cardiovascular Diseases - An in vitro and in silico Approach

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ABSTRACT

Cardiovascular diseases (CVDs) are the leading cause of premature deaths in today's time. Cardiac inflammation-mediated responses promote immune dysregulation leading to the progression of most CVDs. Over the years, bioactive compounds from various herbs have emerged as an effective approach to combat the onset and progression of several CVDs. *Clitoria ternatea* (Butterfly pea) is an edible flowering plant valued for its medicinal and nutraceutical potential in managing various diseases. This study aimed to identify the bioactive compounds and immunomodulatory potential of butterfly pea flower extract using different supportive evidence of in vitro and in silico analysis. The phytochemical screening of bioactive compounds was examined using the HPLC technique. The selected compounds were chosen as ligands to investigate these compound's immunomodulatory activity targeting IL-6, Toll-like receptors (TLR-4), TNF- α and NF-κB receptors. PyRx was used for virtual screening and molecular docking. The compounds selected conformed to drug-likeness criteria and ADME properties using Swiss ADME webserver. Moreover, Molecular dynamics simulation studies were done to examine the docking results to explore their conformational stability. Overall, the results of the study indicated the immunomodulatory potential of butterfly pea flowers and supported the evidence for future in vivo research for the development of herbal therapeutic regimens for the management of CVDs.

Keywords: Immunomodulatory Herbs, Bioactive Compounds, Cardiovascular Diseases, Drug Discovery, Inflammation.

ICABB_F_25

Exploring the Potential Benefits of Fenugreek: From Diabetes Management to Cancer Prevention

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ABSTRACT

In Recent years Ayurveda and Traditional Chinese medicines have gained huge importance in the study of medicinal plants in relation to chemical make-up and various pharmacological effects. Where in-depth preclinical and clinical studies have provided many studies of fenugreek. Use of Fenugreek such as an antidiabetic, antifungal, antioxidant, anticancer, anti-cancer, anti-obesity, antihyperlipidemic, galactogogue, antimicrobial, and for many pharmacological actions, including enhancing effects on the women's health have been recorded in the literature search. Pharmacological effects of fenugreek's have been attributed due to the presence of a broad range of phytoconstituents such as terpenoids, alkaloids, saponins, polyphenols, flavonoids, lipids, carbohydrates, amino acids, and hydrocarbons. With a focus on cellular and molecular pathways, the current review attempts to summarise and critically evaluate the most recent research to understand the potential effects of fenugreek for disease prevention and individuals' health enhancement effects. Also, we have highlighted the complications and future opportunities of fenugreek in the field of pharmacological research.

Keywords: Antioxidant, Cancer, Diabetes, Fenugreek, Phytocompound.

ICABB_F_26

The Phytochemical and Pharmacological Evaluation of Various Extracts of *Curcuma caesia* Collected from Central India

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ABSTRACT

A combinatorial approach of natural products with conventional drugs has brought a paradigm shift in current medical education and practices with a demand for more pharmacological discoveries. The family *Zingiberaceae* have earned widespread recognition in the pharmaceutical industry, but are limited to only a few species e.g., *Curcuma longa*, *Zingiber officinale* and *Alpinia galanga* etc. *Curcuma caesia*, a member of the *Zingiberaceae* family, is frequently employed as a folk medicine but not yet used in the pharmaceutical industry due to irreproducible and insufficient scientific data. The present study aims to detect the phytochemicals present in various extracts of *C. caesia* rhizome with a comparative analysis of their antioxidant and antimicrobial properties. The qualitative and quantitative assays were performed by standard protocol and confirmed through thin layer chromatography (TLC) using gallic acid, quercetin and tannic acid as standards. The total phenolic (47.89 mg Gallic acid (GAE)/g) and flavonoid (73.8 mg Quercetin (QE)/g)content were found to be maximum in ethanol extract and minimum in diethyl ether which is 4.53 mg and 11 mg respectively. The total tannin content was higher in methanol extract (194.7 mg Tannic acid (TAE)/g dry material). The antioxidant potential tested by 2,2-diphenyl-1-picrylhydrazyl (DPPH), Total Anti-oxidant capacity (TAC) and Ferric reducing antioxidant power (FRAP) assay, and antibacterial properties checked against four bacterial species showed maximum activity with ethanol and methanol extracts indicating their therapeutic potential., Through GC-MS analysis, the major active volatile compounds were identified in these two extracts and their possible applications were explored through literature.

Keywords: Phytochemicals, Antioxidant and Antimicrobial Potential, TLC, GC-MS, *Curcuma caesia*.

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ICABB_F_27

Harnessing the Potential of Nanotechnology in the Packaging of Bakery Products

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ABSTRACT

Nanotechnology has emerged as a transformative force in this context, particularly as an antimicrobial packaging material. The study provides a brief overview of the critical aspects of Nanotechnology in food packaging. The findings delve into the integration of nanotechnology in bakery packaging, emphasizing its potential to mitigate microbial contamination and extend the shelf life of products. Nanoparticles, chosen for their antimicrobial properties, are strategically incorporated into packaging materials, creating a dynamic barrier against pathogens. This innovative approach not only inhibits microbial growth but also addresses food safety and quality concerns.

The review explores the potential of these nanomaterials to respond to environmental changes, leading to dynamic and adaptive packaging systems. Consumer perception and acceptance are integral components of the study, recognizing that the success of nanotechnology in bakery packaging relies on consumer trust. The research includes a thorough analysis of consumer attitudes, shedding light on their perceptions of safety and quality concerning bakery products in nanotechnology-based packaging.

In conclusion, this research underscores the transformative potential of nanotechnology as an antimicrobial packaging material in the bakery industry. By addressing microbial challenges, enhancing packaging properties, and aligning with sustainability goals, nanotechnology emerges as a promising frontier for ensuring bakery products' continued freshness and safety.

Keywords: Food Safety, Nanotechnology, Sustainable Food Packaging, Anti-microbial, Bakery Products.

ICABB_F_28

Resistant Starch from Millet: A Sustainable Functional Food Ingredient

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ABSTRACT

Resistant starch has gained major attention due its significant health benefits. Instead of direct digestion in the small intestine, resistant starch is fermented in the large intestine leading to the formation of short chain fatty acids (SCFA). Major portion of resistant starch is consumed in the form of cereals, majorly wheat, rice and maize. Cereals are the major dietary components which are rich sources of carbohydrate and are important for human health. However, the continuous changing climatic conditions have challenged the yield and intensiveness of these crops, therefore necessitating the shift towards more sustainable crops with natural climate resilient features. This resulted in enhanced global interests for millet crops, which are a good source of resistant starch. Recently, the scientific communities have identified several nutraceuticals benefits in millets, which has further attracted the attention towards this crop. In summary, millets are a sustainable source of resistant starch (RS) and have great potential for RS manufacturing. Also, the inherent nutritional qualities and climate resilient traits gave millets an edge over other major cereal crops.

Keywords: Resistant Starch, Functional Properties, Millets, Nutraceutical Properties.

ICABB_F_29

Exploring the Nutritional Values of Fermented Sea Buckthorn Juice and its Oil Fraction

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ABSTRACT

Seabuckthorn is a Himalayan shrub, rich in bioactive compounds like Carotenoids, Vitamins (K, A, C, E, riboflavin, folic acid), phytosterols (Ergosterol, Stigmasterol, Lanosterol, Amyrins), organic acid, some essential acids and polyunsaturated fatty acids. In our study, health benefits have been improved after fermentation of the juice derived from berries of Seabuckthorn Plant. Compounds present in sea buckthorn play a role in inhibiting the ACE activity. Due to the presence of antioxidants, the juice could be used as a supplement for regulating blood pressure. Also, during fermentation of the juice under controlled conditions, a red-coloured oil has been extracted. After Chromatography, various beneficial fatty acids and compounds were found to be present. Essential fatty acids improve blood sugar, inflammation, lowering the risk of rheumatoid arthritis, cancer and heart disease. Consumption of the fermented juice and the oil fraction could be a healthy approach in treating these diseases. The *lactobacillus* present in the fermented juice works as a probiotic improving gut health.

Keywords: Seabuckthorn, Fermentation, Chromatography, Heart Health.

ICABB_F_30

Uncovering the Impact of Natural Fermentation on Indigenous Millet Starch

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ABSTRACT

Millets are gradually entering mainstream agriculture and thus have the potential to be explored as an alternate source of starch. However, starch in its native form finds limited applications in industry. Modification in the structure of starch by chemical means has widely been studied and used in industry but the method is not environment friendly. Fermentation, a process employing microorganisms to transform food properties, has long been practiced and is a green method. Therefore, in this study, we have tried to explore natural fermentation as a means to modify millet starch. We used five different millet varieties of India (pearl, finger, kodo, barnyard, and little) and naturally fermented them for 24 h. A comparative assessment of native and fermented starch was done for its physicochemical, structural, and thermal properties. The results indicate that fermentation affects the relative crystallinity of all the native starches with an improved gel-forming ability. The water and oil holding capacity (OBC) of the starches decreased after fermentation except for little millet starch where OBC increased. Changes in thermal properties were dependent on the type of millet used. In summary, our findings illustrate that fermentation significantly alters critical properties of millet starch with applications in the food industry.

Keywords: Millet, Fermentation, Starch, Modification.

ICABB_F_31

Personalized Nutrition and Gut-Brain-Axis: An Insight Story

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ABSTRACT

Understanding the complex dynamics of the microbiota-gut-brain axis is paramount in the area of the impact of early nutrition on infant development and health. While the influence of infant diet on gut microbiota and its association with gut function and brain development is recognized, integrative investigation of the microbiota-gut-brain axis is lacking. Nutrigenomics, a burgeoning field within nutritional science, examines the intricate interplay between an individual's genetic makeup and their response to dietary factors. This paradigm-shifting approach acknowledges that genetic variations influence how the body processes nutrients, impacting metabolism, nutrient absorption, and overall health outcomes. The advent of personalized diets is a direct outcome of nutrigenomics, where dietary recommendations are customized based on an individual's genetic predispositions. This tailoring of nutrition aims to capitalize on genetic insights to enhance an individual's overall well-being and address specific health concerns. By identifying genetic markers related to nutrient metabolism, food sensitivities, and response to specific dietary components, personalized diets strive to provide a more precise and effective approach to achieving health and nutritional goals. The personalized nutrition also integrates lifestyle, environment, and health status. The goal is to create a holistic understanding of an individual's unique nutritional needs, fostering a proactive and preventive approach to health management.

In essence, nutrigenomics and personalized diets represent a paradigm shift in nutrition science, moving away from generic, one-size-fits-all dietary recommendations. Instead, they embrace the concept that individualized nutrition, informed by genetic insights, has the potential to revolutionize the way we approach health, disease prevention, and overall well-being. As research in this field continues to advance, the integration of nutrigenomics into personalized dietary strategies holds the promise of a more targeted, effective, and personalized approach to nutrition for individuals across diverse populations.

Keywords: Gut-Brain Axis, Nutrigenomics, Diet, Genetic, Nutrition.

ICABB_F_32

A Network Pharmacology-Based Approach in Drug Discovery

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ABSTRACT

With their wide range of bioactive components, medicinal plants are a useful tool for treating a wide range of illnesses. Their affordability, accessibility, and low side effects all contribute to their effectiveness in conventional treatments. In order to create novel treatments, biomedical research is increasingly focusing on these plants' pharmacological targets. Network pharmacology is a systematic paradigm in drug discovery that offers a singular chance to investigate traditional medicines in depth. This transformative method makes it easier to comprehend the complex bioactive components found in medicinal plants. Our research adds to the changing field of drug discovery and development by providing a thorough overview of current network pharmacology including active ingredients, methodologies, resources, and databases. This study would be helpful for discovering novel compounds and delving into the full range of biological potential present in traditionally used plants.

Keywords: Network Pharmacology, Drug Discovery, Medicinal Plants, System Biology.

SESSION - TWO

Medical Biotechnology

ICABB_M_1

Impact of Therapeutics on Carbapenem-Resistant *Acinetobacter baumannii*

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ABSTRACT

Acinetobacter baumannii, a formidable pathogen in healthcare settings, poses a significant threat due to its propensity to cause nosocomial infections. Its resistance to beta-lactam antibiotics and its unique ability to form biofilms - resilient communities of microorganisms adhering to surfaces, offers a protective shield against antibiotics and promotes the exchange of genetic material. This review delves into the intricacies of *A. baumannii*'s resistance to well-known antibiotics, like carbapenems, highlighting biofilm formation, aminoglycoside-modifying enzymes, antibiotic-hydrolysing genes, overexpression of efflux pumps, and alteration of outer membrane porins. Various reasons influence resistance phenotypes and the dissemination of resistance genes within biofilms through mechanisms such as conjugation and transformation. In addition, both intrinsic and extrinsic factors affecting the biofilm formation process, including surface properties, growth conditions, and growth medium. Device-related infections associated with *A. baumannii* colonization are a significant concern in healthcare. The review outlines various strategies for preventing *A. baumannii* resistance, including the use of antibiotic combinations, monoclonal antibodies, natural products, efflux pump inhibitors, antimicrobial peptides, nanoparticles, and phage therapy. Understanding the multifaceted attributes of *A. baumannii*, and its mechanisms of resistance is critical for developing effective interventions to combat this challenging pathogen in healthcare settings.

Keywords: Aminoglycoside-Modifying Enzymes, Antibiotic Resistance, Antimicrobial Peptides, Biofilm, Efflux Pumps, Nosocomial Infections.

ICABB_M_2

Bacterial Type VI Secretion System: An Evolved Molecular Weapon with Diverse Functionality

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ABSTRACT

Bacterial Type VI secretion system 'T6SS' are nanomolecular complexes that release a diverse set of virulence factors/or proteins into its surrounding or translocate to their target host cells. The presence of T6SS is advantageous to many bacteria as it delivers toxins to its neighbour pathogens for competitive survival and also translocates protein effectors to the host cells, leading to disruption of lipid membranes, cell walls, cytoskeletons etc. Recent studies have characterized both anti-prokaryotic and anti-eukaryotic effectors, where T6SS is involved in diverse cellular functions including favouring the colonization, enhancing the survival, adhesive modifications, internalization, and evasion of the immune system. With the evolution of advanced genomics and proteomics tools, there has been an increase in the number of characterized T6SS effectors arsenals and also more clearly information about the adaptive significance of this complex system. The functions of T6SS are generally regulated at the transcription, post-transcription and post-translational level through diverse mechanisms. In the present work, the information about distribution of T6SS in diverse bacteria, any structural similarity/or dissimilarity, effectors proteins, functional significance and regulatory mechanisms have been highlighted. The diverse role played by T6SS in its natural environments and hosts, and further any changes in microbiome is of great importance.

Keywords: Secretion System, Bacteria, Pathogen, T6SS.

ICABB_M_3

Modelling and Annotating pep-MPT of *Leishmania mexicana*

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ABSTRACT

The protozoan parasite *Leishmania*, which causes leishmaniasis, is still a major global public health issue. Deeper knowledge of the biology of the parasite and the discovery of new therapeutic targets are prerequisites for the creation of potent treatments for this neglected tropical disease. In order to shed light on its structure and potential functional roles, we describe an inquiry into the predictive modelling of peptide-specific mannose-1-phosphotransferase, a protein from *Leishmania mexicana*. Pep-MPT is a protein of interest due to its involvement in crucial cellular processes, including regulation by phosphorylation of multiple metabolic pathways of this parasite *Leishmania*, which are essential for their survival. Understanding the structure and function of phosphotransferase could provide information about its function in the parasite life cycle and pave the way for the creation of specific drugs. The ultimate objective is to assist in the creation of novel therapies for a disease that disproportionately affects vulnerable populations in endemic areas.

Keyword: *Leishmania*, Phosphotransferase, Drug Target, Modelling, Annotation.

ICABB_M_5

In Vitro Testing Systems Utilizing Cell Culture for Screening Anti-Cancer Drug

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ABSTRACT

Utilizing in vitro cellular cultivation techniques has markedly propelled the research and innovation of antineoplastic agents, thereby fortifying the ongoing crusade against malignancies. The exact control over cell culture conditions provided by microfluidic technologies makes it easier to research cell activity and drug interactions. The objective of this study is to minimize the knowledge gap between in vitro and in vivo results that are pertinent to clinical trials by concentrating on sophisticated preclinical anticancer drug screening systems. We reviewed the use of many in vitro models, including In vitro tumor cell culture, patient-derived xenografts (PDX), Boyden chambers, microfluidic devices, 2D and 3D cultures. It was observed that to accurately reproduce the tumor microenvironment (TME), 3D bioprinted tumor models were most appropriate and were standardized. It was found that while 3D models offer a physiologically relevant microenvironment, 2D models allow for simple observation. The Boyden chamber was suitable to examine cell invasion and migration, which are vital for understanding metastasis, while In vitro tumor cell culture and patient-derived xenografts (PDX) were efficient, for targeted, and adverse-effect-free therapies. It is concluded that all these models have their individual benefits but modern 3D bioprinting shows promise for enhancing cancer research and customizing therapies and were superior for accurately replicating the TME.

Keywords: Anticancer Drug Discovery, In Vitro Testing, High-Risk Pediatric Cancers, Personalized Treatments, Tumor Microenvironment (TME).

ICABB_M_6

Regenerating Retina: Advanced Retinal Explants and Novel Model Systems for Common Retinal Diseases

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ABSTRACT

In the realm of scientific research, conventional animal models have long been employed to study retinal diseases. Although valuable, these often fall short in replicating human retinal physiology and disease processes. The emergence of species-specific in vitro and ex vivo systems has guided a new era of research, offering more accurate and ethically sound alternatives to animal models. Human cell lines and stem cell retinal models, organ-on-a-chip technology, microfluidics, neuroretina and organotypic retinal explants are at the forefront of this revolutionary change. These models are species-specific so allow the 36iagnostic36d medicine approaches. These progressive methodologies have diverse applications, from high-throughput drug screening and disease modelling to understanding complex cellular interactions, degeneration mechanisms, and drug responses. Collaborative efforts across various disciplines are crucial for reaping the full potential of these models in retinal disease research. It could allow for radical discoveries in retinal diseases treatment, bringing us closer to a future where vision impairment may be effectively improved or even averted. The diverse models discussed in this review cultivate our understanding of retinal diseases, like glaucoma, diabetic retinopathy, and macular degeneration, which pose significant threats to vision, often leading to irreversible blindness.

Keywords: Diabetic Retinopathy, Glaucoma, Human Cell Lines, Macular Degeneration, Microfluidics, Neuroretina, Organ-on-a-chip Technology.

ICABB_M_8

Beyond Vertical: Unraveling the PSP Enigma

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ABSTRACT

Progressive Supranuclear Palsy (PSP) is an aberrant type of Parkinsonian disorder that cognates with progressive axial rigidity, vertical gaze palsy, dysarthria and dysphagia. It is supposed to affect movement, gait, balance, speech, swallowing, vision, movements, mood, behaviour and cognition. PSP increases as per age and its prevalence is 7% per 1 lakh, as reported. PSP is often misdiagnosed with Parkinson's disease; however, PSP progresses more rapidly than Parkinson's. people with PSP develop unique eye movement problems with looking up and down, speech and swallowing problems are much more common and severe in PSP than PD, leaning backwards and extend their neck in PSP (axial rigidity) while in PD -bending happens in forward direction than backward. Tremors are rare for PSP but very common in PD. The three most important primary motor symptoms are: tremors, bradykinesia and rigidity (parkinsonism). Since this disease is termed as taupathy, 4R-tau isoforms aggregate into straight filaments and appear as a major tau doublet (tau64 & 69). The differential diagnosis is very difficult for PSP because many neurodegenerative disorders have similar symptoms and very less discrimination between PSP and other disorders. The main objective of or study is to create awareness about PSP and its overlapping symptoms with PD as well as other and other neurodegerative disorders. However, based upon detailed investigations about, tau and its isoforms, these clinical features may be distinguished. Though, it would require abundant knowledge of the molecular functioning and structure of tau proteins.

Keywords: Tau Protein, Neurodegenerative, Taupathy.

ICABB_M_9

Construction of a Cytochrome c Nanosensor Based on Nano-Engineered Cytochrome Oxidase Enzyme Covalently Immobilized on AuNPs-GrNs Nanocomposite-Modified PG Electrode

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ABSTRACT

Cytochrome c (cyt c) has been suggested as a diagnostic biomarker for non-small cell lung cancer (NSCLC) screening and is a confirmatory method for NSCLC diagnosis. In diagnosed NSCLC patients, the concentration of cyt c in the blood is decreased from the healthy range of ~3nM to about ~1nM. Here, by immobilizing cytochrome oxidase nanoparticles (CoxNPs), onto gold nanoparticles (AuNPs) decorated graphene nanosheets (GrNs) modified pencil graphite electrode (PGE), we have constructed an electrochemical nanosensor for the detection of the cyt c. The proposed cyt c nanosensor performed best at optimal pH and temperature of 7.0 and 35° C, respectively, with a maximum potential of 0.317V. Fabricated cyt c nanosensor showed a wide linear range (0.1nM–5.1nM) and low limit of detection (0.136nM) with satisfactory selectivity and sensitivity ($0.93 mAcm^{-2}nM^{-1}$). It was successfully employed in detecting cyt c levels in sera samples of NSCLC patients and healthy individuals.

Keywords: Cytochrome c, Cytochrome Oxidase Nanoparticles, Graphene, Gold, Pencil Graphite, Nanosensor.

ICABB_M_10

Application of Drug Delivery Using Nano-Technology to Cure Mental Disorders

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ABSTRACT

Nanotechnology involves the manipulation of matter at an atomic scale to create novel structures, materials, and devices. This groundbreaking technology holds immense potential for scientific progress across various domains, including manufacturing, consumer goods, energy, materials, and medicine. In recent times, the field of pharmaceuticals has witnessed a notable surge in the utilization of nanotechnology for the development of innovative medications. Schizophrenia, a neuropsychiatric disorder affecting the central nervous system, results in delusions, social disengagement, as well as visual and auditory hallucinations. The condition primarily arises from imbalances in key neurotransmitters like dopamine and serotonin. Genetic factors, lifestyle changes, and environmental influences also play a role in the development of schizophrenia. To manage the symptoms, atypical antipsychotic medications such as NDMA inhibitors and dopamine receptor D1-D2 antagonists are commonly prescribed. Olanzapine, haloperidol, and clozapine are among the most widely used antipsychotics, being crucial in counteracting the effects of other neurotransmitters and addressing symptomatology.

However, the complex and multifaceted nature of schizophrenia makes it a challenging illness to diagnose and manage. Nanotechnology in medicine aims to utilize tiny carriers to enhance the effectiveness of low-weight molecular therapeutics. Within the field of nanomedicine, the subspecialty of neuropsychiatry focuses specifically on exploring the potential application of nanotechnology in the treatment of mental illnesses. The blood-brain barrier (BBB) poses a significant hurdle when delivering drugs to the central nervous system (CNS). Overcoming these obstacles through nanotherapeutic techniques could greatly improve the delivery, safety, and efficacy of medications.

Keywords: Nanotechnology, Drug Delivery, Mental Disorders, Schizophrenia, Dopamine, Serotonin.

ICABB_M_11

Application of Medicinal Plants to Cure Mental Disorders

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ABSTRACT

The World Health Organization defines mental health as the state of well-being in which individuals recognize their own capacities, effectively manage the typical pressures of life, remain productive and fruitful, and contribute significantly to their communities. The term "*mental illness*" encompasses a wide range of mental and emotional conditions. It is important to differentiate it from other mental impairments, such as mental retardation, organic brain damage, and learning disabilities.

Schizophrenia, a psychological disorder, is characterized by hallucinations and delusions that profoundly affect emotions, behavior, and mental processes. It remains unclear whether schizophrenia is a single disorder or a group of related illnesses. The complexity of the illness makes it difficult to generalize for all individuals diagnosed with schizophrenia. Symptoms of schizophrenia can be categorized as "*negative*" or "*positive*". Negative symptoms encompass social isolation, loss of motivation, and a flat or inappropriate affect. On the other hand, positive symptoms involve hallucinations, delusions, and thought disorders.

The potential of medicinal plants in global healthcare delivery Is immense. This potential holds even greater significance in developing countries, where 70-80% of the population heavily relies on traditional medicine for primary healthcare. Surprisingly, it is estimated that a quarter of the prescribed drugs used in conventional healthcare originated from the traditional usage of these ethnomedicinal plants. Remarkably, medicinal plants continue to offer hope in the search for new treatments for both drug-resistant diseases and conditions that remain unaddressed by conventional prescription drugs.

A thorough examination of the relevant scientific literature has revealed that traditional healers have utilized numerous plants with scientifically proven therapeutic benefits. Additionally, the knowledge passed down through traditional medical practices has greatly contributed to the development of various modern medications. A prominent example is the antipsychotic drug reserpine, derived from the dried root of the *Rauvolfia serpentina* plant, which revolutionized the treatment of schizophrenia. Regardless of the underlying causes, antipsychotic medications play a crucial role in managing symptoms such as hallucinations, delusions, and thought disorders. They serve as the cornerstone for both immediate relief and long-term maintenance in schizophrenia treatment. Herbal medicine has long been integrated into the field of psychiatry, providing effective remedies for mental illnesses like schizophrenia. Numerous phytochemicals are found in plants, and by improving the functions of various human organs, these phytochemicals can help prevent the occurrence of many diseases. It has been demonstrated that many traditional medicinal herbs and their parts have therapeutic value and can be used to prevent, treat, or cure a variety of human diseases.

Keywords: Medicinal Plants, Mental Disorders, Schizophrenia, Antipsychotic Plants.

ICABB_M_12

Sepsis Unveiled: A Silent Storm Within

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ABSTRACT

The majority of the population is unaware of sepsis, a silent killer that takes millions of lives each year. Worldwide, 48.9 million sepsis cases are reported every year and 11 million deaths annually, while in India situation is worse, with an estimated 11 million instances of sepsis and over 3 million deaths each year. In this report, we present symptoms, causes, pathophysiology and diagnosis of sepsis and/or septic shock. Sepsis is a disorder that develops when the bod''s defences against an infection are activated, which can result in shock, death, heart failure, or any other organ failure. It ordinarily begins with an infection, which can be caused by bacteria, viruses, fungi or parasites. The most common sources of infection leading to sepsis include urinary tract infections, pneumonia, abdominal infections and skin infections. Triggering of cascade of events, leads to inflammation and dysfunction of various organs. Symptoms include fever, rapid heart rate, rapid breathing, confusion, low blood pressure and other signs of organ dysfunction. Though sepsis management and treatment has improved over the years however, in-hospital mortality remains as high as 20% of which 80% of the cases begin with treatment in emergency department. In early stages, excessive inflammatory response and cytokine storms are the crucial factors driving the development of sepsis. Appropriate antagonism of the release of inflammatory mediators has evolved as the main targets in drug development in sepsis treatment. Sepsis is not merely a process of systemic inflammatory response, it rather includes changes in the function of multiple organs of the body, like inflammatory response, immune dysfunction, mitochondrial damage, neuroendocrine immune network abnormalities, endoplasmic reticulum stress and autophagy ultimately leading to organ dysfunction. Traditional diagnostic practices are very time consuming, lack sensitivity and specificity contributing to high mortality rates. Better understanding of pathophysiology of sepsis can help in identification of specific biomarkers of sepsis for early diagnosis/identification of infections, identification of appropriate drug targets therapeutic monitoring of organ function prognosis. Although many clinical trials are underway, there is currently no FDA- approved drug for the treatment.

Keywords: Septic Shock, Pathophysiology, Sepsis Biomarkers.

ICABB_M_13

Unraveling the Intricacy of Blood Brain Barrier in Brain Cancer Using Matrix Metalloproteinase-9

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ABSTRACT

Cancer is a complicated disease that has been affecting millions of lives and has been relentlessly challenging the field of medical science since decades. Cancer is characterized by uncontrolled and abnormal growth of cells that form a tumor or lumps of tissues. These tumors may be malignant or benign and can spread to distant parts of the body by the process of metastasis. Brain cancer, also referred to as brain tumors, is the abnormal growth of cells within the brain or its surrounding structures. Being one of the most life-threatening medical conditions, there are several risk factors and challenges in the treatment of the disease. One of the challenges in treating brain tumors is the presence of the blood-brain barrier. The blood-brain barrier is a highly specialized system of microvascular endothelium cells that regulates the influx and efflux of ions, molecules and other substances between blood and the brain. Due to the high selectivity and tight regulatory system of the blood brain barrier, it is difficult for the drugs to reach the tumor during brain cancer treatments. Brain tumors can lead to disruption in the blood brain barrier and as the tumor grows near vessels, there can be problems like ischemic stroke and hemorrhagic stroke. Increased levels of matrix metalloproteinase-9 have been observed after stroke along with subsequent edema formation which can have an impact in the recovery of the patients. MMP-9 is a zinc dependent endopeptidase that plays a role in extracellular matrix degradation and tissue remodeling. MMP-9 compromises with the blood brain barrier and leads to increase in its permeability, allowing harmful substances to enter the brain and result in brain damage along with inflammation. Elevated levels of MMP-9 also contribute in degrading the blood vessel walls, making the blood vessels prone to rupture and causing hemorrhagic stroke. Blockage in blood vessels due to formation of clot during ischemic stroke is also affected by MMP-9. MMP-9 contributes to the breakdown of these blood clots at the site of blockage and can have harmful effects after stroke. Hence, MMP-9 can be a potential therapeutic target in stroke management and other post-stroke outcomes. It can also be studied as a diagnostics and prognostic marker during brain cancer. Development of effective treatment strategies can also be developed in order to target MMP-9 during brain cancer.

Keywords: Brain Tumor, Cancer, Blood Brain Barrier, Ischemic Stroke, Hemorrhagic Stroke, Inflammation, Matrix Metalloproteinase-9, Extracellular Matrix, Prognostics, Onco Therapeutics.

ICABB_M_14

Expression Profiling of Micrornas by Deep Sequencing in Small Intestinal Biopsies of HLA DQ2/DQ8 Positive First-Degree Relatives of Celiac Disease

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ABSTRACT

First-degree relatives (FDRs) of patients with celiac disease (CD) remains at risk for developing CD in their lifetime as they share the same HLA-DQ2/DQ8 haplotypes. The aim of the study was to investigate the role of miRNA-mediated deregulation of the transcriptome in first degree relatives of celiac disease. For the identification of differentially expressed miRNAs, we did small RNA sequencing on RNA isolated from the duodenal biopsy's samples of 11 subjects: five from Seropositive FDRs, 3 from Seronegative FDRs and 3 from Disease control individuals. Using next-generation miRNA-sequencing, we identified 20 miRNAs (16 were upregulated, 4 were downregulated) to be differentially expressed between FDR positive and FDR negative ($p < 0.05$, with a log fold change of $\geq \pm 2$. Our results suggest that there are specific miRNA expression patterns associated with seropositive FDRs and Seronegative FDRs. Whether and/or how these deregulated miRNAs are involved in pathogenesis of celiac disease, needs to be resolved on a large cohort of celiac patients.

Keywords: Celiac disease, Seropositive FDRs, Seronegative FDRs, Anti-transglutaminase, HLA-DQ2/DQ8, MiRNA- sequencing.

ICABB_M_15

Surface Display Technologies for Monoclonal Antibodies Discovery

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ABSTRACT

Surface display technologies are powerful methods for the discovery and engineering of monoclonal antibodies (mAbs) with desired properties and functions. These technologies enable the expression and presentation of large and diverse libraries of antibody fragments or full-length antibodies on the surface of various biological or synthetic platforms, such as bacteriophages, yeast cells, mammalian cells, ribosomes, mRNA, DNA, and bacteria. By using different selection and screening strategies, such as biopanning, magnetic beads, or biosensors, specific antibodies with high affinity and specificity can be isolated from the libraries and further characterized and optimized. Surface display technologies have been widely applied for the generation of therapeutic and44iagnosticics mAbs against various targets, including proteins, peptides, small molecules, and cells. In this study, we have explained the overview of the current state-of-the-art of surface display technologies for antibody discovery and the method for developing monoclonal antibodies for detection of carbapenemases expressed by *Acinetobacter baumannii* to combat antimicrobial resistance by using Phage display technique.

Keywords: Surface Display Technologies, Antibody Discovery, Carbapenemases, Antimicrobial Resistance.

ICABB_M_16

Human Gut Microbes and Their Role in Immune Response

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ABSTRACT

Gut microbes maintain and supply important elements for maintaining human health and immunological balance. The gut microbes comprise millions of microbes which colonize inside the gastrointestinal tract (GI) of humans for metabolic benefit and protection from pathogens. The susceptibility of immune response varies according to the microbiota in terms of food intake, xenobiotics, microbial genetics, pharmaceutics, immunomodulation, supplementation and allergies. Symbiotic interaction has been observed while in a homeostatic state. Novel therapies in terms of fecal microbiota transplantation, proper use of probiotic and prebiotics to target associated diseases have been studied to open a new idea of amelioration of certain disease symptoms. Antigen Presenting Cells (APCs), microbial based immunity, autoimmunity diseases can be flourished under the influence of Gut microbes-host interaction through mucosal response and systemic responses. Under anaerobic conditions, culture media plating has dominated the research field of microbiome while being selective to certain media and bacteria. Moreover, this field is not properly explored, whereby the functional properties of the complex gut microbiome remain less understood. Thereby, studying microbiota-immunity interaction will help in the emergence of new technologies in the pharmaceutical industry.

Keywords: Microbiota, Homeostasis, Immunity, Pharmaceutics, APCs.

ICABB_M_17

Senolytics: Linking Discovery to Translation for Improvements in Long-Term Health

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ABSTRACT

Senescence is a cell fate that typically includes irreversible loss of proliferative potential, resistance to apoptosis caused primarily by telomere shortening and destabilization caused by the expression of the human telomerase enzyme. It can also be stress-induced senescence due to exposure to DNA-damaging agents. Senescent cells (SC) accumulate as we age at anatomical sites associated with a variety of chronic disorders or diseases. SCs have up-regulated anti-apoptotic pathways that render them resistant to apoptosis and defend themselves against their own inflammatory senescence-associated secretory phenotype (SASP), allowing them to survive while harming and killing neighboring cells. These molecular advantages indicate SC to be a logical therapeutic target. Senolytics are a class of drugs that are designed particularly to target the senescent cells in the body. There are different kinds of senolytic compounds like kinase inhibitors, bcl2 family protein inhibitors, natural polyphenols, heat shock protein inhibitors, BET family protein inhibitors, P53 stabilizers, repurposed anti-cancer drugs, cardiac steroids, PPAR alpha agonists, and antibiotics. Senolytic assays and markers can be used in a variety of ways to induce senescence in different cell types, which can have a direct impact on-screen results. A good senolytic medication should decrease senescent cell viability while causing the least amount of damage to non-senescent cells.

Keywords: Senescent Cells, Anti-Apoptotic Pathways, Inflammatory Senescence Associated Secretory Phenotype (SASP), Drug Discovery.

ICABB_M_18

Intranasal Delivery of Herbs and Medicinal Plant: A Promising Approach to Treat Alzheimer's Disease

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ABSTRACT

Alzheimer's disease (AD) is a neurodegenerative disease characterized by loss of memory and cognitive abilities. It significantly impacts the daily life activities of an individual. It can eventually progress to the condition of hindering conversation and responsiveness. There are various factors associated with the development of AD such as lifestyle, environment, genetics, diet, etc, or the accumulation of neurofibrillary tangles and amyloid-β plaques.

Due to the complex etiology, pharmaceutical treatment of Alzheimer's has posed a considerable clinical challenge. Various neuroprotective herbs have gained interest as an alternative approach with potentially more effectiveness. The use of herbs such as Ginkgo biloba, Ginseng, Ashwagandha, etc, and herbal mixtures like Shenwu capsule, and GEPT are some of the current evidences suggests that these therapies exhibit promising cognitive benefits.

Oral drug delivery to the brain has always been challenging, as the drug suffers from hepatic first-pass metabolism and encounters the Blood blood-brain barrier (BBB). To address these issues, intranasal administration is used as a non-invasive, rapid method that bypasses the BBB and directly targets the central nervous system. This review article focuses on various studies and reports the use of several herbs and phytocompounds for the treatment of Alzheimer's disease and their intranasal delivery.

Keywords: Alzheimer's Disease, Herbal Medicine, Neuroprotection, Intranasal Administration.

ICABB_M_19

Signet Ring Cell Carcinoma: An Overview Focusing on Therapeutic Challenges

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ABSTRACT

Signet ring cell adenocarcinomas (SRCCs) are a rare histological subtype of adenocarcinomas with a poor prognosis, typically due to advanced disease at diagnosis. A signet ring cell, mimicking its moniker, contains abundant intracytoplasmic mucin that pushes the nucleus to the periphery. Despite a decrease in the overall incidence of gastric cancer in recent decades, the incidence of SRCC is constantly increasing in Asia, the United States and Europe, accounting for 35% to 45% of gastric adenocarcinoma cases in recent studies. The SRCC is defined according to the WHO's classification as a poorly cohesive carcinoma composed predominantly of tumor cells with prominent cytoplasmic mucin and a crescent-shaped nucleus eccentrically placed. The SRCC is more frequent in the middle stomach than non-SRCC. The SRCC can be inherited or can also occur due to mutation in CDH1 gene which encodes cell-cell adhesion glycoprotein E-cadherin. Also, an infection due to Helicobacter pylori can be a cause of SRCC. When highly differentiated adenocarcinomas lose the capability for cell-cell interaction via a loss of adherins and tight junctions, then the SRCCs are formed. There are very few biomarkers that have been identified so far being associated with SRCC. The prognosis for patients having SRCC is difficult and are generally being diagnosed at advanced stages due to which there's less survival chances. Preoperative chemotherapy as an optional treatment for advanced gastric SRCC gets complicated for several reasons such as chemoresistance and cancer progression during the preoperative regimen. Due to increasing number of cases and poor curative efficacy of chemotherapy on the SRCC patients, it is very crucial to have a deep understanding of SRCC. This review provides an overview of the classification, Biomarkers, current approved therapy, their limitations and recent researches related to signet cell carcinoma.

Keywords: Adenocarcinomas, Biomarker, CDH-1, E-cadherin, Therapy.

ICABB_M_20

Association of NOS2A, TLR4 and MBL2 gene Polymorphisms with Susceptibility to Tuberculosis in Manipuri Population of Northeast India

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ABSTRACT

Single nucleotide polymorphisms (SNPs) have been reported to influence the function of genes involved in the innate immune response to Mycobacterium, and hence they are of crucial importance in Tuberculosis (TB) susceptibility studies. This study aims to investigate the polymorphism in NOS2A (Nitric oxide synthase 2A), TLR4 (Toll-like receptor 4) and MBL2 (Mannose binding lectin 2) genes, and their association with susceptibility to TB in the Manipuri population of northeast India. Serum levels of nitric oxide (NO) were also studied to correlate with the functional changes associated with the polymorphism of NOS2A. In a case-control study including 495 subjects- 220 TB patients and 275 control individuals, the TaqMan allelic discrimination assay was used to study the genetic polymorphism, and Gries's Test was used to determine the serum NO levels. Four SNPs, two for NOS2A (rs8078340 and rs2274894) one for TLR4 (rs4986791) and one for MBL2 (rs11003125), were analyzed in the study. For one of the SNP (rs8078340) of NOS2A, a significant difference in the genotypic and allelic frequencies was observed between the case and control groups ($p<0.05$; AA genotype OR=30.288, 95% CI: 1.703-538.44 and A allele OR=2.937, 95%CI: 1.762-4.896). However, for the second SNP (rs2274894), only the T allele (with OR= 1.464; 95%CI: 1.080-1.983, $p<0.05$) was observed to be associated with susceptibility to TB. For the TLR4 gene, the genotypic and allelic frequencies of the SNP marker (rs4986791) were found to be significantly associated with TB susceptibility ($p<0.05$). Homozygous CC genotype (OR=2.114; 95%CI: 1.081-4.135, $p<0.05$) and C allele (OR=2.30; 95%CI: 1.205-4.39; $p<0.05$) were observed to be associated with TB susceptibility. Analysis of serum NO levels shows significant differences between the study groups. Patients with susceptibility-associated AA genotype for NOS2A (rs8078340) show significantly higher serum NO levels compared to the GG and GA genotypes. However, no significant difference in serum NO levels was observed between different genotype groups for the SNP marker (rs2274894). Significant associations of homozygous AA genotype and allele A of the NOS2A (rs8078340), minor allele T of NOS2A (rs2274894), and allele C and homozygous CC genotype of TLR4 (rs4986791) with TB susceptibility were observed in the study. Patients with the AA genotype of NOS2A (rs8078340) show a higher serum NO level, suggesting its role in greater expression of the NOS2A gene.

Keywords: Nitric Oxide Synthase, Toll-like Receptor 4, Gene Polymorphism, Susceptibility to Tuberculosis, TaqMan Allelic Discrimination Assay.

ICABB_M_21

Liquid Biopsies: Enhancing Therapeutic Strategies in Lung Cancer Treatment

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ABSTRACT

Lung cancer is considered one of the deadliest forms due to its high mortality rate. Factors, including cigarette smoking, industrial risks, environmental exposures, and genetic variations, contribute to the complex nature of lung cancer. Tissue biopsies are regularly used for diagnostics of lung cancer and are associated with many challenges, including last-stage diagnosis, limited options available for screening, etc. They are associated with several limitations like invasiveness, extraction of small tissue samples, tumor heterogeneity, etc. so, to overcome such limitations and challenges liquid biopsies are being investigated as an alternative to the classic techniques used earlier. This advanced method involves analyses of body fluids including, blood, saliva, urine, etc. for detecting the molecular alterations in various molecules, metabolites, and tumor cells. Specific molecules and other entities like DNA and RNA, micro RNA, exosomes, CTCs (Circulating tumor cells), tumor endothelial cells, tumor platelets, etc. are detected and analyzed in liquid biopsies. Currently, it is considered to be one of the innovative approaches to dealing with cancer diagnostics as it allows us to monitor a patient's health in real-time and can become a valuable tool for disease monitoring and treatment guidance. Considering that this technique can better guide us to manage and treat lung cancer more effectively this review discusses the potential of liquid biopsies for the diagnosis of lung cancer.

Keywords: Lung Cancer, Biomarkers, Therapeutics, Liquid Biopsies.

ICABB_M_22

A Comprehensive Exploration of *Nigella sativa* for Lung Cancer Therapeutics

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ABSTRACT

Nigella sativa commonly known as black cumin, is a flowering plant inherent to Southwest Asia, and its seeds are generally referred to as black seeds. They have been used as traditional medicine for ages. They are also rich in bioactive compounds like thymoquinone, which is explored for its anticancer potential in various cancers including, breast, colon, pancreatic, and lung. Lung cancer is a universal global health challenge that demands innovative strategies for treatment due to its high mortality rate. It becomes more difficult to cure as cancer cells are becoming resistant. To deal with such problems natural spices are used as a therapeutic option. Black cumin plays a dual role both as traditional medicines as well as culinary delights. It is widely studied due to its antioxidant and anti-inflammatory effects. Black cumin comes out with an alternative method by studying deep in the concept of molecular pathways like P13K/Akt/mTOR, JAK/STAT, etc. P13K/Akt/mTOR serves as the primary target for thymoquinone by regulating cell proliferation, and survival, and hindering signaling pathways. Additionally, there are many more bioactive compounds like Thymol, dithymoquinone, etc. This review delves into detail to reveal the complex aspects of *Nigella sativa* and its potential for the treatment of lung cancer.

Keywords: *Nigella sativa*, Lung Cancer, Bioactive Compounds, Molecular Pathways.

ICABB_M_23

Integrating Traditional Remedies and Nutritional Boosters for the Treatment of Breast Cancer

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ABSTRACT

Nutritional boosters include a wide range of dietary components rich in essential nutrients. They play an important role in the treatment strategy of various kinds of cancers including breast cancer. Vegetables, fruits, and many other herbs contain bioactive phytochemicals like resveratrol in red grapes, curcumin in turmeric, and epicatechins in green tea which have various pharmacological activities including immune modulating capacity and antioxidant properties. Other than these properties they also interact with specific molecular pathways that are responsible for the progression of breast cancer for example EGCG (epigallocatechin gallate) in green tea targets the PI3K/Akt pathway and results in preventing cell progression. Curcumin shows anti-inflammatory activity by interrupting the NF-κB pathway. Resveratrol modifies genes that are involved in cell cycle regulation and apoptosis. This present review focuses on the impact of these traditional therapies and nutritional boosters for the treatment of breast cancer, targeting various pathways involved in the development, progression, and migration of the same.

Keywords: Nutritional Boosters, Breast Cancer, Anti-Inflammatory, Traditional Therapies.

ICABB_M_24

Significance of HER2 Pathway in Breast Cancer and Its Therapeutics

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ABSTRACT

Human Epidermal Growth Factor Receptor 2 (HER2) is one of the most critical players in breast cancer, contributing substantially to its development and progression. It is a participant of the epidermal growth factor receptor family and is a transmembrane receptor tyrosine kinase. Normally HER2 signaling is involved in the regulation of cell growth differentiation and proliferation, but its irregular activation has become a describing feature for breast cancer. HER2-positive breast cancer is a separate subtype, accounting roughly for 20-25% of all breast cancer cases in the world. It shows the tendency to be more aggressive and linked with a higher risk of recurrence. Clinical management of HER2-positive breast cancer has been transformed via targeted therapies utilizing drugs like trastuzumab (Herceptin) and pertuzumab. These drugs block the HER2 receptor or its downline signaling pathways. The HER2 pathway is elaborately connected with many other signaling networks namely, the PI3K/AKT/mTOR, etc., which additionally stimulate cancer's aggressiveness. Understanding these associations is crucial in expanding effective combination therapies. It is observed that resistance to HER2-targeted agents is arising so there is an urgent need to develop novel treatment strategies. This present review provides a terse overview of the HER2 pathway and its role in breast cancer, emphasizing its clinical therapeutic significance and implications.

Keywords: Breast Cancer, HER2 Receptor, Molecular Pathways, Therapeutics.

ICABB_M_25

Role of RNA in Cancer Treatment

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ABSTRACT

Cancer, the global health challenge, is understood by advances in molecular biology, emphasizing the critical role of RNAin its progression. Messenger RNAs (mRNAs) are a promising approach, especially in the development of mRNA vaccines for cancer immunotherapy, microRNAs (miRNAs) play an important role in oncogenesis by manipulating cellular machinery for immune responses a targeted, which has therapeutic potential by modulating aberrant miRNA expression. Long non–coding RNAs (IncRNAs) influence cancer biology, providing unique therapeutic strategies by targeting their proliferation, apoptosis, and metastasis. In RNA interference (RNAi) technology, small interfering RNAs (siRNAs) select cancer–relevant genes, showing promise in preclinical studies. Combining mRNA vaccines, miRNA modulation, IncRNA targeting, and RNAi technologies provides a comprehensive and scalable approach to address cancer challenges. The potential of RNA–mediated intervention to revolutionize cancer therapy never become clearer as research progresses. This rapid expansion underscores RNA’s contribution to personalized and multifaceted targeted cancer therapies and raises hopes for transformational advances in the field.

Keywords: Cancer, mRNA, miRNA, IncRNA, mRNA Vaccines, Molecular Biology.

ICABB_M_26

Microbiota, Pulmonary Endothelium, and Hypertension: Exploring the LPS Connection

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ABSTRACT

In the dynamic realm of global health, hypertension emerges prominently, sparking exploration into the intricate interplay with host microbiota shifts, potentially shedding light on novel facets of its onset. It is found that the host might experience this as a result of a changed microbiota. The pleomorphic pulmonary endothelium is responsible for circulatory fluid balance maintenance, which functions as a quasi-permeable wall between the vascular space of blood vessels and the underlying tissues. Dysfunction of the pulmonary endothelium barrier is a crucial early stage in the emergence of several high-mortality illnesses, including pulmonary edema. In the presence of persistent inflammatory or infectious mediators, such as lipopolysaccharide (LPS), this endothelial barrier's dysfunction is often observed. LPS is a component of the upper membrane of Gram-negative bacteria that may be released during bacterial cell death. This LPS through various sources, on being through ingestion of contaminated food can be absorbed in the intestines and may translocate from the gut to the bloodstream, triggering an immune response. The disruption of intestinal barrier integrity and reduced expression of tight junction proteins enable unrestricted entry of lipopolysaccharides (LPS) into the bloodstream. This review thus uses available knowledge to incorporate the direct link of LPS with hypertension, and whether possible probiotic intervention may be directed as a technique to regulate the LPS action pathway.

Keywords: Hypertension, Microbiota, Pulmonary Endothelium, Circulatory Balance, Pulmonary Edema, LPS, Inflammatory Mediators, Tight Junction Proteins, Intestinal Barrier, Probiotic Intervention.

ICABB_M_27

Development and in Vitro Evaluation of Chitosan-Coated PLGA Nanoparticles of Pregabalin

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ABSTRACT

The present study reports the optimization, development, and in vitro characterization of Pregabalin-loaded biodegradable nanoparticles of Poly (lactic-co-glycolic acid) (PLGA), coated with chitosan for the sustained release of the drug. The chitosan-coated nanoparticles were prepared by the single emulsion solvent evaporation method. The physicochemical properties of the chitosan-coated nanoparticles were evaluated and the results showed that the particles exhibited a size of 157.3 ± 3.4nm, PDI- 0.228, and Zeta potential of 29.6±7.25 mV. The optimized formulation was selected on the basis of particle size, entrapment efficiency, and drug loading parameters. The entrapment efficiency and drug loading of the surface-modified nanoparticle was reported to be 78.4% and 7.2%. In vitro release of the drug from the nanoparticle's core in Phosphate Buffer Saline (pH 7.4) and Simulated Nasal Fluid (pH5.5) suggested that the nanoparticles showed sustained release of the drug of 63.59% & 76.27% up to 48 hours. In vitro, cytotoxicity on Neuro-2a cells was evaluated using an MTT assay. Results showed that the formulation was nontoxic to the brain cells and uncoated and coated nanoparticles showed comparable % cell viability.

Keywords: Drug Delivery, Nanoparticles, Chitosan, Biodegradable, Pregabalin, Cell Viability.

ICABB_M_28

In-silico modelling of Membrane protein from Human Coronavirus 229E (HCoV-229E)

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ABSTRACT

The human coronavirus-229E is one of the common HCoV which causes mild respiratory tract infections, leading to a symptom like common colds in adults, but can lead to life-threatening illness in people with suppressed immune system. The membrane protein (M-protein) has been speculated as a major player in the process of virus assembly through their interaction with host membrane and numerous viral proteins. In order to shed light on the properties of M-protein, we employed predictive structure modelling of this protein using in silico methods. The quality of the models obtained from various protein structure prediction programs was assessed by using various evaluation programs available. The three-dimensional structure may provide useful insights into the structural and functional properties of this protein. As per the evidence from multiple studies, it is an essential protein in formation of new viral particles inside the host cell. Therefore, the structure can be used to identify possible substrates for use as pharmaceuticals, contributing to development of novel therapies using M-protein of HCoV-229E as a drug target.

Keywords: Membrane Protein, Virus Assembly, Protein Structure Modelling, Drug Target, HCoV-229E.

ICABB_M_29

Gallbladder Cancer: Genetic Alterations and Their Possible Diagnostic, Prognostic and Therapeutic Implications

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ABSTRACT

Gallbladder cancer remains a formidable challenge in oncology due to its aggressive nature and often late-stage diagnosis. In northern India, the incidence rate of Gallbladder Cancer (GBC) is high (21/100,000) with 5-year survival rates of less than 5%. Though early-stage diagnosis can improve survival rates to greater than 75% however, that is incidentally diagnosed. Gallbladder cancer risk increases with chronic cholecystitis and Gallstones and probability increases if left untreated for long. In this review, we present the insights into the most common genetic alteration(s) prevalent in Gall bladder carcinoma such as TP53 mutations, KRAS mutations, HER2 alterations, and PIK3CA mutations. Literature mining for gallbladder cancer using PubMed, EMBASE, Chochrane Library and Web of science shows 62 articles discussing over 3893 GBC samples. The most altered genes (>5% in >5 samples) in GBC involve ATM, ERBB2 and PIK3CA. For solid cancers High tumor mutational burden (TMB-H) and microsatellite instability (MSI-H) are frequently observed. In addition to the above mentioned four mutations, these two additional mutations can be used as potential future molecular panels to enable high precision medicine for GBC patients. The overall systematic review study provides an overview of most frequent genetic alterations and their possible therapeutic implications.

Keywords: Gallbladder, Therapeutics, Cancer, Tumor Mutational Burden.

ICABB_M_30

Comparative Evaluation of Phytocompound Pool and Assessment of Antioxidant Activity of *S.bryopteris* Obtained from the Deccan Terrain of India

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ABSTRACT

Selaginella bryopteris (L.) Baker, is a lithophytic pteridophyte of the *Selaginellaceae* family. It has been reported for its medicinal properties due to its rich phytocompound pool. The current work explores the diversity in the phytocompound pool and the associated bioactive potential of this species from various geolocations. Samples of this species were procured from different locations of deccan terrain of India and subjected to phytochemical analysis by chromatographic and spectroscopic techniques to identify the phytocompound pool and quantify the different classes of secondary metabolites. The bioactivity assessment of the phytoconstituents was conducted. The results revealed significant variations in the phytocompound pool and the bioactivity of *Selaginella bryopteris* from different locations, indicating the influence of environmental factors on its metabolite composition. The present finding offers valuable insight into the correlations between the phytochemical composition and bioactivity accentuating the importance of location specific studies for the assessment of its medicinal properties.

Keywords: Phytocompounds, *Selaginella*, Bioactivity, Extraction, Geolocations.

ICABB_M_31

Structural and Functional Insights into UDGS

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ABSTRACT

Endogenous or exogenous DNA damage needs to be repaired and cells in all three kingdoms have repair pathways for maintaining the integrity of their genetic material. Uracil DNA glycosylases (UDGs) also known as UNGs (uracil-DNA N-glycosylases) are part of the base-excision repair (BER) pathway. These enzymes specifically remove uracil from DNA molecules by cleaving the glycosidic bond between the uracil base and the deoxyribose sugar. UDGs can be broadly classified into six families and all of them share conserved motifs that are critical for substrate recognition and catalysis. Recently an unconventional UDG named UdgX has been identified from the species Mycobacterium smegmatis, which is different from other UDG members in forming an irreversible and extremely stable complex with DNA that is resistant to even harsh denaturants such as SDS, NaOH, and heat. This suicide inactivation mechanism prevents uracil excision and might play a protective role for the genome integrity, as it is seen that under hypoxic conditions bacteria's survival is reduced due to overexpression of MsmUdgX. Due to the importance of UDGs, a number of structures have been solved. Also, high-resolution 3D structures of apo MsmUdgX, as well as uracil and DNA-bound forms, are available in PDB. This review aims to provide insights into the structural basis of Udg and UdgX forming a covalent adduct with DNA and will also discuss the practical utility of this unique feature in detecting incorporated uracils in genomic DNA and diagnostic techniques.

Keywords: Base-Excision Repair, Uracil DNA Glycosylases, UdgX, Structure, Diagnostics.

ICABB_M_32

Emerging Role of Lipids in Mycobacterium - Macrophage Interaction

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ABSTRACT

Tuberculosis, a formidable global health challenge, persists as a silent yet relentless adversary, affecting millions worldwide. It is the 2nd leading cause of infectious disease after COVID-19 and surpasses HIV-AIDS. The cell wall of the causative agent of TB, Mycobacterium tuberculosis (Mtb), is rich in well-established lipid virulence factors such as mycolic acids, lipoarabinomannan (LAM), phthiocerol dimycocerosate (PDIM), sulfoglycolipids, etc., that enables the pathogen to hijack host macrophages for its cellular niche. In this context host-derived lipids aid in reprogramming of macrophages with pro-inflammatory and microbicidal activity to macrophages with attenuated microbicidal function. Numerous studies report impact of dynamic lipid–protein interaction between mycobacterium and host macrophage on modulating host immune responses and directing the outcome of infection. Despite the documented roles of lipids in providing a stable environment for the pathogen, food supply and actively participating in regulation of immune responses, lipid function during infection is not as well studied as their cellular counterpart genes and proteins. In addition to the complex structure of lipids, scarcity of tools and techniques for studying system-level approaches involving lipids have been the impeding factors. This review explores the complex interplay between TB-macrophage lipids with proteins in governing the disease landscape and elucidates how these interactions contribute to the establishment and persistence of TB infections. It also highlights methods of lipid analysis– traditional (thin layer chromatography, enzyme immunoassays, etc) and advanced (mass spectrometry, Fourier-transform infrared spectroscopy, etc) and potential avenues for developing novel antitubercular agents.

Keywords: Mycobacterium Tuberculosis, TB, Macrophages, Lipids, Host Immunity, Persistence, Antitubercular, FTIR.

ICABB_M_33

Deciphering Complex Tripartite Phage-Bacteria-Nanoparticle Interplay: Implications for Novel Antibacterial Therapies and Bioremediation

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ABSTRACT

The global antibiotic resistance crisis necessitates the development of alternative antibacterial strategies. Bacteriophages (phages), viruses that infect and kill bacteria, have emerged as promising substitutes to traditional antibiotics. Phage therapy involves leveraging phages to specifically target and eliminate bacterial infections. Additionally, nanoparticles synthesized via biological routes have exhibited antibacterial effects against pathogenic bacteria. These nanoparticles could potentially act synergistically with phages, enhancing their combined antibacterial capabilities.

Natural freshwater ecosystems often harbour complex trilateral interactions between phages, bacteria, and biologically derived nanoparticles. These intricate interrelationships likely significantly influence bacterial population dynamics and water quality parameters in these environments. However, numerous critical knowledge gaps persist regarding the tripartite interactions between phages, bacteria, and nanoparticles in freshwater habitats.

Addressing these outstanding questions through quantitative in situ examinations is imperative for fully elucidating tripartite phage-bacteria-nanoparticle interplay governing bacterial ecology in natural freshwater ecosystems. Fundamental insights gleaned from probing these complex interrelationships can inform rationally engineering potent mixture antibacterials consisting of phages and nanoparticles. Specifically, knowledge of synergies between biologically synthesized nanoparticles and phages could enable harnessing natural antimicrobial strategies to combat antibiotic resistance.

Keywords: Antimicrobial Resistance, Bacteriophages, Nanoparticles, Novel Therapeutics, Ecosystems.

ICABB_M_34

Structure-Function Insights into Bacterioferritin: An Iron Storage Molecule Involved in Bacterial Pathogenesis and Drug Resistance

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ABSTRACT

Iron, an essential element for most organisms, exists in two oxidation states, Fe^{2+} and Fe^{3+}, and is involved in various biological processes such as oxygen transport, mediating oxygen and electron transfer reactions, mitochondrial respiration, nitrogen fixation, nucleic acid synthesis, etc. Although an abundant element on earth, a biologically useful form is scarce due to limited solubility, which is advantageous since free iron is toxic and generates reactive oxygen species. Therefore, mostly found bound within heme and iron-sulfur clusters. Elaborate strategies have been devised by all living cells, be it pathogenic microorganisms or mammalian cells, to acquire, store, transport, recycle and stringently regulate iron to prevent iron deficiency and toxicity. During infection, both pathogen and host immune cells require iron to carry out their respective tasks and the outcome of the 'Iron tug of war' shapes the disease progression.

Iron storage modulators are integral to iron homeostasis and virulence in bacteria. Bacterioferritin (Bfr) and ferritin (Ftn), are two types of iron-storing proteins, the former specific to bacterial cells while the latter is present in humans as well. Bacterial ferritin and bacterioferritin both are assembly of 24 subunits and each subunit has four-helix bundle and a short C terminal **α** helix perpendicular to bundle forming quaternary structure resembling a hollow nanocage where iron is stored as ferric oxide, thereby preventing iron-induced toxicity and maintaining homeostasis by limiting the cellular iron concentration. Even though structural architecture for both Bfr and Ftn are similar, significant differences exist that affect the function and mechanism. A major difference is presence of Bfr 12 heme groups between the two subunits in Bfr whereas Ftn is free of heme. BfrB is the major iron-storing protein in Psuedomonas aeruginosa and the availability of iron directly affects it's pathogenicity. Mycobacterium tuberculosis synthesizes two iron storing proteins – ferritin-BfrB (Rv3841) and bacterioferritin-BfrA (Rv1876). Lack of BfrA and BfrB results in increased iron concentrations decreasing the resistance of M. tuberculosis strains to various anti-TB drugs including aminoglycosides and fluoroquinolones. This study reviews the structural-functional aspects of Bfrs from various pathogenic bacteria as well as literature documenting the role of bacterioferritin for developing specific therapeutics and similar applications.

Keywords: Bacterioferritin, Iron Storage, Ferritin, Iron- Induced Toxicity, Drug Resistance.

ICABB_M_35

An Insight into Emerging Phytotherapeutic Innovations for Glioblastoma Multiforme Therapeutics

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ABSTRACT

Glioblastoma multiforme is a type of brain tumour, which is associated with high mortality. Glioblastoma can occur at any age but is more common in older adults. Treatment typically involves a combination of surgery, radiation therapy, and chemotherapy but even with aggressive treatment, the recurrence rate is high. The reason for recurrence is mainly resistance against chemotherapy and selectivity of blood-brain barrier against certain therapeutic candidate compounds. Ongoing research and clinical trials are exploring new treatment approaches, including phytotherapy, owing to lesser side effects and ability to cross BBB. This paper analyses some such compounds belonging to different families of phytochemicals. The studies to combat proliferation and migration suggest potential activity of these compounds against GBM cell lines both resistant and non-resistant against chemotherapy. In silico analysis in our study shed light on the possible interactions of these phytocompounds to various receptors involved in GBM.

Keywords: Cell Proliferation, Chemotherapy, Drug Resistance, GBM, Migration, Synergy, Temozolomide, Tyrosine Kinase Receptor.

ICABB_M_36

Effect of Various Naturally Occurring Bio-Active Compounds on Ovarian Cancer

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ABSTRACT

Ovarian cancer ranks as the eighth most prevalent cancer type, and its development is linked to a variety of genetic and epigenetic alterations. Its treatment options include surgery, chemotherapy, and radiotherapy. Platinating agents, such as cisplatin and carboplatin, are commonly used chemotherapeutic drugs, however, they carry the risk of developing chemoresistance and inducing severe side effects, including neurotoxicity, nephrotoxicity, gastric toxicity, and cardiotoxicity.

Naturally occurring compounds are found to be relatively safer, have relatively lesser side effects, are effective and cost efficient. Naturally occurring compounds can be active new biomolecules and hence can be used to combat resistance. There are many different classes of naturally occurring compounds, which use various different and new mechanisms to act on the tumor cells to provide cytotoxic-effects.

Combination therapy is one among the many ways to overcome the resistance, using various types of naturally occurring compounds in combination or using these compounds with various drugs to target multiple pathways rather than just targeting one pathway. There also is the need for the treatment that takes into consideration minimizing the side effects and aims in reducing them.

It is very important to identify and explore various multiple pathways and targets and observe the effects of various biologically active compounds on the diversely explored receptors and targets to counter chemoresistance.

Key words: Bio-Actives, Chemoresistance, Cisplatin, Epigenetic, Genetic, Platinating agents, Toxicity.

ICABB_M_37

Chronic Wound Infection, Antibiotic Resistance and Therapy

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ABSTRACT

Chronic wounds pose a significant health care burden globally, with their management complicated by the escalating thread of antimicrobial resistance. Chronic wounds characterized by prolonged healing periods, often results from underlying conditions such as diabetes, vascular diseases or immune disorders.

Bacterial colonization and biofilm formation in chronic wounds is encouraged by the compromised healing environment, which leads to the development of antimicrobial resistance (AMR). Biofilm has been found to be one of the primary causes of the delay in wound healing, its significance in therapeutic treatment has increased. The urgent need for novel therapeutic approaches is highlighted by the rising incidence of multidrug resistance bacteria in chronic wounds.

Abstract emphasizes on the challenges in wound healing and therapeutic approaches to address the chronic wounds which includes advanced wound dressing, incorporating antimicrobial agents and growth factors. It also addresses the role of phytotherapy, utilizing plant based-compounds, reviews the bioactive compounds of plants that are known for their antimicrobial, antibiofilm, anti-inflammatory and tissue regeneration properties and combinatorial therapeutic approaches to address chronic wounds while mitigating the risk of AMR.

Keywords: Antimicrobial Resistance, Biofilm, Combinatorial Therapy, Phytotherapy.

ICABB_M_38

Study on Impact of Pesticide on Phyllosphere, Rhizosphere Microbes and Isolation of Pesticide Tolerant Microbes

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ABSTRACT

This research endeavours to unravel the complex interplay between plants and endophytic microorganisms using a multifaceted approach involving various technical methodologies. Through experiments such as skim milk testing, Bradford assay analysis, and the isolation of microbial colonies via serial dilution on agar plates, the study aims to decipher the influence and significance of endophytes on plant physiology. The investigation focuses on three distinct plant species - green gram, mustard, and fenugreek - cultivated in controlled pot environments to elucidate the diverse roles of endophytes in enhancing plant health and resilience. The methodologies employed serve specific purposes: skim milk testing allows the assessment of microbial enzymatic activity, providing insights into the metabolic capabilities of endophytic communities. Meanwhile, the Bradford assay facilitates the quantification of proteins, aiding in the evaluation of microbial impact on the plant's protein profile. Furthermore, the isolation of microbial colonies from plant tissues using serial dilution and agar plate culturing offers a glimpse into the diversity and characteristics of endophytic populations associated with the selected plant species. Central to this study is the exploration of how endophytes influence crucial aspects of plant biology, including growth, nutrient uptake, stress responses, and disease resistance. Additionally, the research probes into the potential impacts of pesticide exposure on endophytic communities. This inquiry seeks to understand alterations in endophytic diversity, functions, and their potential ramifications for plant health and ecosystem stability. By examining the intricate relationships between plants and endophytes, this study aims to contribute valuable insights into the mechanisms governing these associations. The findings obtained from these technical methodologies will inform strategies for sustainable agricultural practices and ecosystem management, fostering a deeper understanding of the pivotal roles played by endophytic microorganisms within the plant kingdom.

Keywords: Phyllorhizosphere, Rhizosphere, Pesticide Tolerance, Endophytic Diversity.

ICABB_M_39

Comparative Evaluation of Phytochemical and Antioxidant Activity of *Picrorhiza Kurroa* Using Different Solvents

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ABSTRACT

Picrorhiza kurroa (PK), commonly called kutki is a well-known plant in the Ayurvedic system of medicine due to its reported activities including antidiabetic, antibacterial, antioxidant, antitumor, anti-inflammatory, and hepatoprotective. The present study was designed to investigate the presence of phytochemicals qualitatively and evaluate the antioxidant properties in the extracts of *Picrorhiza kurroa*. For this purpose, PK roots were extracted with ethanol, methanol, chloroform, ethyl acetate, petroleum ether and distilled water and a phytochemical study of the extracts was performed to recognize the total phenolic content (TPC) and total flavonoids content (TFC). The antioxidant activities were determined by DPPH, hydroxyl radical scavenging assay, ferrous reducing antioxidant capacity and ABTS assay methods. The results showed that the ethanolic extract of *Picrorhiza kurroa* showed the highest antioxidant property while the methanolic extract of *Picrorhiza kurroa* showed the least antioxidant property among all the extracts used. Ascorbic acid taken as control showed the highest antioxidant power in the present study. These antioxidant activities could be due to the presence of antioxidants and phytochemicals such as flavonoids, phenols, terpenoids, and saponins among others. Therefore, the therapeutic potential of this plant could be due to its antioxidant properties and could serve as effective free radical inhibitors or scavengers which may be a good candidate for pharmaceutical plant-based products. However, further exploration is necessary for effective use in both modern and traditional systems of medicines.

Keywords: Antioxidant, Medicinal Plants, Oxidative Stress, *Picrorhiza kurroa*.

ICABB_M_40

Phytochemical Analysis and in vitro Antioxidant Activity of *Punica Granatum*

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ABSTRACT

Natural antioxidants products are widely distributed in food and medicinal plants. These natural antioxidants, especially polyphenols, exhibit a wide range of biological activities including anti-cancer, anti-inflammatory, and anti-atherosclerosis activities. Pomegranate (*Punica granatum* L.) is a rich source of polyphenolic components. The core objective of the present investigation was to isolate and quantify antioxidants from *Punica granatum* (Pomegranate) peel extracts. The purpose of this study was to characterize the phenolic composition and flavonoids and tannins content of different solvents-based peel extracts. Our results showed that Ethanolic Peel extract was richer in these compounds than that of the other solvents, DPPH free radical scavenging, ABTS, reducing power (FRAP), and hydrogen peroxide scavenging assays revealed a greater dose-dependent activity of pomegranate peel ethanolic extract compared to aqueous and other volatile solvents. The HPLC, HPTLC and TLC revealed the presence of Gallic acid in the ethanolic extracts which is potential anticancer agent. In the proposed research, different solvents were used for the extraction of antioxidants from peels of Pomegranate. Among these solvents, ethanol resulted in better antioxidant yield compared to aqueous extract. Ethanolic extract of Pomegranate peel showed higher total phenolic contents as compared to aqueous extracts. Pomegranate peel antioxidants have a great potential to be used in various functional foods and the ability to improve storage stability.

Keywords: Natural Antioxidants, Polyphenols, *Punica granatum*.

ICABB_M_42

Isolation, Purification & Characterisation of Bacteriophages Specific to *Mycobacterial* Spp.: Implications in Combating AMR

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ABSTRACT

Tuberculosis infections are getting increasingly difficult to treat because of antibiotic resistance and drug resistant TB is a growing and widespread problem in India and the world. Bacteriophages present potential for an alternative strategy for treating antibiotic-resistant infections.

This study focuses on isolation, purification and characterization of Mycobacteriophages from environmental samples using the non-pathogenic *Mycobacterium smegmatis* as host.

The bacteriophages were purified by a double agar plate method. For further characterization, plaque sizes, plaque morphology and TEM analysis and genome isolation was done which was followed by cluster classification using the primers specific for TMPs of different clusters. Methylation status of the genome was also checked using restriction enzymes.

The above characterization studies resulted in discovery of 20 morphologically distinct bacteriophages.

Genome analysis of phage W2, which has been observed to show lytic activity against *M. tuberculosis* and clinical isolates of NTM revealed 80 unique ORFs including genes coding for lysin enzymes. Lysins hold the promise for acting as potential antimicrobials for therapeutic purposes in treating bacterial infections. Cloning, expression and purification of lysins encoded by this novel Mycobacteriophage as recombinant proteins is underway. Our work has great value addition towards finding alternative solutions to the growing menace of drug-resistant Tuberculosis.

Keywords: Antimicrobial Resistance, Tuberculosis, Mycobacteriophages, Phage Therapy, Lysins.

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ICABB_M_43

Therapeutic Potential of HIF (Hypoxia Inducible Factor) Pathway in Human Diseases

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ABSTRACT

Oxygen plays a vital role in both catabolic and anabolic reactions in mammalian cells. The fundamental process for the survival of every cell or organism involves the uptake of oxygen and its conversion into energy (ATP) through many cellular mechanisms. Hence, mammalian cells maintain a sufficient level of oxygen to ensure their proper physiological functioning. Almost, all cells can sense fluctuations in oxygen levels and activate a set of genes involved in oxygen regulation. When the oxygen concentration decreases physiologically, this situation is called hypoxia. Hypoxia stimulates various downstream signals for adaptation and stress response in the cells. The transcriptional factor-hypoxia inducible factor (HIF), is a key player in sensing and responding to the hypoxic environment in the cells and regulates a wide range of oxygen-responsive genes like EPO (erythropoietin, RBC, and haemoglobin production) and VEGF (vascular endothelial growth factor, vascularization), etc. Hypobaric hypoxia is the hypoxia encountered at high altitudes, due to a fall in partial pressure of oxygen at elevated regions and may lead to illnesses like AMS (acute mountain sickness), HAPE (high altitude pulmonary edema), and HACE (high altitude cerebral edema). Hypobaric hypoxia is a particular matter of concern for travelers, athletes, and adventurers traveling to high altitudes. HIF plays a pivotal role in regulating the biological processes under hypobaric hypoxia exposure as well, such as - cell proliferation, inflammatory responses, redox balance, cell metabolism apoptosis, etc. HIF activation is also implicated in many human diseases like cardiovascular diseases, rheumatoid arthritis, cancer, infectious diseases, COPD, etc. HIF and associated molecular regulators are potential therapeutic targets in the diseases as mentioned earlier. This review provides a detailed description of the biology of HIF, its activation under normal and hypoxic conditions, and its potential as a therapeutic target in high-altitude pathologies and other human diseases. Furthermore, understanding the HIF pathway opens innovative avenues for a range of diseases associated with oxygen sensing.

Keywords: HIF Pathway, Vascular Endothelial Growth Factor, Acute Mountain Sickness, High Altitude Pulmonary Edema, High Altitude Cerebral Edema.

ICABB_M_44

Unlocking the Potential of Zinc Compounds for the Leishmaniasis Vaccine Development

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ABSTRACT

Leishmaniasis, a devastating parasitic disease caused by the *leishmania* parasite and transmitted through sandflies, continues to wreak havoc in Europe, Africa, Asia, and America. The parasite's unique life cycle, alternating between amastigotes and promastigotes in two different hosts, poses a formidable challenge for vaccine development. The absence of long-term drug efficacy underscores the urgency for a viable vaccination strategy. Recent studies have highlighted the anti-leishmanial effects of zinc sulphate, opening new avenues for innovative solutions.

This project delves into the complexities of leishmaniasis, emphasizing the potential of zinc compounds in vaccine development. The discussion extends to ongoing immunotherapy methods and probes, offering insights into promising avenues for combating this relentless disease. By exploring alternative approaches beyond conventional drug treatments, this research aims to contribute to the development of a robust and effective solution against leishmaniasis, ultimately improving public health outcomes.

Keywords: Leishmaniasis, Parasitic Disease, Leishmania Parasite, Sandfly Transmission, Amastigotes, Promastigotes, Vaccine Development, Immunity, Drug Resistance, Zinc Sulphate, Anti-Leishmanial Effects, Immunotherapy, Vaccine Preparation.

ICABB_M_45

ISGylation: A Key Host Cellular Defense Mechanism

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ABSTRACT

ISGylation, a crucial process of the innate immune response, has garnered increasing attention for its involvement in host's defense against pathogenic infections as well in cancer progression. The key player of ISGylation, ISG15, is induced by type I interferons (IFNs). ISG15 covalently binds with viral (influenza NS1A and nucleoproteins) and host (Nedd4, filamin B and CHMP5) target proteins and inhibiting the viral replication process and release of viral particles respectively. The ISGylation process dynamically modifies the immune signalling pathways mediated by NFkB, JNK, and IRF-3. ISG15 has diverse roles beyond ISGylations, for instance the free extracellular ISG15 serves as immunomodulatory cytokine in response to type-I interferon induction and free intracellular ISG15 is involved in stabilization and destabilization of various cellular proteins e.g., Ubiquitin-specific protease 18 (USP18) and Cyclin D1. The reversal of ISGylation is known as deISGylation where USP18 a ISG15 specific protease plays a crucial role. USP18 is a potent inhibitor of interferon signalling thus inculpated in the suppression of innate immune response in host cell. The future prospects of ISGylation research encompass a deeper exploration of its molecular mechanisms, diagnostic utility, crosstalk with other immune responses, and potential therapeutic interventions. This review provides updated literature on state-of-art with respect to ISGylation and its role in providing immunity to human host together with deISGylation process, and techniques to counter deISGylation.

Keywords: ISG15, Innate Immunity, ISGylation, DeISGylation, USP18, Pathogenies.

ICABB_M_46

PDMD: A Comprehensive Repository of Plants Reported for Muscle Related Ailments in Aged Individuals

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ABSTRACT

Plant extracts, purified phytocompounds or combinations thereof are potential interventions against geriatric muscle loss and related ailments such as sarcopenia, cachexia, frailty muscle atrophy etc. A comprehensive online repository of plants reported for muscle related ailments in aged individuals will enable natural compound-based drug discovery. Realizing the importance of a repertoire documenting such medicinal plants, here in this paper we present PDMD (plants database for muscle wasting diseases), a manually curated plants database of more than 250 plants/extracts/phytocompounds reported for muscle wasting diseases containing information(unique ID, plants scientific name, family name, local names, utilized parts, active compounds, PubChem ID, canonical SMILES, kingdom, phytochemical class, phytochemical subclass, mass, extract, part used, geographical location, model organism, disease Target, cellular and molecular targets, anti-Inflammatory property, anti-oxidative property, reference and the PubMed IDs of related articles). Notably, the curation efforts led to the non-redundant scientific information following the rigorous scientific standards to ensure the reliability of this database.

Keywords: PubChem ID, Plant Extracts, Anti-Inflammatory, Anti-Oxidative, PubMed.

ICABB_M_50

Progeria Syndrome Unveiled: A Scientific Odyssey into Premature Aging Mechanisms and Therapeutic Frontiers

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ABSTRACT

Progeria, or Hutchinson-Gilford Progeria Syndrome (HGPS), is a rare and fatal genetic disorder in childhood, exhibiting features akin to premature aging. Despite normal appearances in infancy, affected children face accelerated aging with distinct facial characteristics, including micrognathia, dental malformations, lower body weight, early hair loss, decreased joint mobility, lipodystrophy, etc. The cause of HGPS is a point mutation that occurs at the exon 11 of the LMNA gene which normally produces lamin A protein. This mutation leads to the formation of a mutated lamin A protein known as progerin. Unlike normal lamin A, progerin undergoes incomplete processing and remains permanently farnesylated and carboxymethylated. The persistent farnesylation of progerin disrupts the normal nuclear architecture and function. This abnormality contributes to various cellular defects observed in individuals with HGPS. Different therapeutic strategies are used to target progerin for the treatment of HGPS such as methylation and farnesylation inhibitors, gene therapy, development of biologicals, and a new age CRISPR-CAS9 but none of them can cure it. Despite the considerable work remaining, the progress in understanding progeria holds promise for the development of innovative treatment approaches. This study delves into the mechanism of progerin formation, changes in the body due to progerin, its complications, current therapeutic strategies, and recent advancements.

Keywords: Hutchinson-Gilford Progeria Syndrome (HGPS), Micrognathia, Farnesylation, LMNA Gene Mutation, Progerin, Methylation Inhibitors and Gene Therapy.

ICABB_M_51

ADHD: Current Perspective on Its Medication and Efficacy

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ABSTRACT

Attention Deficit Hyperactivity Disorder (ADHD) is among the most frequent disorders within child and adolescent psychiatry with a prevalence of over 5%. Symptoms like inattention, hyperactivity, impulsivity and emotional dysregulation. Medication is a core stone in the management of ADHD with both stimulants and non-stimulant medications playing vital role. Stimulants like methylphenidate and amphetamines, remain the most commonly prescribed pharmacological interventions for ADHD and they work by increasing the amount neurotransmitters in brain. In spite of having a proven efficacy in controlling the symptoms they are not liked due potential side effects. Non-stimulant medications including atomoxetine, guanfacine and clonidine offer alternative options, specifically for individuals who may not tolerate stimulants. They have a slow response and have less side effects in comparison to stimulants. In addition to this comprehensive ADHD management extend beyond pharmacological interventions to include behavioural therapies, psychoeducation and environmental modifications. The present manuscript describes the basics about ADHD and discusses various options available for its management.

Keywords: ADHD, Methylphenidate, Amphetamines, Atomoxetine, Guanfacine and Clonidine.

ICABB_M_52

Nanoliposomes as Smart Nanocarriers for Greening the Twenty-First Century Biomedical Settings

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ABSTRACT

With the current advancements in the nanosector based drug delivery systems (DDS), the necessity to develop even more effective, biocompatible, and safer treatment methods in biomedical settings is now being focused upon. The nanocarriers available at present still lack the proficiency in drug delivery owing to the stratum corneum layer of the skin thus making the in-practice traditional drug delivery method and therapeutic cues limited. Nanoliposomes, a kind of bilayer lipid vesicles, are in the advent due to their robust properties over traditional DDS. Owing to their production using natural and inexpensive ingredients along with them being biocompatible and biodegradable, makes them the smarter choice in the 21st Century biomedical settings. These lipid carriers have higher surface area-to-volume ratio and their nano-sized properties along with their penetrative capacity make them the excellent choice for dermal application in cases of fungal disease. However, the technology still has to go under many trials because the in vivo fate of Nanoliposomes has still not been identified. Therefore, by incorporating green and sustainable practices into the development and application of nanoliposomes, researchers contribute to the overall goal of greening biomedical technology.

Keywords: Drug Delivery System, Nanoliposomes, Biomedical Technology.

ICABB_M_53

Redox Imbalance and Cancer Cells

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ABSTRACT

ROS are highly reactive molecules derived from oxygen metabolism within the cells and are involved in regulating cellular processes like cell growth, cell differentiation and apoptosis. As the number of cancer cases is increasing there is an urgent need to develop newer medical interventions to reduce the deaths caused due to it. One of the most significant biological events that occur in cancer progression is oxidative stress that leads to higher oxidant level, suggesting a dual therapeutic strategy by regulating redox status, i.e prooxidant therapy. The redox vulnerability of cancer cells, caused by pro-oxidants, is capable of generating excessive ROS, which serves as a potential agent to kill malignant cells. We have explored the recent findings by elucidating the effects of excessive ROS levels as a potent intervention strategy against cancer, triggering programmed cell death or apoptosis. Various mechanisms of action of various synthetic as well as natural pro-oxidants are seen to be capable of generating excessive ROS, via redox cycling compounds, disrupting antioxidant defence mechanisms, and activation of exogenous death receptor pathways. However, the revolutionary clinical approach provided by the pro-oxidants (natural/synthetic) for cancer therapies, poses as a problem in using these prooxidants in cancer therapy.

Keywords: Apoptosis, Redox Cycling Compounds, Cancer Therapies.

ICABB_M_54

Identification of FDA-Approved and Natural Product Based Inhibitors Against RdRp of SARS CoV-2

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ABSTRACT

The global pandemic caused by Severe Acute Respiratory Syndrome Coronavirus-2 (SARS-CoV-2) known as COVID-19, has infected more than 20 million people and has caused 8 million deaths across 188 countries as of August 2022 (GISAID database). This calls for novel and effective therapeutic strategies against COVID-19. Researchers are primarily targeting key viral proteins, including spike proteins, main proteases, RNA-dependent RNA polymerase (RdRp), helicases, and endoribonucleases. The current work focuses on the RdRp complex comprising Nsp7, Nsp8, and Nsp12 the identification of FDA-approved and natural product-based inhibitors. Although various antiviral drugs are available against RdRp (Nsp12), none of them are known to inhibit the protein-protein interactions involved in the complex. Knocking down the RdRp complex is crucial for halting viral replication and transcription, which disturbs the whole viral assembly. In this direction, ~1400 FDA-approved, ~12000 IMPPAT compounds and previously known inhibitors of RdRp were screened against the SARS-CoV-2 RdRp complex via AutoDock Vina. Positive compounds having binding affinity ranges between -5.3 to -8.8 kcal/mol. Among the docked compounds 6 IMPPAT compounds and 10 FDA-approved compounds were selected on the basis of their binding affinity which is more than -8 kcal/mol. Molecular Dynamics (MD) simulation for 100 nanoseconds was done on the selected protein-ligand complexes. For in vitro testing of promising compounds, the recombinant RdRp complex was purified by Ni-NTA affinity chromatography up to a yield of ~1mg/ml. By integrating these processes, this research aims to contribute to developing targeted antiviral drugs against COVID-19.

Keywords: RdRp, Protein-Protein Interaction, Docking, MD Simulation, Ni-NTA Affinity Chromatography.

ICABB_M_55

Combining a Multifactorial Approach of Rational Drug Designing and Therapeutic Repurposing to Fight Leishmaniasis

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ABSTRACT

Leishmaniasis is a vector transmitted; protozoan borne infection that presents a wide range of clinical patterns with a huge global burden. Spread of Leishmaniasis to non-endemic countries and its rapid co-emergence with AIDS has raised alarm for immediate control of this disease. With unavailability of any commercial vaccine, leishmaniasis control lies entirely on chemotherapy that seeks swift rejuvenation. In this regard '*Therapeutic switching*' holds substantial potential especially when it is coupled with an in-silico drug targeting approach. In this work, we screened commercially available drugs against validated drug target(s) of *Leishmania* parasite followed by assessment of their antileishmanial potential in vitro against *L. donovani* and *L. mexicana*. Virtual screening of commercially available drugs was performed against two critical drug targets of *Leishmania* parasite. The drugs exhibiting best binding efficacy were explored further for their in vitro antileishmanial activity and adverse cytotoxicity against mammalian macrophages. Several candidate compounds exhibited critical binding properties against validated drug target(s) in *Leishmania* parasites. These compounds displayed significant antileishmanial activity with impressive IC_{50} values against *L. donovani* and *L. mexicana* promastigotes. Two bioactive compounds (Compound 1 and Compound 2) that exhibited the best safety profile against mammalian macrophages were further investigated for anti-amastigote activity and displayed remarkable reduction of intracellular parasites inside mammalian macrophages. Our study merits further in-depth evaluation of selected commercially available drugs against *Leishmania* parasites. These drugs can prove to be future candidate drugs for leishmaniasis.

Keywords: Leishmaniasis, Visceral Leishmaniasis, Cutaneous Leishmaniasis, *Leishmania*.

ICABB_M_56

Comprehending The Reasons for The Cessation of Effectiveness in Cancer Treatments and Finding Ways to Overcome Treatment Resistance

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ABSTRACT

It's often observed that cancer cells or tumor cells tend to develop resistance against cancer drug therapy known as drug resistance which is one of the most challenging concerns that cancer researchers and patients are currently dealing with. "*Relapse*" is the term for what happens when cancer cells multiply and reorganize tumors in response to chemotherapy drugs that can no longer work on them. A protein present in the cells is responsible for keeping toxic material out of cells known as ATP-binding cassette (ABC) transporters which is also responsible for creating resistance towards the treatment. By producing more glutathione (GSH) and nicotinamide adenine dinucleotide phosphate (NADPH), resistant cells adjust to oxidative stress and preserve intracellular redox equilibrium. Additionally, resistant cells can boost phospholipid production and fatty acid oxidation to preserve the integrity of their cell membrane and get an adequate energy supply to execute cell proliferation. Drug resistance may also come from changes in the epigenetic coding of cancer cells—chemical changes that activate or deactivate genes without changing the DNA code. Sometimes, Resistance can develop quickly, within weeks of starting treatment. In other situations, it takes months or even years for it to appear. To overcome this persistent difficulty faced during the majority of cancer therapies, attaining molecular alterations can effectively allow us to surpass the effects of relapse. Inhibition of ABC transporters and combining drugs to block the resistance mechanism are few of the prevalent approaches to overcome drug resistance in cancer treatment. Patients can possibly resensitize to chemotherapy by taking medications that reverse the epigenetic changes that cause resistance. Altering the tumor microenvironment and simultaneously Testing combinations are various methods which can help cure the issue of drug resistance in cancer cells.

Keywords: Drug Resistance, Relapse, ATP-binding Cassette Transporters, Epigenetic Coding, Glutathione, Nicotinamide Adenine Dinucleotide Phosphate.

ICABB_M_57

Rethinking Type-1 Diabetes Treatment: Emerging Medicines and Managing Expenses

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ABSTRACT

Increasing number of cases, especially in the younger age group, and the lack of accessible clinical solutions, make Type-1 Diabetes (T1D) a growing concern. Gene therapy and transplantation approaches pose a financial burden on those suffering from it, adding to the challenges faced by these advanced techniques. Therefore, it becomes a necessity to develop regular bedside pharmacotherapy that not only curbs β-cell damage but is also financially feasible for the majority of the population. In the present study, authors will discuss various such economic and feasible options such as: α-1 Anti-Trypsin (AAT) therapy using the AAT agent injected along with insulin and C-peptide preservation therapy using drugs like ATG and teplizumab. AAT stimulates the tyrosine phosphorylation of Insulin receptor (IR) and Insulin Receptor Substrate-1 (IRS-1) which is otherwise stimulated by insulin in a non-diabetic individual whereas, the drugs involved in the C-peptide preservation therapy are designed to prevent its depleting levels in T1D patients which is related to the drop in insulin levels. In the present manuscript authors aim to explore the efficiency of these newly emerged therapies in fighting against T1D.

Keywords: Type-1 Diabetes, α-1 Anti-Trypsin, C-peptide, ATG, Teplizumab.

ICABB_M_58

Exploring Ovarian Infertility and Its Novel Treatments

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ABSTRACT

Infertility affects 1 in 6 people globally which reflects upon the alarming need of immediate reproductive care in today's world. This inability to reproduce not only has a concerning impact on the globe but also causes psychological harm to the barren couple. Therefore, it becomes extremely important to understand ovarian infertility and thereby work out its treatments and cures. Sterility is observed in females at a higher rate as compared to males and also is more diverse in its causes that include anomalies in the reproductive organs, functional disorders, metabolic and hormonal imbalance. In the present study, authors will emphasize on the different types of female fertility based on ovulation dysfunction, sperm pathway and implantation disorders. Authors also aim to evaluate the effectiveness of the upcoming treatments such as Mesenchymal Stem Cells (MSC) therapy that aids in the ovarian recovery and in vitro procedures using Platelet-Rich Plasma (PRP) which adds to the quality of ovarian reserves that can increase the probability of conceiving clinically. This study will serve as a review of the latest concepts related to female infertility.

Keywords: Female Infertility, Ovulation Dysfunction, Implantation Disorders, Mesenchymal Stem Cells, Platelet-Rich Plasma.

ICABB_M_59

Novel Nanotherapeutics for the Management for Diabetes

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ABSTRACT

Diabetes is majorly classified into two types, Type 1 and Type 2 Diabetes Mellitus. Diabetes Mellitus is a chronic disorder with dysfunctioned pancreas where, pancreas produces less or no insulin in the body which normally is treated with injectable insulin. In Type 2 Diabetes Mellitus insulin is produced but majorly, body cells like liver cells and straight skeletal muscles, do not response the produced insulin. The major drug therapy for Type 2 Diabetes Mellitus includes alpha glucosidase inhibitors, insulin sensitizers, sodium-glucose co-transporter-2 (SGLT2), insulin secretagogues, biguanides, amylin antagonists, incretin mimetics, and inhibitors. Monotherapy and combination therapies are the preferred therapies to manage type 2 diabetes but over the modest forms of drugs available nowadays, traditional drugs have major side effects and complexities. Currently, nanotechnology-based drug delivery systems are being devised as better options with higher bioavailability and reduced dosage side effects only due to its characteristic of site-specific drug delivery. The present review surveys nanotechnology-based drug delivery systems for diabetic patients.

Keywords: Diabetes, Nanotherapeutics, Monotherapy, Combination Therapy.

SESSION - THREE

Environmental
and
Microbial Biotechnology

ICABB_E_1

Engineering Microbes for Space Mission: A Step Towards Space Microbiology Revitalization

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ABSTRACT

The microorganism response to deteriorating factors of space including high cosmic & UV radiation, space vacuum, and microgravity, etc. are important, as it provides an opportunity to investigate the behavior of microbes under laboratory simulated conditions. The space environment presents an unusual challenge for any forms of life including bacteria and therefore bacteria like tiny microbes show enhanced growth parameter requirements and a demonstrated ability to proliferate. The adverse environment also leads to increased bacterial virulence & pathogenicity, and also possesses health and safety risks to International Space Stations (ISS) crew members. The higher biofilm formation of ISS- microbes also possess a strong threat to astronaut health and equipment integrity. The detailed mechanism leading to several biological responses of bacteria is not yet fully known. In the present proposed work, we have summarized the scope of bacteria especially bioengineered bacteria in terms of plant cultivation, waste management, waste water reuse and atmospheric revitalization. In the present advanced era of newly developed genetic engineered tools, bioengineered microbes can be used for increased production of nutrients, creation and recycling of infrastructure materials, and in-flight therapeutics. The engineered microbes will also contribute to higher plant production, maintenance of soil health systems for future space missions. The developed microbes may act as microbial fuel cells to generate energy from waste, plant decay, and solar light conversion. In the present proposed work, we are presenting hypotheses for the role of newly developed microbes and their possible beneficial or detrimental effects for long-duration space missions. The newly developed microbes can be tested in Earth-based simulated space environment conditions. However, in terms of health and safety risks, the possibility of increased microbial virulence and pathogenicity in spaceflight should also be considered.

Keywords: Microbe, Space, Virulence, Pathogenicity.

ICABB_E_2

Fuel Alcohols from Microalgae

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ABSTRACT

Organic solvents are carbon – based substances that can dissolve one or more substances and can be used as fuel-substitutes. Ethanol and butanol are important organic solvents which can reduce our dependence on fossil fuels and thereby greenhouse gas emission. They can be produced through fermentation and bioprocessing techniques, using microorganisms. Microalgae are unicellular photosynthetic organisms that can efficiently convert carbon dioxide and sunlight into biomass rich in lipids, proteins and carbohydrates. Use of microalgae as a source of starch (19%) for producing these bio-based fuels overcomes many of the limitations associated with the use of conventional sources of starch, and presents a promising and sustainable solution to address the growing demand for renewable and environmentally friendly energy sources. Certain microalgae like *Chlorella sorokiniana*, *Chlorella vulgaris* and *Chloroidium saccharophilum* have been widely studied for the production of fuel alcohols. This review paper is focused on the production of these dual alcohols form microalgae via the starch route.

Keywords: Bio-Based Fuel, Organic Solvent, Ethanol, Butanol.

ICABB_E_3

Biosensors in Environmental Monitoring

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ABSTRACT

As the number and concentration of toxic pollutants in the environment are elevating, it necessitates the call for fast and cost-effective analytical techniques to be used for the development of a monitoring device. One such group of pollutants are Parabens, which is also an endocrine disruptor. A device that can be used for correct analysis to limit the increasing amounts of Parabens in the environment at a sensitive range of nanograms. Various sensors are already reported to detect paraben, so, to improve the accuracy, sensitivity of detection, an enzyme-based biosensor is being proposed in the current study. The signal produced by the sensor is equivalent to the quantity of the compound, the enzyme immobilized will increase the specificity. To further improve the specificity, a group of three enzymes (i.e. esterase, decarboxylase and oxidase) will be utilized on the sensor.

The biosensor utilizes biological molecules for the recognition of a target molecule or a specific event. Biosensors can be classified on the basis of different bio-recognition elements and transducing methods. Various types of bioreceptors, immobilization techniques, transducing element and transduction process could be combined for the detection of different types of analytes (like enzymes, antibodies, microorganisms etc.). Biosensors including genosensors, immunosensors, aptasensors, and enzymatic biosensors have been reported for the detection and monitoring of various environmental pollutants using nucleic acids, immunoglobulins, aptamers, and enzymes as recognition elements, respectively. Due to the ability of biosensors to be repeatedly calibrated, they can be used to determine the concentration of an analyte of interest in biological media and are easily distinguishable from bioanalytical systems, which require various processing steps to reduce the complexity of the biological sample through the addition of reagents. Different Food contaminants, adulterants, and environmental pollutants call for the same sensitivity, stability, and limit of detection as medical applications; however, such parameters as the volume of the sample, matrix complexity and requirement for on-site continuous monitoring make mounting these biosensors much more intricate.

Keywords: Biosensor, Environmental Pollutants, Signal, Bio-Recognition.

ICABB_E_4

Chlorpyrifos Exposure-Induced Alterations in Acetylcholinesterase Activity and Oxidative Stress Parameters in *Channa punctatus*

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ABSTRACT

This study investigated the impact of chlorpyrifos exposure on various biological parameters in *Channa punctatus* fish, including acetylcholinesterase (AChE) activity, lipid peroxidation, and antioxidant enzyme activities in kidney and liver tissues. The fish were subjected to three sub-lethal concentrations of chlorpyrifos (0.6 ppm, 0.3 ppm, and 0.16 ppm) along with a control group for comparison. The findings revealed a significant dose-dependent and time-dependent reduction in AChE activity in bith tissues of fish exposed to chlorpyrifos. Moreover, elevated levels of malondialdehyde (MDA), an indicator of lipid peroxidation, were observed in both tissues of chlorpyrifos-exposed fish, exhibiting dose-dependent and time-dependent effects. Additionally, glutathione peroxidase (GPx) activity exhibited significant alterations across both tissues, with higher doses and prolonged exposure leading to more pronounced effects. Glutathione S transferase (GST) activity was significantly increased in all treatment groups, with the highest activity observed in the high dose group at all-time points. These results suggest that chlorpyrifos exposure significantly inhibits AChE activity and induces oxidative stress in multiple tissues of *C. punctatus* fish. These findings highlight the potential adverse effects on fish health and survival, emphasizing the importance of monitoring and regulating pesticide use in aquatic environments.

Keywords: *Channa Punctatus*, Chlorpyrifos, AChE, Lipid Peroxidation, Glutathione.

ICABB_E_5

Gut Feelings: The Microbiome's Impact on Mental Health

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ABSTRACT

The microbiota, a varied ecology of bacteria, viruses, and fungi that live inside the human body, is present. The microbiota and various neuropsychiatric disorders, including major depressive disorder, schizophrenia, bipolar disorder, autism spectrum disorder, and attention-deficit hyperactivity disorder, are the subject of increasing current research. Due to its enormous abundance and probable involvement in mental and neurological diseases, the gut microbiota in the digestive system has drawn special interest. Although less prevalent, the microbiota found in other bodily tissues nonetheless has a significant impact on human homeostasis and the immune system, which also affects the onset and course of neuropsychiatric illnesses. Our gut health and brain function are greatly influenced by our diet. Certain diets, such as the fish oil-based Mediterranean diet, may help lower depression. Research on vegetarian and vegan diets, however, is conflicting. While some studies claim they have no effect or have benefits, others believe they may raise the risk of depression. Refined sugar-rich diets are bad for the brain because they can cause oxidative stress and inflammation. A high-refined-sugar diet has been linked to altered brain function, including increasing signs of mood disorders including depression. Patients with psychiatric problems have been found to have reduced relative abundances of the butyrate-producing *Faecalibacterium* and greater relative abundances of the taxa *Lactobacillus*, *Eggerthella*, and *Streptococcus*.

Keywords: Gut-Brain Communication, Neurotransmitters, Clinical Depression, Digestive System, Homeostasis, Gut Flora.

ICABB_E_6

Bioremediating Oil Spills as a Promising Strategy

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ABSTRACT

Bioremediation is an ongoing approach that harnesses the ability of microorganisms using approaches such as biodegradation, biotransformation, and biosorption to alleviate or stabilize contaminants from soil and water. An overview of the key concepts and applications of bioremediation is provided in this work, particularly of surface oil spills. The spilling of liquid petroleum, usually into rivers, oceans, etc., is called an oil spill. Three significant spills (>700 tons) were reported for 2022; two happened in Asia and Africa impairing aquatic life. Crude oils are primarily composed of hydrogen and carbon, resulting in an exceptionally poor solubility in water, causing a surface slick to form and spread quickly, covering a large area with a thin layer of oil. This can be physically removed by in situ burning, dispersant application, etc., and chemically by herding, dispersing, and gelling, which results in more toxicity. Compared to these methods' bioremediation offers benefits, such as cost and environmental savings. Consequently, fertilizers incorporating wheat bran (cheap non-toxic agro-residues) and marine bacterial consortia are introduced that include a variety of bacteria like *Pseudomonas putida*, also known as oil guzzlers, fungi and archaea (white rote fungi) (*Marinobacter*, *Oceanospiralles*, *Pseudomonas*) degrade oil using enzymes such as lipases, peroxidases, and dehydrogenases, catalyzing the breakdown of oil components into simpler, less harmful compounds. In summary, using microorganisms in the control of oil spills offers a long-term solution to lessen the effects of spills on the ecosystem. Sustained investigation into this area could enhance the effectiveness of microbial bioremediation as a crucial instrument in response plans for oil spills.

Keywords: Bioremediation, Biodegradation, Biotransformation, Biosorption, *Pseudomonas Putida*.

ICABB_E_7

Efficacy of Bioremediation in Cleaning Oil Contaminated Soil

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ABSTRACT

The contamination of soil by machine oil, petrol or such petroleum hydrocarbons poses a significant threat to the environment. These substances are highly toxic as they are a complex mixture of polycyclic aromatic hydrocarbons (PAH) such as paraffins and naphthene etc. as they are more reactive with the ozone layer than the alkanes developing a negative impact on the ecosystem and human beings as well. This disturbs the chemical balance of the soil. It also affects the production of reactive oxygen species (free radicals), antioxidant defenses and causes low availability of nutrients required for vegetation. Additionally, it is found that petroleum oil contamination affects processes like seed germination, photosynthesis resulting in barren land. Therefore, there is an urgent need to clean up this contamination from the soil. Bioremediation is an ecofriendly and environmentally conscious solution to this problem. As bioremediation utilizes the natural metabolic processes of microorganisms, such as bacteria and fungi, which assist in degrading and converting oil compounds into less harmful byproducts. Along with microorganisms, plants are also known for the remediation of such contaminates from the soil. Therefore, use of microbes and plants for cleaning of this contamination from the soil is one of the most appropriate and cost-effective strategy, unlike physical and chemical methods for the remediation of oil. This review highlights the potential and mechanism of microbes and plants for the remediation of oil contaminated soil.

Keywords: Bioaccumulation, Bioremediation, Contamination, Microorganism, Oil, Soil.

ICABB_E_8

Biopolymers: A Novel Approach and Sustainable Way to Remove Contaminants and Treat Wastewater. Existing Conditions and Future Prospective

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ABSTRACT

Biopolymers are defined as naturally occurring substances or polymeric materials synthesized from biological sources and considered to be environmental-friendly and sustainable. However, various synthetic polymers are produced from coal as raw materials and making them not compatible with environment because they cannot be incorporated with natural recycling system. In order to adaptability, sustainability, biodegradability and non-toxicity, applications of biopolymers have been suggested in a variety of areas such as food industries, pharmaceutical, biomedical industries and particularly in wastewater treatment. The wastewater mainly consist pollutants like persistent organic pollutants, phosphates, chlorine complexes, heavy metals, dyeing constituents, toxic cations, dissolved solids, and suspended solids. In order to remove pollutants from wastewater and industrial effluents, naturally occurring biopolymers have now emerged as interesting sorbents with enormous potential to replace conventional technologies. The biopolymers exhibit remarkable characteristics such as high efficiency, bioactivity, non-toxicity, elasticity, anti-microbial activity, large surface area, and ease of synthesis. Furthermore, their adsorption qualities can be modified by employing efficient fabrication techniques. Naturally generated biopolymers such as chitosan, lignin, cellulose, carrageen, pectin etc. exhibited extremely effective sorption capabilities for the remediation of contamination and categorised as low-cost sorbents. They can also be used to address current research gaps and potential challenges related to various contaminations because it is an important component of circular bioeconomy (CBE) also. The CBE model framework also makes recommendations for potential approaches to applying CBE principles in the wastewater management sector, with a particular emphasis on societal and institutional and technological advancements. This chapter covers the applications of natural biopolymers and grafted copolymers to treat wastewater for heavy metals, oils, dyes, and other chemicals, as well as the difficulties, current perspective and potential future developments in the field of biopolymer development.

Keywords: Biopolymers, Wastewater Treatment, Bio-Flocculants, Circular Bioeconomy.

ICABB_E_9

Exploring the Versatility of Fungal Chitosan: Its Application & Advancement in Enzyme Immobilization

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ABSTRACT

Fungal chitosan is a biopolymer derived from fungal cell walls, β-1,4-linked glucosamine units, with some of the glucosamine residues deacetylated to form N-acetyl-D-glucosamine (NAG) units. There are various applications like enzyme immobilization, wound healing, food preservation, and biomedical purposes. Immobilizing enzymes has been explored in various fields, including nonaqueous media, water purification, and nanogel-based systems. The market for fungal chitosan is projected to grow at a CAGR of 12.2% and reach USD 1.2 billion by the upcoming year Enzyme immobilization using chitosan involves preparing chitosan with a specific degree of deacetylation (influencing amino acid binding capacity and affinity for the enzyme), mixing the enzyme with a suitable buffer solution, to facilitate its interaction with the activated chitosan matrix. and ultimately concluding with washing and recovery steps. Significant progress has been made in enzyme immobilization, particularly leveraging fungal chitosan, with potential for increased industrial applications. The versatility and potential of fungal chitosan across various scientific and industrial domains pave the way for further research and applications in the future, indicating its expanding role in enhancing enzyme immobilization technologies.

Keywords: Chitosan, Biopolymer, Nonaqueous, Nanogels, Antioxidant Activity.

ICABB_E_10

Development of Antibody-Based Immunoreagents for the Detection of Drug-Resistant *Acinetobacter baumannii*

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ABSTRACT

Multi-drug resistant (MDR) strains of *Acinetobacter baumannii* (*A. baumannii*) are known for causing nosocomial infections globally resulting in significant mortality rates. Carbapenems are considered the last-resort treatment of choice for MDR *A. baumannii*. However, the emergence of carbapenem-resistant *A. baumannii* (CRAB) has been now reported world-wide, and WHO has listed it as the ‘critical priority 1’ pathogen for research and development. Development of reliable, rapid, and easy-to-use diagnostic reagents is an important aspect for the timely treatment of the patients for improved clinical outcomes and to ensure controlled use of carbapenem drugs and effective management of infection spread. At present, the detection of CRAB is performed using tests which are either time-consuming, laborious, or expensive. Further, no single platform allows rapid, efficient, sensitive, specific, and cost-effective detection of CRAB. In this work, using a major carbapenemase as a target, specific antibodies have been developed using phage display technology to enable rapid detection of carbapenem resistance in drug-resistant *A. baumannii*. Six antibodies have been selected and produced in soluble form for further validation and use as reagents for diagnosis of drug-resistant *A. baumannii*.

Keywords: Carbapenems, Drug-Resistant *Acinetobacter baumannii*, Antibody, Phage Display.

ICABB_E_11

Current Advancements and Emerging Trends of Nanoparticles as Photocatalysts for Treatment of Dye Waste-water

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ABSTRACT

Environmental contamination from textile dyes is a worldwide issue, and treating wastewater has become an extremely difficult challenge in recent years. The primary sources of dyes in the environment are the textile, paper, and pulp industries, dye intermediate, tannery and craft bleaching industries etc. The amount of oxygen in water gets disrupted by dyes and affecting the ecological balance of aquatic ecosystem and making water unsuitable for drinking, irrigation, and recreation purposes therefore, it must be removed from the environment. Various physical and chemical methods such as adsorption, chemical precipitation, photolysis and electrochemical treatment have been used for dye removal from the wastewater which is not sustainable. The limitations of conventional wastewater treatment has been overcome by use of various nanoparticles such as TiO_2, ZnO, and Fe_3O_4 which exhibit greater potential of dye degradation because of their nano-size, electrochemical stability, high surface reactivity, high electron mobility and large surface area. Therefore, present review mainly emphasises the significance, mechanism and application of nanoparticles as photocatalyst to make them more practical in wastewater treatment. This review also offers valuable insights for environmentally friendly techniques like nanoparticles utilization for dye removal along with varying perspectives on the limitations and effectiveness of nanoparticles on dye degradation.

Keywords: Textile Dyes, Nanoparticles, Zinc Oxide, Titanium Dioxide, Remediation, Photocatalyst.

ICABB_E_12

Fermentative Production of 2, 3-Butanediol Using Food Waste – A Sustainable Method for Food Waste Management

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ABSTRACT

This is an era of resource scarcity for human population, with the need for a clean environment and demands for cost available resources. Approximately thirty percent of all food intended for human consumption is wasted, which causes serious environmental impact. Therefore, the high amount of food waste (FW) is a concern for the entire world. Considering the high population energy demand, the uses of edible substrates from food industry can considered as alternative and renewable bioresource to produce valuable product such as 2, 3-butanediol (BDO). BDO extensively used in production of printing inks, fragrances, fumigants, and softening agents, and plasticizers such as polyvinyl chloride, cellulose nitrate, polyacrylates and chemical industries and transformed into beneficial derivatives like methyl ethyl ketone, diacetyl, and 1,3-butadiene. FW has the potential source of biomolecules which is considered as a feasible alternative feedstock for the fermentation-based chemical production and provide alternative solution against conventional waste management techniques. Food waste such as bread is starch-rich material and clean source of fermentable sugars, which required various enzymatic pretreatment for release of fermentable sugars. The present study illustrates an environmentally friendly solution in converting food waste into 2, 3-Butanediol and the associated solid residues produced during fermentation and hydrolysis into biogas.

Keywords: Bioresource, Fermentation, 2, 3-butanediol, Biomolecules, Lactic Acid.

ICABB_E_13

De-Extinction: Bringing Back the Long Lost

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ABSTRACT

The duality of Mother Nature rests in her ability to bestow her bountiful gifts upon us and, in equal measure, to reclaim them, and we as human beings have always been fascinated by the idea of bringing back what has been taken from us by Mother Nature. The concept of de extinction, as defined by the International Union for the Conservation of Nature (IUCN) is "*The process of creating an organism that resembles an extinct species*". With every passing day, the idea for bringing back extinct species is becoming more of a reality rather than sci-fi, and the idea is not limited to species, buried inside our genome right now are molecular fossils-bits of DNA that are so broken that they no longer work (like- the UoX gene that codes for uricase) and these bits of DNA can be recovered using the right techniques. Here we focus on the concept of species and molecular De-extinction as well as our hypothesis on how to trace back the lineage of the ancient molecules, using Ancestral Sequence Reconstruction methods.

Keywords: De-extinction, Ancestral Genome Reconstruction, Uricase, IUCN.

ICABB_E_14

Physicochemical Characterization of Bacterial Cellulose Produced by *Gluconacetobacter liquefaciens* MTCC 3135 Under Static and Agitated Culture

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ABSTRACT

Bacterial cellulose (BC) is a significantly required biopolymer in the biomedical and industrial sectors because of its superior crystalline structure, water retention, biocompatibility, and biodegradability. However, the high operating cost, expensive culture media components and low productivity often limits its widespread industrial usage. In our study, bacterial cellulose production by *Gluconacetobacter liquefaciens* MTCC 3135 was investigated under static and agitated culture conditions in Hestrin–Schramm (HS) medium. Growth kinetic studies were done for 7 days under static and agitated culture conditions and specific growth rate and doubling time were calculated. Under static culture conditions, *Gluconacetobacter liquefaciens* gave maximum BC yield of 3.43±0.24 g/L in HS medium at 30°C at pH 6.0. BC samples produced under static and agitated culture were purified using NaOH treatment and were subjected to physicochemical characterization using FTIR, XRD and DSC. FTIR spectra showed peak shifting and variations in peak intensities for BC samples produced under agitation and static culture, while compared to commercial cellulose (Himedia, India). BC produced under static culture was more crystalline compared to BC samples produced under agitation, as determined by FTIR and XRD.

Keywords: Bacterial Cellulose, *Gluconacetobacter liquefaciens,* Static, Agitation, FTIR, XRD, DSC.

ICABB_E_15

Screening and Isolation of Polyhydroxyalkanoate (PHA) Producing Bacterial Isolates from Oil-Contaminated Soil

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ABSTRACT

Petrochemical based plastic materials are contributing to significant environmental impacts due to their stable structure and poor degradability, which has created increased interest in development of biodegradable polymeric materials. This has led to the development of economically viable biodegradable polymers with distinct physicochemical properties. Polyhydroxyalkanoates (PHA) are microbial esters with distinctive properties, making them a suitable candidate for replacing synthetic polymers. PHA production process largely depends on the type of microbial strain, their metabolism & bioprocess parameters. Choice of a potential microbial strain is crucial for PHA production. In this study, we aim to screen and isolate PHA producing bacteria from oil-contaminated soil. Ten isolates were obtained on nutrient agar plates after serial dilution method. Isolates were then subjected to Sudan black B staining for further screening. 4 isolates showed black-blue coloration when stained with Sudan black B which is used as a preliminary screening dye for identification of lipophilic compounds, out of them 2 isolates showed positive result with Nile blue A staining which is used as a confirmatory dye and specific dye for PHA accumulation. Selected isolates were analyzed for PHA production in Mineral salt medium (MSM).

Keywords: Polyhydroxyalkanoates, Sudan Black B, Nile Blue A, Mineral Salt Medium.

ICABB_E_16

Cost Effective Production of Fungal Chitosan from *Trichoderma reesei* in Solid State Fermentation Using Agroindustrial Residues

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ABSTRACT

Chitosan is the second abundant biopolymer on the earth and is found in exoskeleton of arthropods and crustaceans. Chemically, chitosan is the deacetylated form of chitin, which is produced via treatment with harsh chemicals on the commercial scale. This is adversely affecting the environment. An alternative approach for the production of chitosan is via using a fungal system as chitin is an integral part of fungal cell wall. Replacing the expensive synthetic culture media with agro-industrial residues present a sustainable production strategy for cost effective production of chitosan. Solid state fermentation (SSF) offers the advantage of producing large fungal biomass quantities compared to submerged fermentation (Smf), resulting in improved potential of chitosan production. SSF for biomass production using agro-industrial waste such as paddy straw, sugarcane bagasse, potato peel, banana peel and wheat bran can be cost-effective nutritional supplement. A significant amount of carbohydrates in agro industrial waste enhances fungal biomass production to achieve a circular bio economy. The presence of fermentable sugars in agro industrial waste act as a viable substrate for scaling up fungal chitosan production. In our study, solid state fermentation of *Trichoderma reesei* on banana peel and wheat husk was done for fungal chitosan production using an alkaline treatment with modifications. Extracted polymer was analyzed for physicochemical characteristics and was compared with commercial chitosan. The FT-IR spectra of fungal chitosan revealed signature absorption peaks, confirming the polymer to be chitosan. DSC thermogram showed that fungal chitosan was stable at room temperature along with two degradation peaks.

Keywords: Fungal Chitosan, Solid State Fermentation, Agro Industrial Waste, FTIR, DSC.

ICABB_E_18

Holistic Approaches to Health: Probiotics and Beyond

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ABSTRACT

In the pursuit of health and disease management, the intricate dynamics among probiotics, postbiotics, prebiotics, paraprobiotics, and synbiotics have surfaced as a promising frontier. Recent studies highlight the adverse impacts of synthetic drugs, preservatives, and fertilizers on both human health and the environment, underscoring the urgent need for innovative, non-toxic solutions. Probiotics, renowned for promoting health through diverse mechanisms, offer a practical alternative for treating infectious and non-infectious diseases with minimal side effects. Their role in forming colonies that inhibit pathogens, producing inhibitory substances, and the emergence of paraprobiotics as a potent therapeutic form demonstrate the evolving landscape of health interventions. Prebiotics, functioning as substrates for probiotic growth, contribute to energy through fermentation despite evading digestion. Synbiotics, a synergistic blend of prebiotics and probiotics, further amplifies their potential to enhance human or animal health. Understanding the profound impact of probiotics on gut microbiota and their ability to influence immune responses through toll-like receptors on dendritic cells, especially with *Lactobacilli*, emphasizes their pivotal role in maintaining overall well-being. As society grapples with environmental challenges and health complexities, embracing these holistic approaches becomes imperative for fostering sustainable and effective solutions. The convergence of scientific advancements in probiotics, prebiotics, and their derivatives unveils a multifaceted strategy in the pursuit of a healthier future.

Keywords: Probiotics, Prebiotics, Paraprobiotics, Synbiotics, *Lactobacilli*.

ICABB_E_19

Application of Polypyrrole Modified Stainless Steel Mesh as an Effective Anode Catalyst for Efficient Power Generation in Saline Microbial Fuel Cell

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ABSTRACT

Microbial fuel cell (MFC) is an emerging technology for power generation and simultaneous wastewater treatment. The anode material is one of the key factors which determines the power density and cost of the MFC system. Stainless steel (SS) mesh is considered one of the suitable anode materials in MFC due to its low cost and high mechanical strength. However, its low conductivity and poor biocompatibility limit its use in MFC. In this study, SS mesh modified with polypyrrole (PPy) using in-situ electro polymerization, was used as an anode material in a saline MFC. Under highly saline conditions, electrode stability and corrosion are the biggest challenge. Ppy has good environmental stability, biocompatibility, and high electrical conductivity. Many studies have been done already using Ppy as a conductive material for the anode in MFC. This is the first study using SS/Ppy anode in a saline MFC. Halophilic bacteria enriched from seawater (Arabian Sea, Mumbai) was used as inoculum source for treating saline wastewater. Sodium chloride (NaCl) concentration of 40 g/L was used in the anode chamber. Nitrate was used as electron acceptor at the biocathode. The maximum power density of 272.90 mW/m2 was achieved using SS/PPy electrode which was 1.9 times higher as compared to bare SS anode (146.06 mW/m2). Higher OCV (open circuit voltage) of 730 mV was achieved in SS/PPy as compared to bare SS (590 mV). SEM analysis revealed rough and porous microstructures in the SS/PPy electrode surface which facilitated the attachment of microorganisms. Cyclic Voltammetry analysis revealed the high electrochemical activity in SS/PPy anode. The electrode capacitance was also 11 times higher in SS/PPy anode as compared to bare SS. Thus, this study demonstrates that higher conductivity and surface area contribute to higher power density in SS/Ppy which makes it a suitable catalyst in saline MFC.

Keywords: Microbial Fuel Cell, Halophilic Bacteria, Denitrification, Salinity, Charge Transfer Resistance, Power Production.

ICABB_E_20

Revitalizing Antimicrobial Strategies: A Comprehensive Exploration of Bacteriophage Therapy to Combat Antibiotic-Resistant Infections

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ABSTRACT

The escalating problem of antibiotic infections requires an approach to fighting against them. Traditional antibiotics are becoming less effective which emphasizes the need for treatments. In this review we discuss the resurgence of phage therapy as a solution to tackle incurable infections. To address the issue of resistance we suggest a targeted approach that involves isolating and studying bacteriophages. Our focus is on identifying the characteristics that make them effective in therapy especially when dealing with biofilms. Recognizing the limitations of phages and the constant challenge of resistance we propose a strategy that involves modifying the genomes of known phage isolates with desired properties. Successful cases like using engineered phages to treat *Mycobacterium abscessus* infections demonstrate the potential of this approach. Moving beyond applications we explore uses for phages, including their role in military medicine. We delve into both the genotypic and phenotypic properties that make a "*therapeutic phage*" and discuss ongoing efforts to enhance their effectiveness in treating pathogens. In addition to uses we highlight how phages can be valuable, for pathogen detection targeted drug delivery, vaccine development and decontaminating food or surfaces.

To sum up this review highlights the changing field of phage applications and their potential, in tackling the problem of resistance. With conventional treatments becoming less effective a concentrated investigation into bacteriophage therapy emerges as a path to combat antibiotic infections.

Keywords: Bacteriophage Therapy, Antibiotic Resistance, Phage Isolation, Genetic Engineering, Biofilm Infections, Clinical Applications.

ICABB_E_21

Understanding Maternal Microbiota Influence on Offspring Development and Health

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ABSTRACT

Microbial metabolites are transferred to the fetus even before birth, where the mother's microbiota influences the development of the progeny. Therefore, the fetus's exposure to a particular chemical environment throughout its gestation in the womb is shaped, in part, by the metabolic processes of the mother microbiota, and vary depending on the gender. The numerous systemic regions inside the body receive a varied array of metabolites that arise from the commensal microbiota that lives in the maternal body. Fetal development of specific pathogen-free (SPF) and germ-free (GF) mouse dams kept in a sterile environment is examined in relation to the impact of the maternal microbiome. The embryonic organs of GF and SPF mice differed significantly based on 3680 molecular characteristics and 101 annotated metabolites studied. Gene expression differences become noticeable in develop in the placenta, brains, and intestines. Strongly differentiable expression was observed for several genes related to synaptic signaling and neuronal development. Immunity, intestinal host-microbe interactions, and xenobiotic metabolism are all impacted by these genes, which include mucins, interferon and cytokine signaling genes, interleukins and their receptors, etc. In order to guide individualized interventions and provide prospective biomarkers for health evaluation, it is imperative to comprehend how the fetal metabolome is influenced by the mother microbiome in medical applications. The goals of this review are to improve overall healthcare outcomes by promoting early detection and intervention.

Keywords: Maternal Microbiota, Microbial Metabolites, Fetal Development, Potential Biomarker, Medical Applications.

ICABB_E_22

Isolation of Halotolerant Bacteria with Potential Biotechnological Applications

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ABSTRACT

Halotolerant bacteria can be identified as those which can grow in salt deficient conditions and sustain their life cycles under salt stress too. Such microbes have been identified with significant potential in remediation and production of commercially relevant hydrolases. In this study isolation of halotolerant bacteria from Sambhar Salt Lake, Rajasthan led to eight strains which were characterized using phenotypic and genotypic methods. These isolates grew under mildly acidic to alkaline conditions and between 25–37°C. Among these four were gram positive and other four were gram negative. Catalase, oxidase and citrate activities were found to be positive for the majority of the isolates with a negative result obtained majorly for indole, MR-VP, gelatine liquification and urease. Fatty acid methyl ester (FAME) analysis exhibited accumulation of saturated fatty acids across all isolates, suggesting a shared lipid composition within the group while FTIR spectrum confirmed them to be members of eubacteria supporting the staining results. Taxonomic delineation through 16S rRNA gene sequencing showed 2 species *Salisediminibacterium*, 2 of *Halomonas* belonging to γ-Proteobacteria. In gram positives, 3 genera were identified in *Firmicutes* as *Marinococcus*, *Ornithinibacillus*, and *Alkalicoccus*, with *Enteractinococcus* in *Actinobacteria*.

Keywords: Halotolerant, Halophile, Sambhar Lake, Phenotypic Studies, Genotypic Studies, 16s rRNA Sequencing, FAME.

ICABB_E_23

Insights into Yamuna River Bacteriophages: Isolation and TEM Examination

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ABSTRACT

In nations grappling with waterborne illnesses, ensuring safe and cost-effective drinking water production faces increasing challenges due to heightened river pollution. The Yamuna, considered sacred, is at risk of contamination, introducing bacteria carrying antibiotic resistance genes (ARGs). Bacteriophages are advocated as an alternative treatment for antibiotic-resistant pathogens, targeting various pathogenic bacteria. The revival of phage treatment offers a strategy against antibiotic resistance and provides a viable means of combating harmful microorganisms. This study aims to assess bacteriophages abundance and evaluate Yamuna water quality, obtaining high-magnification images and employing detailed collection protocols and electron microscopy. Samples from the Yamuna underwent filtration using 0.22µm and viral titration against E. coli and Pseudomonas using a plaque assay method. Bacteriophages morphology was confirmed through Transmission Electron Microscope (TEM) analysis. The phages exhibited diverse effectiveness in managing bacterial infections, offering compelling data to support prospective phage therapy applications. A comprehensive understanding of phages necessitates further exploration.

Keywords: Antibiotic Resistance Genes, Bacteriophages, Plaque Assay, Transmission Electron Microscope, Yamuna River.

ICABB_E_25

A Comprehensive Review on *Aureobasidium* sp and its Utility for Medical Applications

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ABSTRACT

Aureobasidium sp., a ubiquitous genus of dematiaceous fungi, has gained increasing attention in recent years due to its diverse ecological roles and potential applications in various biotechnological fields. This review provides a comprehensive overview of the taxonomy, ecology, and biotechnological relevance of *Aureobasidium* sp. Taxonomically, *Aureobasidium* is a complex genus with numerous species exhibiting morphological and genetic diversity. Advances in molecular techniques have facilitated a more accurate classification, shedding light on the phylogenetic relationships within the genus. The review highlights the challenges associated with species identification and the need for continued research to refine the taxonomy of *Aureobasidium*. Ecologically, *Aureobasidium* sp. demonstrates adaptability to a wide range of environments, including terrestrial, aquatic, and extreme conditions. The fungus is commonly found on plant surfaces, in air, and even in extreme habitats such as hypersaline environments and cold ecosystems. Understanding its ecological niche and interactions with other microorganisms is crucial for appreciating its ecological significance. The biotechnological potential of *Aureobasidium* sp. is explored in the context of various applications, including industrial enzymes, biocontrol agents, and bioremediation. The fungus produces extracellular enzymes with applications in industries such as food, textile, and pharmaceuticals. Additionally, *Aureobasidium* sp. has demonstrated biocontrol capabilities against plant pathogens and potential for bioremediation of pollutants. Despite the promising attributes, challenges and gaps in knowledge regarding the biology and applications of *Aureobasidium* sp. are discussed. This review aims to consolidate existing knowledge, stimulate further research, and inspire the utilization of *Aureobasidium* sp. in diverse scientific and industrial applications.

Keywords: Dematiaceous Fungi, Pharmaceuticals, Extracellular Enzymes, Biocontrol, Extreme Habitats.

ICABB_E_27

Population Structure Analysis of Swamp Buffaloes Using High-Density SNP Chip in North East India and Adjoining Regions

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ABSTRACT

India boasts a widely distributed buffalo population, displaying variable densities across different states and union territories. The two primary classifications of these buffaloes are the swamp buffalo and river buffalo. Swamp buffaloes, prevalent in Southeast Asia, exhibit a compact and robust physique, playing a crucial role in agricultural activities, particularly in drought-related operations in Southeast Asia. This study focuses on characterizing the population structure of Swamp buffaloes using high-density SNP Chip in North East India and adjoining states. Two methodologies, Principal Component Analysis and Admixture for efficient estimation of admixture proportion interference, were employed for this purpose. The analysis revealed distinct patterns among various buffalo populations. The Luit buffaloes exhibited contiguity, while Tripura buffaloes formed a separate contiguous group. In contrast, Manipuri buffaloes predominated and were distinctly clustered apart from the rest of the population. Chilika buffalo constituted a unique cluster, and Chhattisgarhi and Kalahandi buffaloes formed a single cluster that remained inseparable even at Principal Component Six. The results imply that Luit buffaloes are not confined to a specific location but are widely dispersed. This study highlights the presence of a distinct pattern among different buffalo populations, providing valuable insights into the genetic diversity and distribution of swamp buffaloes in the specified regions.

Keywords: Swamp Buffaloes, SNP Chip, Admixture Proportion Interference.

ICABB_E_28

Edible Herb Plant(s) of Manipur: Waste to Wealth

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ABSTRACT

Manipur, one the North eastern state of India, is well known for her rich biodiversity and her food habits. Wetland with its bio-resources plays an important role in human life. There is consideration of the wetland as the main source of livelihood of sustainable societies and its plants also play a crucial and significant role. Consuming of plant(s) from wetlands as food is one of the old practices in Manipur. It is one of the old practiced in the state, and also most significant techniques adopting by the Manipuri's in their food processing. Neglected plant(s) species from wetlands is reviewed in the present investigation. Survey has been conducted following questionnaire on food habits by location-wise for obtaining maximum information. In further, the study includes the efficacy of food items as medicines. The collected data shall be properly document in order to validate the traditional practicing.

From this investigation, one could reveal the traditional practices (especially eating habits) in different districts of the state need to be documented. Currently, traditional knowledge and practices are in danger state, the effective of local food items from wetlands are not well known, so documentation is must. The young generation is not aware and not interested to carry out this traditional food habit; consequently, there is need of proper maintenance of wasted wetlands that could support wasted to wealth and also this revision may reflect some light on the value of preserving the wetlands.

Keywords: Edible Neglected Plant(S), Wetlands, Manipur, Traditional Knowledge.

ICABB_E_29

Role of *Ocimum basilicum* in Phytoremediation and Bioaccumulation of Lead and Cadmium Present in Soil

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ABSTRACT

Soil contamination with heavy metals like lead (Pb) and cadmium (Cd) poses a serious risk to ecosystem and human health. These heavy metals can be removed from the soil using various physical and chemical techniques but these conventional remediation techniques can have negative ecological effects and are expensive. Aim of this study was to use ecofriendly options for the removal of Pb & Cd and to investigate the efficacy of *Ocimum basilicum* (Tulsi plant) in remediating Pb & Cd from the soil. This research examines the ability of *Ocimum* plant to absorb, translocate and tolerate high concentration of these metals. Pot-based experiments in a natural environment were used in the experimental design to simulate soil spiked with Pb & Cd. In order to determine the phytoremediation potential of selected plant, various parameters like plant growth, chlorophyll content, metal uptake, translocation and other physiological parameters were evaluated. Results reflect that *Ocimum basilicum* plant can remediate Pb through phytostabilization while Cd by phytoextraction. *Ocimum* is a potential phytoremediator and has an ability to accumulate heavy metals. This study helps to understand the properties and potential of *Ocimum basilicum* in sustainable and cost-effective strategy for remediation of heavy metal contaminated soil.

Keywords: Environment, *Ocimum basilicum*, Phytoremediation, Phytostabilization, Phytoextraction.

ICABB_E_30

Indian Mustard (*Brassica juncea*): A Promising Phytoremediator for Ciprofloxacin

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ABSTRACT

The antibiotic selected for investigation was ciprofloxacin, primarily due to its prevalent usage in both human and veterinary medicine, making it the most commonly administered drug. The aim of the present study was to evaluate the capability of Indian mustard (*Brassica juncea*) in phytoremediation of ciprofloxacin. Germinated seeds of *B. juncea* were grown with different concentrations of ciprofloxacin ranging from 50 mgkg-1 to 300 mgkg-1 for a duration of three weeks. The examination of antibiotics in plant samples was conducted using HPTLC. Parameters such as remediation rates, translocation factor, and various toxicity indicators including fresh and dry weight, root and shoot length, variations in chlorophyll, and carotenoid content were calculated to evaluate the uptake of antibiotics by *B. juncea*. The findings demonstrated a dose-dependent effect on the biomass and growth of plants. Under the influence of ciprofloxacin stress, it was seen that there was an increase in total chlorophyll, carotenoid, and flavonoid content. The remediation outcomes indicated that the chosen plant exhibited a remediation potential of 65.71% at 100 mgkg-1 of ciprofloxacin concentration, but signs of toxicity emerged after exposure to 200 mgkg-1. Overall results indicate that *Brassica juncea* is exhibiting a very encouraging rate of phytoremediation, and it has also demonstrated toxicological impacts on plants. As a result, the study was effective in removing the antibiotic ciprofloxacin from soil and can now be carried out on a wide scale.

Keywords: Antibiotics, Contamination, Ciprofloxacin, HPTLC, Phytoremediation.

ICABB_E_31

A Sustainable Approach for Degradation of Azo Dyes in Wastewater Through Biogenic Palladium Nanoparticles

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ABSTRACT

Dyes are the coloured substances that are applied on different substrates such as textiles, leather and paper products, etc. Azo dyes release from the industries are toxic and recalcitrant wastewater pollutants therefore it is necessary to degrade these pollutants from water. In this study, the palladium (0) nanoparticles (PdNPs) were generated through the biological process and exhibited for the catalytic degradation of azo dye. The palladium nanoparticles (PdNPs) were synthesized by using the extract of fungal strain Rhizopus sp. (SG-01) from anhydrous $PdCl_2$ therefore it may be called as biogenic PdNPs, which significantly degrade the azo dye (methyl orange). The amount of catalyst was optimized by varying the concentration of PdNPs (1 mg/mL to 4 mg/mL) for 10 mL of 50 ppm methyl orange (MO) dye separately. The time dependent study demonstrates the biogenic PdNPs could effectively degrade the methyl orange dye up to 98.7% with minimum concentration (3 mg/mL) of PdNPs within 24 h of reaction. The long-term stability and effective catalytic potential up to five repeated cycles of biogenic PdNPs have good significance for acceleration the degradation of azo dyes. Thus, the use of biogenic palladium nanoparticles for dye degradation as reported in the present study, can provide an alternative and cost-effective process for the generation of PdNPs as well as degradation of azo dyes present in wastewater and helpful to design effective approach in textile effluent remediation.

Keywords: Azo Dyes, Wastewater treatment, Biogenic, Palladium, Degradation.

ICABB_E_32

Enhancing Air Quality through Plant-Mediated Dust Interception: A Review of Common Roadside Plant Species in Delhi NCR

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ABSTRACT

Rapid urbanization and industrialization have led to a surge in air pollution, particularly in regions like Delhi National Capital Region (NCR), where the ambient Air Quality Index (AQI) is escalating at an alarming rate. This phenomenon poses a significant threat to plant species growing alongside roads, as elevated levels of dust in the atmosphere visibly impact photosynthetic and respiratory rates. Recognizing the urgency of this issue, the primary objective of this review paper is to investigate the resistance mechanisms employed by various plant species to counteract the deleterious effects of a polluted environment. Central to this exploration is the crucial role of dust interception in mitigating air pollution near plants. Leaves covered with dust experience reduced light exposure, leading to diminished photosynthetic efficiency and overall productivity. This study sheds light on the dust deposition efficiency of common roadside plant species, emphasizing their diverse responses to dust accumulation on the biochemical aspects of leaves, such as total chlorophyll content. Understanding the impact of polluted air on plant species is vital for assessing their ability to thrive in challenging environments. This review serves as a comprehensive resource for estimating the resilience of different plants to pollution, ultimately identifying species that can serve as effective mediums for restoring air quality balance. The specific plant species that can be strategically employed to enhance air purification in homes. As society grapples with the escalating challenge of air pollution, the insights provided in this paper contribute to the ongoing discourse on sustainable solutions for maintaining a healthier environment.

Keywords: Air Quality Index, Chlorophyll, Environment, Photosynthetic Rate, Pollution.

ICABB_E_33

A Perspective Review on Role of Environmental Pollutants in Developing Neurodegenerative Diseases

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ABSTRACT

As human society progresses towards industrialization, an excess amount of environmental pollutants are released which significantly contribute to causing various health issues primarily associated with neurodegenerative diseases such as cognitive disorder, dementia, anxiety, Alzheimer, Parkinson etc. Because of their high global occurrence, these diseases have attracted attention in recent decades, however, the etiology of these diseases remains unclear. Pollutants are discharged into the environment by natural events such as volcanic eruptions and wildfires, as well as by man-made activities such as industrial and laboratory waste, pesticide residues, automotive exhaust and the burning of terrestrial waste that pollute the water, air, and soil causing neurological diseases in inhabitants. These pollutants enter the body by inhalation, oral absorption and ingestion and reach to the central nervous system (CNS), where they induce tissue damage and disrupt molecular and cellular processes. Numerous investigations on humans, animals, and cell cultures have shown how these pollutants affect the blood-brain barrier causing neuroinflammation, CNS oxidative stress, neurodegeneration, and the cerebrovascular system damages. The current review discusses diverse sources of pollutants, their neurotoxic effect, molecular mechanisms of distinct pollutants involved in the etiology of various neurological diseases and their management strategy. In addition, this study intends to address current understanding of the relationship between environmental toxins and human health in order to bridge this knowledge gap.

Keywords: Pollutants, Sources, Neurodegenerative Diseases, Human Health, Management Strategy.

ICABB_E_34

Cysteine and Methionine Biosynthetic Pathways in *Pseudomonas aeruginosa*: Unravelling Targets for Innovative Antibiotic Development

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ABSTRACT

The increased multidrug resistance in *Pseudomonas aeruginosa* necessitates innovative approaches for treating associated infections. In general, any microbial system's central metabolic pathways are important for synthesizing biomolecules and as such are promising targets for therapeutic interventions. For that purpose, sulfur-containing two amino acids i.e., cysteine and methionine are essential for microorganisms. Most bacterial cells synthesize cysteine via the de novo pathway (sulfate assimilation pathway) from L-Serine, while methionine biosynthesis follows the transsulfuration pathway starting with L-cysteine. The former pathway of cysteine biosynthesis is predominantly used by prokaryotes and plants; whereas other eukaryotes and humans use reverse transsulfuration pathway (RTS). Interestingly, *Pseudomonas aeruginosa* synthesizes Cysteine via both these pathways. For methionine biosynthesis, in addition to the normal transsulfuration pathway, it also utilizes homocysteine as a direct precursor (Direct sulfhydralation pathway). The presence of multiple pathways for synthesis of sulfur containing amino acids accentuates the importance of sulphur source for the growth and survival of the *P. aeruginosa*. This review contributes the updated knowledge and significance of the enzymes involved in these pathways for identifying novel drug targets in the organism.

Keywords: *Pseudomonas aeruginosa*, Cysteine, Methionine, Multidrug Resistance, Sulfur Metabolism.

ICABB_E_35

A Review on Sustainable Bioplastic Production from *Eichhornia crassipes*

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ABSTRACT

Water hyacinth, known as *Eichhornia crassipes*, is listed as invasive aquatic weed, commonly found grown in water bodies, dams, irrigation channels and drains across South Asia, including India. Due to its fast growth rate, it generally grows over an entire waterway and can double its mass every 5 days. Water hyacinth, originally introduced for its beauty, has become a menacing weed in places like Bengal. Despite its origins in the Amazon basin, it's now a severe issue in India, requiring significant annual government spending for its removal from affected lakes. The large infestations of water hyacinth impact negatively on agriculture and infrastructure. Water hyacinth also has negative impacts on people and the environment in several ways. Petroleum-based plastics, dominating the global solid waste stream, pose significant environmental challenges. In response, eco-friendly bioplastics, synthesized from starch and natural fibres, presents a promising avenue to alleviate the ecological burden caused by conventional plastics.

The abundance of water hyacinth in Indian water bodies, as an unwanted weed, allows for scalability and cost minimization making up for its low starch content, addressing the issue of excess water hyacinth in lakes. To leverage the massive amounts of waste produced from the extraction of water hyacinth from lakes and other water bodies, a strategy was devised to separate and utilize the cellulose to form a bioplastic with comparable tensile strength to that of single use plastic (13.5MPa) and of currently available bioplastics (1.63 - 9.29 MPa). FTIR, SEM and thermogravimetric analysis were performed to measure their physicochemical properties. Inclusion of 4% zinc oxide as a catalyst into the cellulose - starch matrix showed significant increase in the tensile strength affecting its overall durability

Keywords: Water Hyacinth, Petroleum-Based Plastics, Bioplastics, Waste Utilization, Zinc Oxide (ZnO).

ICABB_E_36

Evaluating the Ecological Health of the Ganges River in Uttarakhand and Uttar Pradesh: A Comprehensive Bioassessment Utilizing Benthic Macroinvertebrates as Indicator Species

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ABSTRACT

Environment deterioration is the result of the rapid industrial & growth of the population. Pollution refers to changes in the physical, chemical, or biological character of water, air and soil that have adverse effects on the health of living organisms. Pollution caused by sewage and industrial discharge from the cities, villages and towns is the primary cause of degradation of water bodies. Biological testing (Biomonitoring) of River Ganga at 23 different locations including 03 tributaries is carried out in Post-Monsoon Season (2018-2019). The aim of the study was to investigate the potential use of macro invertebrates as an indicator system of water quality using Biological Water Quality Criteria (BWQC) developed by Central Pollution Control Board, Delhi. The presence and absence of species including quantification in terms of Saprobic Score and Diversity Score indicates the pollution level. Out of 23 studied locations, 03 locations were found to be in Slight pollution range whereas locations were in Moderate Pollution category. The sampling location of 02 tributaries viz., River Pandu in Kanpur (UP29) and River Varuna in Varanasi (UP54) were found to be heavily polluted. Only 01 locations on the mainstream of River Ganga i.e., UK8b (Jagjeetpur STP downstream) was found to be heavily polluted. This may be due to discharge of partially treated sewage from STP outlets. Continuous and long-term monitoring is essential to confirm the ecological health of River Ganga and impact of anthropogenic inputs to take remedial measures.

Keywords: Benthic Macro-invertebrates, Pollution, Biological Testing, Water Quality, Anthropogenic Activities, Environment.

ICABB_E_37

Antibiotics: An Overview of Their Environmental Occurrence, Toxic Exposure, Degradation, and Remediation Methods

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ABSTRACT

Antibiotics are bioactive compounds that are frequently employed in human and veterinary medicine. Many antibiotics have been found in the environment as a result of their widespread production and use, as well as the shortage of proper treatment processes. Antibiotic contamination in the environment has created global concern due to the capability to harm the ecosystem and human health. The most commonly detected compounds in the environment are macrolides, fluoroquinolones, tetracyclines, amoxicillin and sulfonamides. Wastewater had a higher concentration of antibiotic and its residues than surface and groundwater which showed toxic impact to non-target organisms, such as algae and fish. Antibiotics can be removed by the process of adsorption, photodegradation and phytoremediation. Further research into the long-term impact of antibiotics at levels that are environmentally relevant on the ecosystem was urgently required in order to comprehend the risks of antibiotics. In this article comprehensive overview on (1) presence of antibiotics in various environmental compartments (2) Antibiotic toxicity to non-target organisms, such as aquatic and terrestrial organisms (3) Current antibiotic degradation and removal technologies (4) bioaccumulation and translocation of antibiotics in various edible crop tissues in field settings are discussed.

Keywords: Antibiotics, Toxicity, Tetracycline, Photodegradation, Phytoremediation.

ICABB_E_38

Actinomycetes from Sulphur-Rich Reservoirs: Pioneering Healthcare Innovations

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ABSTRACT

This investigation delves into the biopharmaceutical potential of two uncommon *actinomycetes*, *Microbacterium proteolyticum* (GKB-017) and *Kocuria flava* (GKB-021), isolated from a 13th-century sulfur-rich stepwell. Employing molecular techniques, including 16S rRNA gene sequencing and phylogenetic analysis, their genetic distinctiveness and distinctive evolutionary traits are unveiled. Ethyl acetate extracts from these strains manifest notable antimicrobial efficacy against both Gram-positive and Gram-negative bacteria, encompassing clinical isolates, coupled with significant antioxidant potential.

Metabolite profiling via gas chromatography-mass spectrometry (GC-MS) identifies a diverse array of bioactive compounds, primarily comprising fatty acid methyl esters (FAMEs), fatty alcohols, ethers, cyclohexanol, and lactones. Specific compounds, such as 1-undecene, 9-methyl-,fatty alcohols, lactones, fatty esters, and bactericidal diterenoids, demonstrate promising bioactivity against various microbial entities, including bacteria, fungi, cancer cells, viruses, and inflammation. Additionally, methylated fatty acids and tetrahydrocurcumin exhibit associations with antioxidant properties. This study accentuates the biotechnological potential of actinomycetes sourced from sulfur-rich environments, with *Microbacterium proteolyticum* and *Kocuria flava* showcasing versatile bioactivities.

Keywords: *Actinomycetes*, Natural Products, Bioactive Metabolites, Sulphur-rich Water.

ICABB_E_39

AMR's Hidden Allies: Biocides in Personal Care

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ABSTRACT

The rise in antibiotic resistance presents substantial threats to both public health and ecological systems. While the excessive use of antibiotics in healthcare and agriculture is widely acknowledged, there is an increasing awareness of the contributory role of personal care products containing antimicrobials (PCPPs) in exacerbating antimicrobial resistance (AMR). Diverging from prior research, which predominantly approached biocide compounds from a toxicological standpoint, this paper emphasizes their involvement in AMR. The review meticulously examines the impacts and mechanisms of biocides in PCPPs on AMR development in the environment. Additionally, it delves into the potential cross-resistance between commonly used biocides and clinically relevant antimicrobial agents, highlighting broader implications for public health. Most of the existing research focuses on community shifts in water systems, particularly within wastewater treatment plants, with specific attention to Triclosan—the predominant biocide succeeding the 2016 ban on Triclocarban. There is insufficient evidence to undertake a critical assessment of the impact, and further targeted in-field studies are necessary to provide the required evidence. Moreover, stress the importance of informed strategies for reducing the impact of biocides, promoting a balanced approach to infection control in pharmaceutical and personal care industries.

Keywords: Triclosan, Triclocarban, Biocides, Personal Care Products, Antimicrobial Resistance.

ICABB_E_40

Fitness Risk and Resistance Assessment on Exposure to Ethion and Chlorpyrifos in *Drosophila melanogaster* and *Drosophila simulans*

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ABSTRACT

Ethion (ET) and chlorpyrifos (CP) are a widely used organophosphate class of insecticides and known for their neurotoxic properties. Although these insecticides are applied to control the insect pest species of agriculture and medical importance, they also affect the normal life cycle of non-targets along with target species. The major focus of our study is two- fold, i.e. to assess: I) fitness risk and II) resistance development on exposure to lower concentrations of these two organophosphates using Drosophila model. Drosophila is a well-known model in toxicology due to its well-defined system. To this respect, it can be attributed valuable insights into both targets as well as non-target species. In the present study, two Drosophila species i.e., *D. melanogaster* and *D. simulans* flies were initially exposed to different concentrations of ET and CP for a duration of 24, 48 and 72 hrs and LC_{50} was calculated in each case. For experimental purpose, two sub lethal concentrations of ET (1.25ppm, 1.88ppm) and CP (0.3ppm and 0.5ppm) were selected and various biological parameters e.g., fecundity, larva crawling, pupation height and adult climbing were measured after exposing the flies to insecticide-treated and untreated(control) culture media for 10 generations. Both the resistance and detrimental effects of these insecticides were assessed through LC_{50} (F_0 vs F_{10}) and by comparative analysis of control with insecticide-exposed flies of F_1 and F_{10} generations. A significant reduction was noticed in all parameters tested in insecticide-treated F_1 flies in both species, however, the adverse effect was less in F_{10} flies due to the development of resistance, which is evidenced through LC_{50} and life history traits.

Keywords: Organophosphate, Fitness Risk, Resistance, Non-Targets, Drosophila.

ICABB_E_42

Evolution of Infant Gut Microbiota: Role of Diet

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ABSTRACT

In infant, development in the initial days plays a crucial role as our gut microbiota establishes during this time, which may influence the health status of an individual during the life span. Therefore, it is imperative to understand the role of various factors which play pivotal role in determining complex microbial colonization patterns during infant developmental stages. During the life span of an individual, the gut microbiota composition changes substantially during infancy and toddlerhood in terms of both taxonomic composition and diversity.

There are several studies using animal model to investigate the complex interactions between newborn feeding, the microbiota-gut-brain axis, and early developmental consequences.

Early nutrition has a dramatic impact on many areas of growth, immune system maturation, and cognitive function. Optimizing development methods requires an understanding of the complex link between newborn nutrition and physiological outcomes. The investigation of the microbiota-gut-brain axis, a complex interaction between the gastrointestinal tract, its resident microbial communities, and the central nervous system, is one new area of pediatric research. Unique microbial profiles found in piglets feeding human milk highlight how diet shapes the gut microbiota and highlight the significance of microbial communities linked to good health. The examination of microbiota revealed specific microbial profiles linked to every feeding schedule, underscoring the diverse bacterial communities nurtured by human milk.

Studies done on piglet models raised on human milk showed distinct microbial fingerprints, indicating a possible function in forming the gut ecology. Neurochemical differences were shown by gut-brain axis research, suggesting that neurotransmitter levels and neuropeptide expression are influenced by early feeding in both the gastrointestinal system and important brain regions.

The variations in the gastrointestinal tract and important brain areas demonstrates how closely the stomach and central nervous system communicate. The investigation of both microbial and neurodevelopmental components of the study is thorough, which adds to our understanding of the complex structure of the microbiota-gut-brain axis. The nutritional differences in nutrition between human milk and baby formula highlight the difficulties in creating synthetic alternatives that accurately reflect the complex makeup of human milk. Future developments in formula creation will be based on this understanding of the intrinsic complexity of human milk.

Keywords: Gut Microbiota, Infant, Human Milk, Gut-Brain-Axis, Diet.

ICABB_E_43

Bioremediation of Wastewater Contaminated with Mercury: Present and Future Prospective

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ABSTRACT

Heavy metals are toxic pollutants that are released into the environment by many anthropogenic activities. Mercury is one of the examples of heavy metals entering the environment through both natural processes and human activities. Many industries such as pharmaceuticals, paint, disinfectants, and pulp and paper industries are major sources of mercury pollution in water and soil. It is a persistent, bioaccumulative, and toxic pollutant in nature. It can release into the environment and accumulates in water-laid sediments where it converts into toxic methylmercury and enters the food chain. Mercury has a lethal effect on humans. It can easily enter the bloodstream and affect the brain functions. This review specifically focuses on the bioremediation mechanism of mercury using microorganisms to remove mercury contamination from the environment. Certain bacteria such as *Shewanella oneidensis*, *Geobacter sulfurreducens*, *Geobacter metallireducens* can convert toxic mercury compounds through different genes (merA) into less harmful forms. Some strategies to mitigate mercury contamination in the environment include phytoremediation with microbial assistance, biofilm formation, and the application of mercury-reducing bacteria to convert it into a less toxic form.

Keywords: Bioremediation, Heavy Metals, Mercury Contamination, Wastewater, Biofilm.

ICABB_E_44

Metabolites Profiling of Fungal Isolate Using Chromatography and their Bioactivity Assessment

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ABSTRACT

The increasing fascination with both well-known and lesser-explored organic compounds derived from diverse mycobiota has become a focal point of scientific interest. This is attributed to their diverse properties and potential applications across various sectors. The heterogeneity of fungal isolates originating from distinct geo-climatic habitats highlights each organism's uniqueness, presenting an opportunity for exploration in the quest for novel biomolecules. In the ongoing study, the metabolites of *Aspergillus flavus*, obtained from agricultural soil in pine tree areas, were examined. The Gas Chromatography–Mass Spectrometry (GC-MS) investigation of the extract and the metabolites showed different bioactivities as antioxidants, antimicrobials, and anti-cancerous compounds. Moreover, analysis using Liquid Chromatography-Mass Spectrometry (LC-MS) unveiled the presence of organic compounds, polysaccharides, and amino acid derivatives. The in-silico pharmacokinetic evaluation of the extract, conducted through Swiss ADME analysis, indicated the bioavailability of promising bioactive constituents. The growth kinetic studies spanning six days consistently demonstrated a substantial production of flavonoids and antioxidant activity in the extract. Designing an effective downstream processing method for obtaining mycotoxin-free bioactive compound consortia from the isolate is feasible. The uniqueness of this study lies in its exploration of bioactive compounds from the isolated *Aspergillus flavus*, a feature not documented in the majority of previously reported *Aspergillus flavus* isolates. Nonetheless, validation of the bioactive compound consortia using alternative techniques is imperative.

Keywords Bioactive Molecule, Gas Chromatography-Mass Spectrometry, Liquid Chromatography-Mass Spectrometry.

ICABB_E_45

Artificial Intelligence and Sustainable Waste Management

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ABSTRACT

Solid waste management is an essential part of sustainable development and involves the set of practices and strategies used to reduce the negative environmental impacts of waste disposal. It includes reducing the amount of waste generated, reusing and recycling materials, and composting organic waste. Sustainable waste management practices can help businesses and communities to create economic and social benefits. The ever-increasing volumes of different categories of solid wastes generated worldwide is inducing various environmental and public health hazards, calling for new strategies to improve the waste ecosystem, such as the use of artificial intelligence. Artificial Intelligence can be milestone to monitor, segregate, recycle. Studies have shown that artificial intelligence has been integrated with waste management in waste-to-energy, smart bins, waste-sorting robots, waste generation models, waste monitoring and tracking, plastic pyrolysis, distinguishing fossil and modern materials, logistics, disposal, illegal dumping, resource recovery, smart cities, process efficiency, cost savings, and improving public health. Incorporating AI with waste stream results in reduced cost of waste logistics, cost and time savings by up to approximately 13- 28%. AI-based technologies allow easy identification and sorting of waste for effective waste management with up to 99.95 % accuracy. Combining AI with chemical analysis (proximate and ultimate analysis) yields improved rate of waste pyrolysis, fixed carbon determination and improved energy conversion during waste-to-energy processes.

Keywords: Artificial Intelligence, Waste Management, Pyrolysis, Chemical Analysis, Waste to Energy.

SESSION - FOUR

Omics-Based Technologies

ICABB_O_1

Transcriptome Response of T6ss Bacterium *Enterobacter* Sp. S-33 Unveils the Role of T6ss Effectors in Stress Protection

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ABSTRACT

Acidic environments naturally occur worldwide and uncontrolled use of agricultural practices may also cause acidification of soils. The development of acidic conditions disturbs the establishment of efficient microbial populations in their natural niches. Moreover, the survival of Enterobacter species under acidic stress remains poorly understood. This study aimed to investigate the survival of an environmental isolate *Enterobacter* sp. S-33 under acidic stress and to identify the various genes involved in stress protection at the global gene transcription level. The obtained results provide new targets that will allow understanding the in-depth mechanisms involved in the adaptation of bacteria to environmental pH changes. We used next-generation sequencing (NGS) method to analyze the expression (up-regulation & down-regulation) of genes under varying pH conditions. A total of 4214 genes were differentially expressed under acidic conditions (pH 5.0), with 294 up-regulated and 167 down-regulated. At pH 6.0, 50 genes were significantly expressed, of which 34 and 16 were identified as up-regulated and down-regulated, respectively. Many of the up-regulated genes were involved in carbohydrate metabolism, amino acid transport & metabolism, and the most down-regulated genes were related to post-translational modification, lipid transport & metabolism, etc. The observed transcriptomic regulation of genes and pathways identified that Enterobacter reduced its post-translational modification, lipid transport & metabolism, and increased carbohydrate metabolism, amino acid metabolism & transport, energy production & conversion, to adapt and grow in acidic stress. The present work provides in-depth information on the characterization of genes associated with tolerance or adaptation to acidic stress of Enterobacter bacterium.

Keywords: Umami, *Enterobacter*, Post-Translational Modification, Next-Generation Sequencing (NGS).

ICABB_O_2

Artificial Intelligence and Machine Learning Approaches for Predicting the Multi-Drug Resistance Mutations in *Mycobacterium Tuberculosis*: Analysis of Genes, Proteins, and Drug Interactions

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ABSTRACT

Tuberculosis, the most prominent cause of death from recoverable and contagious diseases among young adults, resulting from the transmission of *Mycobacterium tuberculosis* has been increasing for many years. To combat multi-drug resistant mutations, it has become a necessity to supplement drug discovery with machine learning (ML) based prediction models for forecasting the likelihood of further modifications. High throughput sequencing approaches aid in the detection of *Mycobacterium tuberculosis* DNA in samples, providing insights into multi drug resistance (MDR-TB) mutations and drug susceptibility. Studies have demonstrated the usage of artificial intelligence (AI) and machine learning (ML) approaches in predicting the resistance in the genes such as rpoB, inhA, katG, pncA, gyrA and gyrB against several drugs such as isoniazid, rifampicin, fluoroquinolones, and pyrazinamide. Respective gene sequences and structural features of encoded proteins have been used to depict the single nucleotide variations, demonstrating the effect of these mutations on the specific proteins encoded by each gene. Prevalent ML algorithms that are used to design any model's base for operations and compute the feature engineering necessary for a predictive label are: naïve bayes, k-nearest neighbour, support vector machine, and artificial neural networks (ANNs). The algorithms generate models capable of classifying with an accuracy up-to 85% when trained and tested against a previously unknown dataset. Moreover, the studies involved the comparison of conformational changes in mutant proteins with wild type proteins by using molecular docking and dynamics simulations to understand the mechanism of predicted drug resistance.

Keywords: Tuberculosis, Multi-Drug Resistance Mutations, Genes, Proteins, Machine Learning Algorithms, Artificial Intelligence, Dataset, Molecular Docking, Molecular Dynamics Simulations, Anti-TB Drug Complexes (NGS).

ICABB_O_3

In-depth Genome Analysis and Characterization of a Halotolerant Probiotic Bacterium *Paenibacillus* sp. S-12

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ABSTRACT

Members of the *Paenibacillus* genus have been reported from a wide variety of environments and attracted great attention due to their multifarious properties. Considering their limited genome information, we have characterized the genome of a halotolerant environmental bacterium *Paenibacillus* sp. S-12. Molecular identification by 16S rRNA gene sequencing showed its closest match to other *Paenibacillus* species. The complete genome size of S-12 was 5.69 Mb, with a GC content 46.5%. The genome analysis unraveled the presence of an open reading frame (ORF) encoding the functions related to environmental stress tolerance, adhesion processes, multidrug efflux systems, and heavy metal resistance. Additionally, it showed the presence of CAZymes, probiotics, and stress-protected genes that equipped the strain for industrial and agricultural purposes. The antiSMASH analysis identified genes for antimicrobial peptides (AMPs), secondary metabolite production, NRPSs, and PK synthesis. Various NRPs regions related to Paenibacterin, guadinomine, polymyxin B, chejuenolide A / chejuenolide B, fusaricidin, pelgipeptin, and octapeptin-C4 were identified. The pangenome analysis indicates the S-12 strain harbors many unique genes that are not shared by other strains and thereby gene pool size would further increase the number of genomes incorporated in the analysis. Many genes related to probiotic features were identified in the S-12 genome. Overall, the study suggests that S-12 strain can be used for biotechnological applications after monitoring its safety assessment using a suitable animal/or host system.

Keywords: Characterization, Halotolerant Bacterium, Probiotics, Genome Analysis.

ICABB_O_4

Gut Microbiota Allies Against Cancer: A Closer Look at Pharmacomicrobiomics

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ABSTRACT

Extensive exploration delves into the intricate interplay between gut microbiota and commonly used drugs in oncological diseases, underlining the substantial impact of gut microbiota on the effectiveness and safety of traditional anticancer agents. It also explores a range of strategies for modulating the gut microbiota, encompassing prebiotics, probiotics, antibiotics, and fecal microbiota transplantation (FMT), all aimed at improving clinical outcomes for cancer patients. Prebiotics, with their capacity to promote beneficial bacterial growth, diminish pathogenic microorganisms, and exert anti-inflammatory and immunomodulatory effects, have been examined for their therapeutic potential. On the other hand, probiotics, live microorganisms that confer health benefits, have emerged as non-invasive adjuncts in cancer therapy. The exploration briefly touches on bacterial-based anticancer technologies that leverage tumor-associated bacteria for tumor targeting and drug biotransformation. Crucially, the stress of the importance of employing multi-omics approaches and integrating machine and deep learning techniques to unveil the intricate interactions between gut microbiota, drugs, and the host. These insights have held promise for the development of personalized precision therapies that could revolutionize cancer treatment.

Keywords: Gut Microbiota, Oncological Drugs, Prebiotics, Probiotics, Antibiotics, FMT, Anticancer Technologies, Multi-Omics, Precision Therapies.

ICABB_O_5

Unraveling Possible Alternative Methods for Determining Acute Systemic Toxicity

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ABSTRACT

Acute systemic toxicity refers to the adverse effects of a chemical on an organism after being exposed for a definite time. The traditional orthodox method for figuring out acute systemic toxicity was the LD50 (lethal dose up to 50% survival rate) test using animals is now being replaced by various other in vitro and in silico techniques. The 3R's concept encourages the replacement and reduction of direct testing on animals and instead the application and refinement of various alternatives to conservative techniques. Animal cell culture, embryo-larval fish models (Zebrafish), human 3D organ-on-chip modeling techniques and in silico techniques (ex-QSAR) which utilize computer models, are being utilized to predict toxicity levels these days. With assistance from regulatory norms like The National Toxicology Program Interagency Center for the Evaluation of Alternative Toxicological Methods (NICEATM), The Association for Assessment and Accreditation of Laboratory Animal Care (AAALAC), and other potential sites like The National Library of Medicine provides strategies and roadmaps to the awareness about the alternative methods to assess toxicity testing. The present review describes the need to understand acute systemic toxicity and possible methods of checking toxicity levels with high accuracy reducing the direct testing on animals.

Keywords: Umami Systemic Toxicity, In Vitro, Data, LD_{50}, In Silico, Embryo-larval fish models, Organ on Chip Models, NICEATM, AAALAC, 3R's Concept.

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ICABB_O_6

Pharmacomicrobiomics and Drug–Infection Interactions

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ABSTRACT

The abstract explores the intricate relationships between microorganisms and humans. Focusing on the burgeoning field of pharmacomicrobiomics, it investigates how variations in the microbiome significantly influence drug disposition, efficacy, and potential toxicity. Additionally, the emerging sciences of toxicomicrobiomics and pharmacoecology complement this exploration by studying the reciprocal impacts of the microbiome on drug metabolism and toxicity. The abstract introduces the innovative concept of "drug-infection interaction," shedding light on the influence of pathogenic microorganisms on drug responses.

It not only emphasizes the importance of these interactions but also identifies promising areas for future research. The term "drug-infection interaction" is proposed to extend the scope of pharmacomicrobiomics, offering a nuanced perspective on the complex interplay between drugs and pathogenic infections. In summary, the abstract serves as a roadmap for exploring the dynamic connections between microorganisms and drug responses, urging further investigation into this evolving field for a more comprehensive understanding of pharmacological outcomes in the presence of diverse microbial influences.

Keywords: Pharmacomicrobiomics, Toxicomicrobiomics, Pharmacoecology, Drug–Infection Interaction, Microbiome.

ICABB_O_7

Macronutrient Management Strategies in Type 2 Diabetes: A Focus on Insulin Resistance and Glucose Homeostasis

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ABSTRACT

Type 2 diabetes mellitus (T2DM) is caused by systemic insulin resistance leading to state of overnutrition and nutrient-induced GLP-1 secretion, impairing insulin sensitivity. Impaired insulin sensitivity, causes alleviated blood glucose levels and affects functioning of organs. Insulin and glucagon are pivotal hormones in glucose homeostasis, within Forkhead box O1 (FoxO1)[1] protein plays a role of mediator by connecting glucagon and insulin signalling by regulating several genes. Short-term protein feeding improves glucose homeostasis, which may be attributed to the increased release of gut hormones, including GLP-1 and GIP. FoxO1-induced transcriptional changes leads to insulin resistance. Insulin resistance through increasing hepatic lipogenesis and impairing gut immunity, thereby attenuating insulin sensitivity by inducing pro-inflammatory activity and activating signalling pathway. Understanding the molecular mechanisms of diet-gene interactions will help us apply precision-nutrition to clinical practice by integrating multi-omics approaches.

Keywords: T2DM, GLP-1, Insulin, FoxO1, Glucose Homeostasis, Insulin Signalling.

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[1] *Forkhead box protein O1 (FOXO1), also known as forkhead in rhabdomyosarcoma (FKHR), is a protein that in humans is encoded by the FOXO1 gene. FOXO1 is a transcription factor that plays important roles in regulation of gluconeogenesis and glycogenolysis by insulin signalling, and is also central to the decision for a preadipocyte to commit to adipogenesis. It is primarily regulated through phosphorylation on multiple residues; its transcriptional activity is dependent on its phosphorylation state.*

ICABB_O_8

Combining Virtual Screening, Molecular Docking Analysis: Assessing Natural Compounds Interaction with the NMDA Receptor

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ABSTRACT

Alzheimer’s disease is a progressive neurodegenerative disorder and associated with aging, characterized by cognitive deficit. It has been reviewed that with Alzheimer’s disease, over 50 million individuals globally are impacted, and it will be a leading threat to global health with a potential increase to 150 million by the year 2050. The N-methyl-D-aspartate receptor (NMDAR) has gained approval for the treatment of Alzheimer’s disease and can be considered as a viable therapeutic approach through the effectual way of inhibitory ligands. Several pharmaceutical drugs such as tacrine, donepezil, rivastigmine, galantamine, memantine, and others, work on a comparable principle of inhibiting the NMDA receptor. In the literature survey, several natural compounds demonstrated anti-Alzheimer’s effect with fewer side effects. In the present study natural compounds and phytochemicals were virtually screened followed by molecular docking and molecular visualization. Docking was conducted between the selected natural compounds and as well as with a standard drug memantine. Among the selected compounds, a few of them exhibited binding energy equivalent to standard drug memantine. Withaferin A showed the best binding energy of -11.7 kcal/mol against the NMDA receptor. The outcomes predicted that these compounds were potentially neuroprotective and results further need to be validated.

Keywords: Alzheimer’s, N-methyl-D-Aspartate Receptor, Virtual Screening, Docking, Binding Energy, Natural Compounds.

ICABB_O_9

Biological Networks and its Significance

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ABSTRACT

Biological networks have profound relevance in systems biology and can be used as a tool for identification of Patho-physiological pathways. Networks, of any kind, are strongly grounded in mathematical principles and are constructed using the 'graph theory'. The diverse nature of biological networks in forms of DNA-Protein and Protein-Protein interactions at the molecular levels. We reviewed the topological parameters and how they are mathematically defined by arithmetic formulas that provide us an outlook of the nature of the network. The network topological parameter (degree distribution, centralities, path length etc.) provides us information about the kind of interaction that a biological entity (protein, gene, etc.) is having with other biological entities and lead us to identify the potential targets/genes. The study of biological networks is vital for emerging biological fields and can be applied to solve real life problems such as diagnosis of rare diseases, metabolic malfunctions and therapeutics.

Keywords: Biological Network, Systems Biology, Therapeutics, Graph Theory.

ICABB_O_10

Exploring Mutational Dynamics and Ligand Binding on a Peptide GPCR, Melanocortin-1-Receptor (MC1R)

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ABSTRACT

MC1R, a peptide-GPCR, is one of the key regulators of human skin pigmentation. It is known to be highly polymorphic with several variants associated with melanoma and non-melanoma skin cancers. Due to the absence of crystal structure, the underlying structural changes responsible for protein functional selectivity and the precise role of protein dynamics in skin-cancer mutations are not known. Here, we studied structure and dynamics of wild-type MC1R and 15 disease-associated mutations using all-atom molecular dynamics simulations (130 μs). Analysis of the ligand-bound MC1R trajectories revealed unique contacts for inverse-agonist (ASIP) and antagonist (βD3), suggesting a differential mode of regulation. We observed agonist (α-MSH) induced specific conformational changes in MC1R, leading to activation and opening of the intracellular region. Further, the dynamic profiling of 15 mutations showed a complete alteration of global and local networks of contacts. Our results reveal atomistic insights into MC1R-ligand activation and structural principles governing protein dynamics in skin cancer mutations that may guide de novo design of future skin-cancer therapeutics.

Keywords: MC1R, Molecular Dynamics Simulation, Mutations, Ligand Binding.

ICABB_O_11

Genomic Pioneering in Pulmonary Disorders: Single-Molecule Profiling and Nanopore Sequencing for Diagnosing Lung Cancer

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ABSTRACT

Recent breakthroughs in genetic research have revolutionized the way we understand and diagnose lung-related problems including lung cancer. Which gives us various powerful tools who look deep into our DNA, helping us uncover crucial information about our health. One such genetic tool discussed here involves analyzing cell-free DNA (cfDNA) methylation using single-molecule sequencing. This method not only provides more accurate results but is also scalable and robust, making it a game-changer in monitoring cancer treatment progress. The integration of single molecule analysis with smart computer techniques enhances our ability to detect lung issues early on. By studying the entire genetic makeup of diverse groups of people, we've learned that different lung tumors have unique genetic fingerprints. For instance, tumors in individuals exposed to smoking exhibit an average of 52,209 mutations per genome. This sensitive approach, detectable even in tiny amounts of tumor DNA, positions single-molecule sequencing as a crucial tool in liquid biopsy diagnostics, especially for respiratory problems. It showcases how single-molecule genome-wide mutation profiling is reshaping our understanding of lung health. It not only helps in early detection and personalized treatment but also provides us with a deeper knowledge of the genetic factors influencing lung-related diseases. This review explores how single-molecule genome-wide mutation profiling and nanopore sequencing have transformed the landscape of lung health diagnostics.

Keywords: Single-Molecule Sequencing, Liquid Biopsy, cfDNA Methylation, Nanopore Sequencing.

ICABB_O_12

Aptamers As Potent Tool for Designing Highly Sensitive Biosensors

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ABSTRACT

Aptamers, the single-stranded DNA or RNA molecules, have emerged as potential cornerstones in biosensor technology owing to their specific binding properties. An In-vitro specialized technique called Systematic Evolution of Ligands by EXponential enrichment (SELEX) selection technique has been used widely to generate aptamers, that bind to target molecules precisely. This review encapsulates the science behind aptamers, from their synthesis via the SELEX process to their diverse applications. Particularly, their role in cancer diagnosis and the strategies employed for various disease detections are deliberated. With the advancements in the aptamer databases, their computational design, and the ongoing research, aptamers promise a revolution in sensitive biosensor design. Newer In- silico search algorithms have made it possible to predict the extremely stable aptamer/target molecule complex. Such tools enable the prediction of the reliable and functional molecular structure of aptamers for accurate biosensing. Therefore, it is rightly believed that optimizing high affinity aptamers by using a combination of In-vitro and In-silico techniques is essential for enhancing the aptamer-substrate binding affinities.

Keywords: Aptamers, SELEX, Biosensors, Aptamers, Binding Affinity, In-silico Aptamer Designing.

ICABB_O_14

Microbiome Modulation and Machine Learning in Preventing Chronic Obstructive Pulmonary Readmission

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ABSTRACT

Chronic Obstructive Pulmonary Disease (COPD) is among the leading causes of morbidity and mortality in the world, affecting millions worldwide. COPD is a progressive pulmonary disease including symptoms like coughing, wheezing, shortness of breath and chest tightness. COPD is a multifactorial respiratory condition influenced by various risk factors. These risk factors include tobacco smoking, environmental air pollution, occupational exposures, occupational exposures, genetic factors, and other comorbidities. This review focuses on two aspects for COPD, diagnosis, and therapeutics based on Microbial dysbiosis and Machine learning tools. Primarily this study explores the pivotal role of Artificial intelligence (AI) and machine learning (ML) tools in early diagnosis of the disease by extracting meaningful information from COPD data, generated by various diagnostic techniques such as CT scans and several indices of pulmonary function.

In recent years, there has been growing interest in understanding the intricate relationship between microbial Dysbiosis and COPD. Studies have suggested that alterations in the composition and function of the respiratory and gut microbiota, known as microbial dysbiosis, may play a crucial role in the pathogenesis and readmission of COPD. The biomarkers associated with this microbiome are being used for diagnosis of the disease. The focus of this study is to highlight the latest research related to microbial dysbiosis in COPD and explore the possibility of applying AI tools for novel diagnostics and therapeutic strategies.

Keywords: COPD, Readmission, Microbial Dysbiosis, Artificial Intelligence, Machine Learning.

ICABB_O_16

Unveiling Nature's Potential: In-Silico Exploration and Identification of Herbal Remedies for Major Depressive Disorder through Molecular Interaction Studies

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ABSTRACT

Major depressive disorder, a globally discussed mental health condition, has drawn significant attention due to its unique and intricate nature. It is marked by enduring presence of negative emotions, stemming from a lack of interest, diminished self-esteem, and excessive rumination. Despite the widespread availability of various antidepressant medications, their effectiveness is hindered by low response rates, prolonged treatment durations, and the prevalence of side effects such as headaches, dizziness, insomnia, and oversleeping. This underscores the pressing demand for alternative therapeutic approaches. In this study, a network biology approach was employed to identify candidate genes associated with Major Depressive Disorder (MDD). Among the identified genes, Brain-derived neurotrophic factor (BDNF) emerged as a potential target for further investigation. BDNF was subjected to molecular docking studies, utilizing various drugs commonly prescribed for MDD treatment. Notably, the drug Paroxetine demonstrated a superior docking score of -9.3 kcal/mol.

Expanding our exploration to plant-derived natural compounds (phytochemicals), we investigated substances from Brahmi (*Bacopa monnieri*), Shatavari (*Asparagus racemosus*), Ash Gourd (*Benincasa hispida*), and Marijuana (*Cannabis*). Phytochemicals such as quercitin, kaempferol (from Shatavari), and Dronabinol (from Marijuana) exhibited compelling docking scores of -10.6 kcal/mol, 9.9 kcal/mol, and 9.6 kcal/mol, respectively. These findings underscore the potential of phytochemicals as alternative therapeutic agents for MDD, providing valuable insights for future research and development in the field of mental health.

Keywords: Drugs, Natural Compound, Molecular Docking, Major Depressive Disorder, Marijuana.

ICABB_O_17

Prioritizing Hub Genes in Duchenne Muscular Dystrophy: A Protein-Protein Interaction Study

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ABSTRACT

Duchenne Muscular Dystrophy (DMD) is a rare, X chromosome linked, lethal and progressive disorder affects 1 in 3500 in young children especially boys. Generally, it caused by mutation in X chromosome leads to reducing and depletion of structure and function of dystrophin protein. Dystrophin protein is generally responsible for providing structure, stability and functions to the skeleton muscles. Improper functioning in muscle tissue of respiratory and cardiac system leads to premature death of the patient. To explore the targets, and key genes in DMD, we used the system biology approach by using 491 genes to construct Protein-Protein Interaction Network (PPIN) using the STRING database. This study focus on finding the hubs based on the protein - protein interaction of DMD genes and identification of modules with similar functions. DMD-PPIN follows a hierarchical scale-free nature of the network. We have identified top degree nodes such as ACTB, TNF, FN1, IL6, VEGFA, IL1B, MYC, CASP3, MMP9, CD4. Functional analysis revealed various molecular function like signaling receptor binding, extracellular matrix structural constituent, cytokine activity, molecular function activator activity while biological processes like cell surface receptor signaling pathway, locomotion, cell migration and these are located in extracellular region, collagen-containing extracellular matrix, extracellular space in the cell. Disease association study revealed that these are associated in disorders like Proteoglycans in cancer, IL-17 signaling pathway, Chagas disease, pathway in cancer. Further investigation of these key genes can provide understanding of role in pathophysiology of DMD and can identify potential targets for precise therapeutic interventions.

Keywords: Dystrophin, Protein-Protein Interaction Network, Key Genes, Hubs, Therapeutic Target.

ICABB_O_20

Recombinant production of SARS CoV-2 RdRp-NSP7-NSP8 Complex and insilico Discovery of FDA Approved and Natural Origin Inhibitors

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ABSTRACT

The global pandemic caused by Severe Acute Respiratory Syndrome Coronavirus-2 (SARS-CoV-2) and known as COVID-19, has infected more than 20 million people and has caused 8 million deaths across 188 countries as of August 2022 (GISAID database). This calls for novel and effective therapeutic strategies against COVID-19. Researchers are primarily targeting key viral proteins, including spike proteins, main proteases, RNA dependent RNA polymerase (RdRp), helicases, and endoribonucleases. SARS-CoV-2 RdRp (Nsp12) associates with Nsp7 and Nsp8 cofactors for efficient polymerase activity and structure as well as dynamic assembly of RdRp with accessories proteins have been reported. The current work reports purification of the complex (yield of ~1mg/ml) and identification of FDA approved and natural product-based inhibitors. Although various antiviral drugs are available against RdRp, none of them are known to inhibit the protein-protein interactions involved in the complex. Knocking down the RdRp complex is crucial for halting viral replication and transcription and subsequently the viral assembly. In this direction, ~1400 FDA approved, ~12000 natural compounds from IMPPAT database were docked against the SARS-CoV-2 RdRp complex via AutoDock Vina. On the basis of binding affinity, followed by Molecular Dynamics Simulations of top scoring IMPPAT and FDA approved compound promising compounds will be tested for inhibitory activity. By integrating these processes, this research aims to contribute to the development of specific antiviral against SARS-CoV disease.

Keywords: RdRp-Nsp7-Nsp8, Protein-Protein Interaction, Docking, MD Simulation, Protein Purification.

ICABB_O_22

Molecular Docking of Bioactive Compounds Derived from Strain TD-062 of *Aureobasidum* sp. with p53 Protein in the Apoptosis Pathway of MCF-7 Breast Cancer and A375D Myeloma Cancer Cell Lines

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ABSTRACT

Aureobasidium sp. is emerging as a highly sought-after medicinal fungus due to its rich repertoire of bioactive compounds with potential therapeutic applications. Notably, certain bioactive compounds derived from *Aureobasidium* sp. Strain TD-062 exhibit promising anti-cancer properties against MCF-7 breast cancer and A375D myeloma cancer cell lines. This research investigates the interaction dynamics between these selected bioactive compounds and the apoptosis-regulating protein p53, aiming to discern their potential in inducing apoptosis post-mutation in p53. To assess the safety and drug-likeness of the chosen bioactive compound from *Aureobasidium* sp., adherence to Lipinski's Rule of Five is evaluated. Molecular docking analyses are conducted to determine the binding affinity between the bioactive compounds and the targeted apoptosis protein p53, identifying the most potent inhibitor against the selected target. The study reveals compelling docking interactions between the bioactive compounds and the targeted apoptosis protein p53. Among the compounds investigated, squalene emerges as the most potent bioactive compound, exhibiting significant affinity, while Delta-Tocophenol demonstrates a comparatively lower binding affinity towards the targeted p53 protein within the apoptosis pathway. These findings offer valuable insights for the isolation of bioactive compounds from *Aureobasidium* sp. Strain TD-062, enabling structural analysis and paving the way for in-vivo experiments on cancer cell lines. In conclusion, this research contributes to a deeper understanding of the medicinal potential of *Aureobasidium* sp. Strain TD-062-derived bioactive compounds, specifically their interaction with the apoptosis-regulating protein p53. The identified compounds, particularly squalene, hold promise for further exploration in drug development and cancer treatment strategies, opening avenues for future investigations and applications in the field of oncology.

Keywords: *Aureobasidium* sp., Protein p53, Squalene, Delta-Tocophenol, MCF-7 Breast Cancer, A375D Myeloma Cancer.

ICABB_O_23

Unravelling the Transcriptome Response of *Enterobacter* sp. S-33 Under Varying Temperature

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ABSTRACT

Enterobacter genus includes the bacteria occupying every aspect of environment, however, their adaptability at varying temperature is not clear. In the present study, we analyzed the transcriptome response of *Enterobacter* sp. S-33 and their functional genes under various temperatures (30 ℃ to 45 ℃) that were expressed and accumulated in cells under temperature stress. During a temperature shift from 37 ℃ to 45 ℃, 165 genes showed differential expression including 112 up-regulated and 53 down-regulated. In particular, heat-shock genes such as CspA, 16 kDa heat shock protein A/B and transcriptional regulators such as LysR, TetR, and LuxR were differentially expressed, indicating the role of complex molecular mechanism of Enterobacter adapting to temperature stress. Similarly, genes associated to signal transduction, ABC transporters, iron homeostasis, and quorum sensing were also induced. The Gene ontology enrichment analysis of differentially expressed genes (DEGs) were categorized into "transmembrane transport", "tRNA binding", "hydrogen sulfide biosynthetic process" and "sulfate assimilation" terms. In addition, Kyoto Encyclopedia of Genes and Genomes pathways showed that ABC transporter as well as quorum sensing pathways were significantly enriched. Overall, current study has contributed to explore the adaptive molecular mechanisms of *Enterobacter* spp. upon temperature change, which further opens new avenues for future in-depth functional studies.

Keywords: *Enterobacter*, RNASeq, Signalling, Temperature, Transcriptome.

ICABB_O_24

Decoding the Genomic Tapestry: Unraveling Lichen *Pyxine subcinerea*'s Metagenome and Microbial Interactions for Insights into Lichen Metabolism

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ABSTRACT

The study delves into the intricate web of interactions within the lichen *Pyxine subcinerea* by comprehensively sequencing its entire metagenome. Recognizing the pivotal role of lichen microbe interactions in the synthesis of lichen metabolites, the investigation employed 16S rRNA sequencing and ITS sequencing to unravel the genomic makeup of both fungal and algal components. Through a systematic application of bioinformatics tools such as BLAST, KEGG, and COG, the obtained sequences underwent meticulous analysis. The metagenomic exploration revealed a diverse composition, highlighting the prevalence of cyanobacteria (4.22%), fungi (33.7%), and algae (1.4%). Notably, a significant portion of the encoded genes pertained to cellular signaling and processing, elucidating the sophisticated molecular machinery orchestrating the dynamic relationships within the lichen symbiosis. This comprehensive genomic insight into lichen *Pyxine subcinerea* sheds light on the genetic foundations governing the cooperative interactions between different microbial components, ultimately contributing to the understanding of lichen metabolism. The study paves the way for further exploration of the intricate biochemical pathways and ecological significance embedded in lichen-microbe collaborations.

Keywords: Metagenome Sequencing, Lichen Microbe Interactions, 16S rRNA Sequencing, Lichen Metabolism, Ecological Significance.

ICABB_O_25

An Insilco Toxicity Study of the Phytocompounds Found in *Pongamia innata* Leaves Using the ProTox-II Web Server

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ABSTRACT

The current study aimed to determine the *Insilco* toxicity of the phytocompound present in the leaves of *Pongamia pinnata*. The leaves of *Pongamia pinnata* have long been used in traditional medicine for their therapeutic properties. Nowadays, herbal toxicity is a common problem caused by incorrect dosage. The FDA reviews the safety and effectiveness of herbal products only in response to complaints from patients or healthcare providers—issues with them, such as side effects, interactions, and allergies. ProTox-II is a web server that uses computational methods to predict the toxicity of small molecules. It is a virtual laboratory that uses factors such as most common features, molecular similarity, and fragment propensities to predict a variety of toxicity endpoints, including immunotoxicity, carcinogenicity, mutagenicity, acute toxicity, hepatotoxicity, cytotoxicity, adverse signalling pathways (Tox21), and toxicity targets. The server receives a two-dimensional chemical structure as input and returns likely toxicity profiles for the compound. Based on the bioactive compounds we wish to study further; we selected bioactive compounds from *Pongamia pinnata* leaves from several published studies. The bioactive compounds rutin, methyl hexadecenoate, isoquercitrin, pongagallon B, pongagallon A, bis(2-methylheptyl) phthalate, vitexin, vecinin-2, 2H-1-benzopyran-6-ol, 3,4-dihydro-2, 8-dimethyl -2-[4,8,12-trimethyltridecyl], 12ahydroxy-alpha-toxicarol were selected for the insilico toxicity study. According to our findings, among the ten bioactive hexadecanoic acid methyl esters, 2H-1-benzopyran-6-ol,3,4-dihydro-2,8-dimethyl-2-[4,8,12-trimethyltridecyl] all toxicity classes are inactive. Based on the oral LD_{50} dose value prediction of ten phytocompounds, only 12 α-hydroxy-toxiccarol are toxic. However, other researchers found numerous positive effects in vitro.

Keywords: Insilco Toxicity, ProTox-II Webserver, *Pongamia innata* Bioactive Compound, Herbal Medicine.

ICABB_O_26

Microbial Diversity and Its Attributes of Gandhak-ki-baoli Water: A Metagenomic Analysis

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ABSTRACT

Throughout the centuries, numerous wells were constructed in northwestern India, yet the majority now lie abandoned, their functionality compromised. Despite this, a significant stepwell in Delhi, known as Gandhak-ki-baoli, stands as an exception, retaining its water and boasting a notable sulfur content believed to harbor medicinal properties. In this regard, the present study focused on the metagenomic analysis of sulphur enriched water. The analysis yielded a total of 17,488 Operational Taxonomic Unit (OTU) sequences, with *Sulfuricurvum kujiense* and other sulfur-reducing bacteria as predominant strains that impart to the water's medicinal attributes. Additionally, *Pseudomonas*, *Methylotenera*, *Flavobacterium*, *Dechloromonas*, and *Arcobacter* emerging as the most abundant genera, constituting 30%, 16.73%, 9.12%, 7.59%, and 6.01%, respectively. The taxonomic scrutiny further revealed that these bacterial species play pivotal roles in pollutant degradation (phenols, biphenyl, heavy metals, hydrocarbons, aromatic compounds), function as soil inoculants in agriculture and horticulture, serve as probiotic sources, and contribute to the production of industrially relevant compounds, such as butyrate. Thus, this investigation underscores the diverse applications of water enriched with sulfur.

Keywords: Sulphur Water, Gandhak-ki-baoli, Metagenomics, *Sulfuricurvum Kujiense*.

ICABB_O_27

Molecular Docking and Molecular Dynamic Simulation Based Virtual Screening of Natural Bioactive Phytocompounds for Interaction with Modulators of Urolithiasis

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ABSTRACT

Urolithiasis is a common pathological condition in which renal stones are formed in the urinary system. Most common type of urolithiasis involves the formation of calcium oxalate (CaOx) or phosphate (CaP) stones (80%). Formation of stones includes multiple steps starting with crystal nucleation, growth, aggregation and eventually adhesion and retention to renal epithelial cells. Terpinyl acetate, beta caryophyllene, gamma sitosterol and eucalyptol are the phytocompounds which are found in many of the plants like *Herniaria hersuta, Tribulus terrestris, Ocimum sanctum, Boerhaavia diffusa, Bryophyllum pinnatum, Macrotyloma uniflorum* herbal extracts. As per the clinical and experimental investigations, phytocompounds present in these extracts are capable of regulating the urinary concentration of promoters and inhibitors thus inhibit crystallization process.

In the present study we aim to investigate the role of these phytocompounds in modulating selected modulators of urolithiasis such as calgranulin, CD-44, Fibronectin and human serum albumin through *in silico* study. Gold docking scores revealed that albumin exhibited highest fitness level with all the selected ligands with gold fitness score ranging from 34.13 to 46.17 and binding free energies ranging from -7.51 to -9.09 Kcal/Mol. Among other modulators, calgranulin also exhibited good fitness score with gamma sitosterol with the gold docking score of 45.69 and predicted binding affinity of -8.78 Kcal/Mol. X-scores also confirmed good interactions of albumin and calgranulin with all the selected ligands. On the basis of drug likeliness test and conventional use of these compounds, they can also be considered for prophylactic measures against recurrence of the disease.

Keywords: Urolithiasis, Modulators, In Silico, Docking, Phytocompounds.

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EDITORS' PROFILE

Prof. Pammi Gauba, joined as Dean A and R on 1st feb 2023.She is also Dean International affairs and sponsored projects and Head Department of Biotechnology. She has a vast experience of 35 years in teaching and research at different institutes in India and abroad. Her current research work focuses on Inorganic and organic pollutants and their remediation. She has published more than 60 research articles in reputed international journals and several book chapters .edited 4 books and 3 patents filed. She is supervising close to 10 PhD scholars in JIIT. She holds several sponsored R&D research projects from ICMR, MOEF, DRDO and AYUSH.

Prof. Indira P. Sarethy has been in teaching and research for more than twenty years, working at Lady Doak College, Madurai, The Energy and Resources Institute (TERI), New Delhi and Amity Institute of Biotechnology, Noida before taking up the present assignment at Jaypee Institute of Information Technology, Noida. Her research interest is in bioresources, specifically natural products (for therapeutic and industrial applications) from microbial and plant biodiversity. Based on a culture-dependent approach, microorganisms from niche habitats (desert, forest, limestone rock, monuments, endophytic, fermented food and water bodies) are identified and characterized for bioactive compounds. Metagenomics-based approaches focus on eliciting production of natural products from environmental DNA. The group leverages capabilities to taxonomically characterize and study microbial diversity (cultivable and metagenomic) for products of use in environment waste management and of industrial importance. Many novel bacteria, fungi and lichens have been identified. Bacteriophage-based therapeutic approaches are currently being studied.

Dr. Smriti Gaur joined the Department of Biotechnology in 2010. She did her graduation in Botany (Honours) and an advance certificate course of two year duration in Cell Biotechnology from Dayalbagh Educational Institute, Agra. She did her Masters in Applied Microbiology from Cancer Hospital and Research Institute, Jiwaji University, Gwalior and PhD from JIIT, Noida. She has several publications to her credit. She is presently focused in the area of Functional food, Food Biotechnology and Microbial Biotechnology. Currently our research focuses on development of novel functional foods (rich in anti-oxidative and prebiotic properties) which could improve the quality of life by stimulating probiotics growth in gut, helps in managing diabetes, cholesterolemia as well as other lifestyle disorders and reduces the dependence on drugs having high cost and side effects.

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