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Chief Editor : Prof. Pammi Gauba
Editors: Prof. Rachana and Dr. Shazia Haider

THEME

**Innovations in Life Sciences and Computational Biology
(20 - 22 January, 2022)**

Organised By:

Department of Biotechnology

JAYPEE INSTITUTE OF INFORMATION TECHNOLOGY

A-10, Sector 62, Noida - 201 309 (UP) (India)

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CHIEF EDITOR

Prof. Pammi Gauba

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Prof. Rachana and Dr. Shazia Haider



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Manoj Gaur
Chancellor

Jaypee Institute of Information Technology

(Declared Deemed to be University U/S 3 of the UGC Act 1956)

January 07, 2022



Message

It is indeed a matter of great pleasure for me to know that **the Department of Biotechnology, Jaypee Institute of Information Technology, Noida** is organizing the **"International Conference on Advances in Biosciences and Biotechnology (ICABB – 2022)"** on the theme **"Innovations in Life Sciences and Computational Biology"** from 20 – 22 January 2022.

The world is currently facing a global pandemic without precedence in our lifetime. Conferences are a pivotal part of the scientific enterprise, as the pandemic experience has shown, online meetings are a viable alternative. Scientific conferences are important avenues for researchers to share and discuss research findings, to exchange ideas and insights, and to network for collaboration and career development.

This conference aimed at expanding the program by including all aspects in various discipline of Life Sciences and Computational Biology as multidisciplinary approach for essential sustainable society. The diversity of specializations and related themes will enable us to achieve our targeted mandate and vision. The role of research and scientists from across the globe is paramount to address the leading problems.

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

With best wishes,

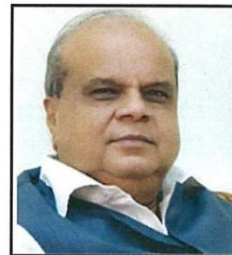


(Manoj Gaur)



Prof. S.C. Saxena
Pro-Chancellor

January 07, 2022



Message

It gives me a great pleasure to know that **Department of Biotechnology, Jaypee Institute of Information Technology, Noida** is organizing the "**International Conference on Advances in Biosciences and Biotechnology (ICABB – 2022)**" on the theme "**Innovations in Life Sciences and Computational Biology**" from 20 – 22 January 2022.

Organizing inclusive and useful scientific meetings is a significant responsibility shared by researchers, scientific societies, and other organizations worldwide. Due to the COVID-19 pandemic, a major shift has occurred towards virtual conferencing formats, triggering discussions in the scientific community on the current and future formats and organization of conferences. The current challenging time has taught us the importance of robust ecosystems for dealing with the global crisis.

I am certain that these three days of conference will be of enormous value to all the participating delegates and will bring out innovative ideas among the participants paving way for new inventions and technologies in Life Sciences and Computational Biology.

I welcome all the delegates to this conference and hope that the theme will benefit the scientific fraternity and students. I convey my best wishes to the organizers and grand success to the event.

With best wishes


(S.C. Saxena)



Jaypee Institute of Information Technology

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

Vice Chancellor
Prof. Yog Raj Sood

January 10, 2022



Message

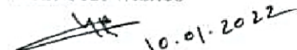
I take pride in introducing Jaypee Institute of Information Technology, Noida which has been recognized as a center of excellence in higher education through knowledge, creation and dissemination. By sheer dint of hard work, focused, attention and dedication in respective disciplines of engineering, biotechnology, management, humanities and the energetic and qualitative support of the students, teaching and non-teaching staff, the JIIT has shown exemplified growth. JIIT is striving to impart quality education to meet national and international challenges.

I am glad 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 – 2022)"** from 20 – 22 January 2022 on its theme as **"Innovations in Life Sciences and Computational Biology"**. The Department of Biotechnology at JIIT, Noida, established in 2002, remains committed to provide research informed teaching and learning, vibrant R & D environment.

This conference will be a good starting point for national and international universities to interchange knowledge and skills in the area of Life Sciences and Computational Biology. We are looking forward to find new solutions in this area and forecast future trends to contribute to global needs. I would like to congratulate the department of biotechnology for superb drive in organizing this conference.

It is a great pleasure to welcome all delegates and participants to this conference. I am very certain that this occasion will be able to provide a platform towards strengthening our relationships in knowledge sharing while at the same time provide the necessary thrust in joint research collaborations and product commercialization within the research society. It is my aspiration that this conference will be a foundation for the growth of new ideas towards a better tomorrow.

With best wishes


Prof. Yog Raj Sood



Jaypee Institute of Information Technology

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

Message from Organizers

It is our great pleasure to welcome all the delegates to ICABB 2022, the 5th International Conference on “**Advances in Biosciences and Biotechnology**”, theme **Innovations in Life Sciences and Computational Biology**, being organized by the Department of Biotechnology, JIIT, Noida, from 20 – 22 January 2022.

Computational Biology is one of the most important aspects of Life Sciences research, especially in such a time when the world is reeling under a health crisis due to the global pandemic COVID-19. The conference will provide a vibrant platform to share the advancement and research findings and would provide an enriching experience to all the participants. The three-day scientific program consists of technical sessions with eminent speakers covering a wide range of topics in various aspects in the area of Life Sciences and Computational Biology including Computational Biology and Applications, Medical and Microbial Biotechnology, Food, Agriculture and Natural Products, Environmental and Industrial Biotechnology and Nanotechnology and Drug Delivery.

We thank Prof S.C. Saxena, Hon’ble Pro-Chancellor, and Prof. Yog Raj Sood, Hon’ble Vice-Chancellor, for his constant motivation, guidance, valuable inputs, and support extended to make this conference a success. Without their cooperation and full support, this conference would not have been possible.

We take this opportunity to thank all the National and International speakers for accepting our invitations. We are also thankful to our Advisory Committee Members for their continuous support and guidance. The event has been made possible with the sincere efforts of all the faculty members of the Department of Biotechnology, Staff from the administrative and finance department. The constant efforts of the student volunteers who have worked round the clock are appreciated immensely. The support from our publishing partners is highly acknowledged.

We hope that you will find the conference informative and interactive with eminent speakers that would enhance our knowledge and provide an enriching experience. Thank you all once again, and we look forward to a productive event.

Prof. Pammi Gauba
Chairperson

Prof. Rachana
Convener

Dr. Shazia Haider
Convener

ICABB 2022

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Speakers Abstract

Guest of Honor

Pharmacopoeial Standards for Biotechnology Based Therapeutics

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ABSTRACT

Biotechnology-based therapeutics are gaining extreme importance worldwide as it is preferred for the treatment of chronic diseases like rheumatoid arthritis, various cancers, psoriasis etc. In India, the biotherapeutic industry is recording exponential growth and the domestic market is expected to reach \$40 billion by 2030. To ensure the quality of these medicines in the country, standards are developed by the Indian Pharmacopoeia Commission (IPC), an autonomous institution under the Ministry of Health & Family Welfare, Government of India. The developed standards are published as monographs in Indian Pharmacopoeia (IP), a book of standards for Drugs and Pharmaceuticals including biotechnology-based therapeutics. In order to fulfill the intended purpose of IP monographs, IPC also provides IP Reference Substances (IPRS). The standards laid down in IP are authoritative and legally enforceable as per The Second Schedule of Drugs and Cosmetics Act 1940. IP standards are designed to ensure the quality and consistency of these therapeutics by defining quality attributes using multiple and orthogonal tests, due to their complex and heterogeneous nature. IP monographs prescribe a set of analytical methods and their acceptance criteria to assess the identity, purity, and potency of the product using physicochemical, immunochemical property, and biological activity which are needs to be complied with throughout the life cycle of the products or till its expiry. The current edition IP 2018 provides quality standards for more than 40 biotechnology-based therapeutics such as insulin and its analogue, interferons, cytokines, hormones etc. Quality attributes in the monograph are able to assess protein variants that have a similar biological activity to the parent molecule, protein variants that do not have a similar biological activity to the parent molecule, process-related impurities, potency, and appearance. Methods in the pharmacopoeia monographs are also amended if the majority of the stakeholder's face difficulty in adopting it. For example, in the case of the Recombinant Follicle Stimulating Hormone (rFSH) monograph in IP 2018 it was observed that manufacturers faced challenges in using a large number of vials for testing Follitropin oligomers as per IP method. To minimize this challenge the new method was developed and amended through an amendment list to IP 2018. This amendment reduced the burden of using the large number of vials for one single test. The stakeholders were also explained that the interpretation of IP monographs, must be in accordance with all general requirements, testing methods, texts, and notices pertaining to it, in the IP.

Keywords: Indian Pharmacopoeia Commission (IPC), Recombinant Follicle Stimulating Hormone (rFSH), IP monographs.

International Speakers

Environmental Inhaled Nanoparticles in the Lungs: Interaction and Induced Toxicity

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ABSTRACT

The presentation is organized around two parts that could lead to developments in the field of environmental biotechnology. In the first part, we address the issue of air pollution which is now recognized as a major threat to human health. Traffic exhaust Particulate Matter (PM_{2.5} and PM₁₀) is considered to be a significant contributor to this threat. Until now, little attention has been paid to non-exhaust PMs, such as brake wear particles emitted by transport vehicles. We have studied brake wear PM_{2.5} from distinct sources and shown that they contain large amounts of metallic particles smaller than 100 nm (NPs), raising concerns about their ability to cross the respiratory barrier. Brake wear NPs were found to be cytotoxic to human bronchial cells while exhibiting attenuated inflammatory effects. These results should be able to guide manufacturers towards the production of environment-friendly automotive equipment. In a second part, we study the impact of engineering model NPs reaching the deep lung region, and interacting with the pulmonary surfactant, a thin lipid film lining the alveolar epithelium. It is found that cationic silica (SiO₂, 42 nm) and alumina (Al₂O₃, 40 nm) interact strongly with the lung fluid and induce profound modifications of its flow (viscosity) properties, even at low concentrations. We find that silica causes fluidification, while alumina induces a liquid-to-solid transition. It is suggested that the structure and viscosity changes could impair the fluid reorganization and recirculation occurring during breathing.

Keywords: PM_{2.5}, Particulate Matter, Alumina, Environmental Biotechnology.

Bioengineered Growth Factor Delivery Systems for Vascular Applications

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ABSTRACT

Regenerative medicine strategies that promote robust angiogenesis remain elusive and have the potential to enable the treatment of a range of conditions. Growth factors are key signalling molecules in angiogenesis; however, they are in low abundance and when delivered exogenously are rapidly cleared by proteolytic processes. The glycosaminoglycan chains of proteoglycans are the natural binding, protective, and signalling partners for growth factors. However, the yield of proteoglycans isolated from natural sources is low, supporting the alternative approach of recombinant production. This presentation will cover recent research into bioengineering proteoglycans containing functional glycosaminoglycans and their presentation in biomaterial scaffolds. The preclinical assessment of these bioengineered systems for vascular applications will be presented utilizing *in vitro* and *in vivo* assays.

Keywords: Growth factors, Angiogenesis, Regenerative Medicine, Glycosaminoglycans.

Nanoparticles as Versatile Nanozymes: Oxidant and Antioxidant Applications

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ABSTRACT

Several metal and metal oxide nanoparticles show unique abilities to mimic the function of enzymes. Most of these nanoparticles mimic the activity of oxido-reductase enzymes and can oxidize or reduce the biomolecules, dyes, or other analytes making them perfect candidates for various applications requiring oxidation or reduction reactions. This talk will introduce the field of nanozymes by giving examples of two specific nanoparticles – cerium oxide and iron oxide. The first half of the talk will focus on the use of cerium oxide nanoparticles ‘nanoceria’ as novel antioxidant material. For example, nanoceria is used as a novel antioxidant that mimics the function of Reactive Oxygen Species (ROS) scavenging enzymes such as superoxide dismutase, catalase, and glutathione to maintain redox homeostasis. This antioxidant property has been exploited in the prevention and treatment of multiple human and plant conditions mediated by oxidative stress. The ability to reversibly switch its oxidation state between Ce^{3+} and Ce^{4+} is fundamental to these applications and this talk will review the current understanding of the mechanism of interaction and the role of ligands in tuning this activity. The second half of the talk will focus on the use of iron oxide nanoparticles as oxidant nanozymes that mimic the activity of peroxidases. It will introduce one of the major drawbacks of iron oxide nanoparticles in its application as a peroxidase mimic and summarize how we overcame this crucial drawback. This opened the door for the application of iron oxide nanoparticles in sensing and antimicrobial applications that will be presented during this talk.

Keywords: Metal Oxide Nanoparticles, Oxido-reductase Enzymes, Reactive Oxygen Species & Antimicrobial Applications.

National Speakers

Medicinal Plants of Western Ghats - Issues & Challenges

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ABSTRACT

Medicinal plants are played an important role during the Covid-19 pandemic and also their utilization in the day today life for boosting the immunity against coronavirus infections. In the natural vegetations, Kashmir Himalayas, Western Ghats, and the Eastern Ghats regions in different parts of the country are rich in medicinal plants diversity. Among these, the Western Ghats Mountain range runs parallel to the West coast of Peninsular India for about 1600km. It has a very rich floristic diversity of about 4000 indigenous angiosperm species which includes 1500 endemic plant species. The Western Ghats is a global biodiversity hotspot which comprises endemic status of 78% Amphibians, 62% Reptiles, 38% Plants and 12% Mammals are Endemic to the W. Ghats. As for drug identification are concern many of the studies are involved in the plant drug identification process. Among them, some of the studies and techniques are Biological origin, Geographical distribution & history, Cultivation & Collection, Plant protection, Macroscopic characters or Morphological characters (Organoleptic studies), Microscopic characters (Histology), Chemical constituents present in the crude drugs, Chemical test for un-organized drugs, Therapeutic and pharmaceutical uses, etc. In addition, the adulteration and substitution of crude drugs is a challenging issue in the present scenario. The main objective of this presentation is to make awareness of the status of the medicinal plants in the southern Western Ghats and plant drug identification issues as well and this will be very useful for drug discovery and drug development research activities of indigenous systems of medicine.

Keywords: Western Ghats, Plant Identification, Adulteration.

Protein Kinases and Phosphatases: Role in Virulence and Survival of Pathogenic Bacteria

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ABSTRACT

Protein phosphorylation at specific amino acid residues regulates multiple cellular processes in the living organism which include metabolic pathways, cell division, stress response, sporulation, and even virulence in pathogens. The master players of these events are specific proteins like kinases and phosphatases that are reported as essential for the survival and virulence of pathogenic bacteria. Earlier, we showed that a secretory tyrosine phosphatase (MtpB) in *Mycobacterium tuberculosis* is essential for infection and the mutant strain lacking mtpB was about a hundred-fold less virulent. We also showed that a serine/threonine phosphatase (PstP) is essential for the survival of *Mycobacterium tuberculosis*. In another pathogenic bacterium, *Bacillus anthracis*, we demonstrated the regulation of bacterial chain length – a potential virulence determinant by a ser/thr protein kinase, PrkC. Deletion of PrkC caused reduced chain length, reduced cell wall thickness, and multi-septation. Recently, we characterized a second serine/threonine phosphatase in *Bacillus anthracis* and observed that it regulates sporulation and toxin production. Overall, we have conclusively shown the importance of kinases and phosphatases in multiple processes of *Mycobacterium tuberculosis* and *Bacillus anthracis* that are associated with virulence and survival and these can thus serve as potential drug targets.

Keywords: *Mycobacterium tuberculosis*, *Bacillus anthracis*, ser/thr protein kinase, PrkC, ser/thr Protein Kinase.

***Aspergillus Niger* Acidogenic Metabolism: A Peek at its Carbon-Nitrogen Interface**

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ABSTRACT

Aspergilli are endowed with abilities to produce organic acids, bioactive compounds and to secrete extracellular enzymes. Many of these have matured into technologies through industrial fermentations. *Aspergillus niger*, a filamentous fungus of our interest, is a major citric acid producer. Over a century of research has endeavored to elucidate the underlying biochemical mechanisms of acidogenesis-largely focusing on carbon metabolism. Yet definitive and simple answers have been elusive and hence the acidogenic metabolism of *A. niger* provides an excellent paradigm for research. Our laboratory is interested in elucidating the connections between nitrogen metabolism and acidogenesis. These are exciting times since many *Aspergillus* genomes are sequenced. Genetic manipulation tools have allowed us the ability to explore and exploit *A. niger* metabolism. Few leads and mechanistic insights to acidogenic metabolism gleaned by us will be presented.

Keywords: *Aspergillus niger*, *Aspergillus* Genomes, Citric Acid Producer, Filamentous Fungus.

Systems and Synthetic Biology: Concepts to Applications

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ABSTRACT

Systems biology is an approach to understand higher-level cellular behaviors as a function of group molecular interactions. This calls for capturing multi-level and contextual biological data using mathematical equations and computational algorithms. The hope is to understand molecular network design principles that interface the expression layer with its corresponding phenotypic outcome. In the first part of my talk, I will introduce the foundational concept and key developments in Systems Biology. The second part of my talk will touch upon the need to design biological systems from scratch. This is a new area of Synthetic Biology. Specifically, I shall examine key biological issues using an engineering approach. In both sections of my talk, I shall move from general concepts to applications and touch upon our work. My hope is to generate curiosity leading to the identification of good unanswered questions. Currently, we neither know the natural network design principles nor the rules of designing biological systems de novo. In my view, it is a grand challenge and also a grand opportunity.

Keywords: Systems Biology, Computational Algorithms, Synthetic Biology, Natural Network Design Principles.

Microbiome: Human Health, Environment and Society

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ABSTRACT

Recent advances in genomics and metagenomics have unraveled many aspects of the microbiome. These findings have now paved the way to develop technologies to maintain human health, and resolve many environmental issues. These findings have also necessitated to step up our efforts to educate society and children about the role of the microbiome in our daily life. Our efforts in this direction during the past 5 years will be presented.

Keywords: Genomics, Metagenomics, Microbiome.

Network Science Applications in Biology: Identifying Significant Key Regulators

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ABSTRACT

Complex biological systems are often represented as networks, where the sub-units are linked together to form the whole. Protein-protein interaction networks or gene-regulatory networks are a few of the favorite examples. Interestingly, the topological characteristics of biological networks enable us to identify the key nodes in terms of modularity. However, due to the large size of the biological networks with many hubs and functional modules across intertwined layers within the network, it often becomes difficult to accomplish the task of identifying potential key regulators. As an example, we demonstrate the use of a generalized formalism of "Hamiltonian Energy" with a recursive approach to identify significant key regulators in an Apoptosis Regulatory Gene Network.

Keywords: Hamiltonian Energy, Apoptosis Regulatory Gene Network, Biological Networks.

Exploration of Specialized Metabolic Pathways and Their Regulation in Plants

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ABSTRACT

Plants produce an amazing diversity of compounds termed “specialized or secondary metabolites” as means of defense and interaction with the surrounding environment. Besides their importance to the plant, specialized metabolites are useful to mankind for their immense medicinal and aromatic properties. Specialized metabolites in plants are produced at low levels in tissue and response specific manner due to which the production cost is generally expensive, which can be overcome by metabolic engineering of plant and microbial production platforms if genes and metabolic pathway steps are characterized. To this end, our group has been working on understanding the biosynthesis and regulation of anticancer alkaloids in Periwinkle (*Catharanthus roseus*) and medicinally important withanolides in Ashwagandha (*Withania somnifera*). This talk will cover the general aspects of plant specialized metabolism and metabolic engineering along with the latest research on specialized metabolism and its regulation in Periwinkle and Ashwagandha.

Keywords: *Withania somnifera*, *Catharanthus roseus*, Secondary metabolites, Ashwagandha.

SESSION I
Computational Biology
and
Applications

ICABB_C101_Ruch

Identification of Co-Occurring Mutations in IL7R gene in Patients with High-Grade Serous Carcinoma

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ABSTRACT

The lack of specific and sensitive biomarkers for diagnosis and prognosis of ovarian cancer is a major cause of mortality in the disease. Finding mutations in genes involved in important oncogenic pathways is a significant step in the identification and development of new biomarkers. Whole exome sequencing (WES) is an effective tool for detecting cancer-causing mutations. Through computational analysis of WES, the current research aims to uncover functionally damaging mutations in patients with high-grade serous ovarian cancer (HGSC). WES data from HGSC patients was acquired from the genomic literature available in the sequence read archive, the variations were identified, and a detailed structural and functional analysis was carried out in this study. Intriguingly, I66T and V138I mutations in the IL7R gene were found to be co-occurring in four of the five HGSC patient samples examined in the present study. The V138I mutation was located in the fibronectin type-3 domain and was found to have a disruptive effect on the structure and dynamics of the IL7R protein by computational analysis. This mutation was identified in the same domain as the neutral I66T mutation, which compensated for the V138I variant's disruptive effects. These investigations show that the IL7R gene has a substantial role in ovarian cancer that has been previously undiscovered. The work is expected to lay the groundwork for the development of a new biomarker that might be used in molecular profiling and disease prognostic prediction.

Keywords: Whole Exome Sequencing, Ovarian Cancer, High Grade Serous Ovarian Carcinoma, Biomarkers, Clinical Prognosis, IL7R, Co-Occurring Mutations.

ICABB_C103_Mee

Genome Sequencing and Comparative Analysis of Antibiotic Resistance Plasmids in Carbapenem-Resistant *Escherichia coli* Isolated from Indian Cattle

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ABSTRACT

The present study illustrates plasmidome and resistome profile of two carbapenem-resistant *Escherichia coli* isolates from milk of two different cows with recurrent subclinical mastitis from semi-urban region of Kolkata, India. Both *E. coli* strains (IVRI Kol CP4 and CM IVRI Kol-1) were sequenced and subreads were *de novo* assembled. Genome annotation data revealed the presence of multi-resistance plasmids conferring resistance to β -lactams, sulphonamide, tetracycline, trimethoprim, and aminoglycosides and even to the last-resort drugs carbapenem in both the strains. The strain IVRI Kol CP4 carried 3 plasmids: a 92840 bp IncFII plasmid with *bla*_{TEM-1B}, *bla*_{NDM-5}, *sul-1*, *dfra12*, *rmtB*, *aadA2* genes; a 50882 bp IncI plasmid with *bla*_{CMY-42} gene and a 28652 bp undermined replicon type plasmid having *bla*_{TEM-1B}, *mphA* and *tet(A)* gene. Other strain CM IVRI Kol-1 also had 3 plasmids: a 146286 bp IncFIA plasmid with *bla*_{TEM-1B}, *bla*_{NDM-5}, *mph(A)*, *sul1*, *tet(A)*, *dfra12*, *rmtB*, *aadA2*, and *tetR* genes; a 62055 bp IncI plasmid with two copy of *bla*_{CMY-42} and a 6346 bp plasmid of unknown replicon type. We compare our plasmid sequences with other publicly available data, to know the evolutionary picture of MDR plasmids from different locations. In addition, we also found virulence genes belonging to adherence, iron acquisition and secretion system which are responsible for the pathogenicity of the strains. This first-ever study on the whole genome sequence of NDM-5 producing *E. coli* from bovine milk in India highlights the role of IncF type plasmid as a common vehicle for carriage and spread of NDM-5 gene in food animals.

Keywords: *Escherichia Coli*; Plasmid, Whole Genome, Antibiotic Resistance, β -lactams.

ICABB_C104_Sur

***In-silico* Modeling and Identification of Common Potent Inhibitor/s Against the Most Poisonous Toxins**

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ABSTRACT

Botulinum neurotoxins (BoNTs) are causative agents of life-threatening disease botulism and the most potent group of toxins currently known. They block the release of acetylcholine at the neuromuscular junctions and cause flaccid paralysis. Due to extreme toxicity and potential use of BoNTs as biowarfare agent, development of medical countermeasures is a high-priority research area. There are seven distinct serotypes of BoNT and various subtypes exist within a serotype. Since the identification of a specific serotype is a time-consuming process, development of common small molecule non-peptidic inhibitors (SMNPIs) is the area of concern. Virtual screening methods have been proved to be a proficient approach in the drug discovery process. In present study, the ligand-based *in-silico* approach was applied for identification of the potent pan active inhibitor of human botulism causing BoNT/A, B, E, and F. The studied compounds are the derivatives of NSC1012 an 8-hydroxy chloroquinoline (8-HQ). The synthetic versatility of 8-HQ makes it a privileged molecule that helps in developing numerous compounds with good efficacy and low toxicity. The selected derivatives against each serotype were then studied for *in-silico* ADME/T properties and all of them were filtered on the basis of Lipinski's rule. Here, we report three SMNPIs A11, A18, and A20 which are providing better binding affinities with the target BoNTs. These compounds could be developed as potential pan active BoNTs inhibitors that can be progressed to new antidote/s.

Keywords: Botulinum Neurotoxin; 8-HQ; Small Molecule Non-Peptidic Inhibitors; Molecular Docking; ADMET Studies.

ICABB_C105_Nab

Evaluation of Binding of Small Molecule Inhibitors against SARS-CoV-2 Variants of Concern

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ABSTRACT

SARS-CoV-2, being one of the largest known RNA viruses, is highly prone to undergo mutations in its genome. There are several identified variants of the virus which are more infectious (also known as Variants of Concern or VOC). Till date, Alpha, Beta, Gamma, Delta and Omicron variants have been identified for the virus. The mutations facilitate the virus to evade immune responses or escape therapeutic efforts. SARS-CoV-2 interacts with the host Angiotensin Converting Enzyme 2 (ACE2) receptor protein *via* its Spike glycoprotein. While several drug candidates are under study to inhibit the Spike protein, the binding of the inhibitors with the newly generated variants would be different. Here, in our work, we have studied the efficacy of three drugs Remsdivir, Saquinavir and Stavudine against Spike protein. We have carried out the molecular docking and structural analysis by using Autodock docking and Pymol visualization software. Our detailed molecular analysis shows the differential binding of the inhibitors to SARS-CoV-2 Wild-type and its Variants. Our detailed molecular analysis would be very useful in rational drug designing strategies against the virus.

Keywords: SARS-CoV-2, Variants, VOC, ACE2, COVID19.

ICABB_C106_Kri

Identification of Gedunin: A Natural Compounds as Drug Like Inhibitors Against FabG1 of *Mycobacterium tuberculosis*: an *In Silico* Approach

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ABSTRACT

Tuberculosis (TB) continuously poses a major public health concern around the globe, with a mounting death toll of approximately 1.4 million in 2019. It is a major cause of death across the globe and kills 1.5 million people per annum, thereby persisting as a challenge for the scientific community. Drug-resistant strains often undergo mutations, adopt other pathways and express drug efflux pumps to reduce or block the entry of drugs. *Mycobacterium tuberculosis* (*M.tb.*) has an extremely rigid cell wall containing mycolic acids that play an important role in the virulence and persistence of *M.tb.* Fatty acid biosynthesis in *M.tb.* is mediated by fatty acid synthesis I and II. The type II fatty acid biosynthesis system (FAS-II) is present in bacteria, plants, and organisms of the phylum Apicomplexa, but generally considered to be absent from mammals. It has been shown that MabA is essential for *M. tuberculosis* survival thus it is considered as an important target for new drug development. The current study is undertaken with an objective directed towards the identification of potential inhibitor(s) for mycobacterial protein FabG1, an essential and functional gene for bacterial growth, survival and fatty acid synthesis. In the present study, 1000 secondary metabolites from ethnomedicinal plants, reported against TB were compiled and subjected to *in silico* pharmacokinetic analysis followed by Lipinski's Rule of Five to check drug-likeness and ADMET. Molecular docking was finally done along with TB drugs (Isoniazid) to check binding affinity with FabG1. Pharmacokinetic analyses revealed that 15 natural compounds satisfy all ADMET criteria and also those of Lipinski's Rule of Five. These natural compounds docked successfully within the active site of FabG1. Among the compounds tested, Gedunin showed the best docking profile and exhibited lowest binding energy indicating high affinity for Fabg1, suggesting its potential as a putative antimycobacterial agent.

Keywords: *Mycobacterium*, FabG1, Molecular Docking, Ethanomedicinal Plant.

ICABB_C107_Akv

A Multi-Omics Analysis to Reveal the Significant Correlation of SMYD2 with Different Cancers using TCGA Dataset

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ABSTRACT

SET and MYND domain-containing protein 2 (SMYD2) is a protein lysine methyltransferase (PKMT) from the family SMYD. It can regulate gene transcription by catalysing the methylation of lysine residues of protein substrates that play an important role in tumorigenesis. Although emerging evidence supports the association of SMYD2 in cancer progression. But the relation of SMYD2 expression in cancer progression remains unknown with concrete evidence. Therefore, a multi-omics analysis was performed using the TCGA (The Cancer Genome Atlas) data, to analyse the therapeutic potential of SMYD2 as a biomarker for multiple human cancers. The transcriptional expression, mutations, survival rate, gene ontology and enriched pathways associated with SMYD2 were determined by using different bioinformatics-based analyses. In addition, the protein-protein interaction (PPI) analysis was performed, and examined the correlation between genes co-expressed with SMYD2. We found that SMYD2 was highly expressed in tumor tissues compared to normal tissues in queried datasets of multiple human malignancies. A total 15 missenses, 4 truncating, and 5 other mutations were detected. In PPI analysis, out of 50 protein partners, majorities of these indicated significant co-expression. The gene GNPAT was the most positively correlated gene which is involved in various other regulatory processes. Gene ontological characteristics and pathways were significantly associated with the development of cancer. Collectively, our data-driven research provides a relatively comprehensive understanding of the carcinogenic effect of SMYD2. We believe that it can be used as a target for new biomarkers of various human cancers.

Keywords: SMYD2; Cancer; Multi-Omics; Survival Analysis; Mutational Analysis; Pathways Analysis.

ICABB_C108_Tiy

Computational Investigations of Alzheimer’s Disease Related Pathways with Special Relevance to DNA Repair and Autophagy

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ABSTRACT

Alzheimer’s disease (AD), also known as senile dementia, is a neurodegenerative disease and the most common form of chronic dementia that shows progressive loss of memory, synaptic function, cognitive capacity and atrophy in different brain areas in the elderly. Epidemiological studies highlighted AD as a multifactorial disease i.e.; it occurs due to complex interactions between various intrinsic and extrinsic factors. The pathology of AD involves a combination of intrinsic genomic susceptibility and environmental factors. It entails a continual dynamic interplay between dysfunctional pathways and central homeostatic networks of nerve cells. Employing a systems biology approach to integrate protein alterations provides a link between multiple molecular abnormalities leading to memory impairment revealing a broadly dispersed and multi-molecular targeting pathogenic process. Both DNA damage and repair (DDR) pathways and autophagy process hold constitutive roles in AD. We have retrieved several pathways related to DNA damage, DNA repair and autophagy from the KEGG and other databases. Relevant information was retrieved from literature and interaction pathways of the key genes related to these pathways were retrieved from the STRING database. All this information was compiled carefully to implement further analysis. Only those genes (like PARP1, BECN1, mTORC1, UVRAG etc.) were selected which can establish a link between the DDR pathways with the autophagy. We have created a Protein-protein interaction (PPI) network and then that network will be analyzed to explore the role of these integrations. We would like to identify hub genes and anticipate that these hub genes can act as potential therapeutic targets or biomarkers for the AD.

Keywords: Alzheimer’s Disease, Systems Biology, Protein-Protein Interaction, DNA Repair, Autophagy.

ICABB_C109_Was

Identification of Novel and Potential Inhibitors of Lanosterol-14 Alpha Demethylase: Structure Based Drug Designing Approach

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ABSTRACT

Candida glabrata is the second most common cause of invasive fungal infection. In the limited antifungal drugs, azole antifungals are commonly used to treat candidiasis. Lanosterol 14 alpha demethylase (L14aD) is the main target of the azole antifungals. High level resistance against the azoles antifungal indicates the need of novel inhibitors of L14aD. In this study we have screened a large number of small molecules from different chemical databases (Zinc, Drugbank, ChEMBL and ChEMDIV antifungal) to find out novel and potential inhibitors of L14aD. As a result, from more than 100000 molecules, four best candidates (ZINC000095786149, ChEMBL4081680, ChEMBL263611, ChEMBL3133986) were selected from the top scoring compounds, and further validated in molecular dynamic simulation. Glide score of selected compounds ZINC000095786149, ChEMBL4081680, ChEMBL263611 and ChEMBL3133986 were -19.13, -15.52, -15.08 and -14.65 kcal/mol suggesting that these compounds bind with L14aD with higher binding affinity than the benchmark compound (Itraconazole) which has Glide score -6.85 kcal/mol. Protein-ligand complexes of selected molecules also show good stability during molecular dynamic simulation.

Keywords: Lanosterol 14-a Demethylase, SBDD, Molecular Docking, Molecular Dynamic Simulation.

ICABB_C110_Pri

Molecular Insights to the Binding Mechanism of APNS Containing HIV-protease inhibitors to SARS-CoV-2 M^{pro} through MD Simulations and Binding Free Energy Calculations

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ABSTRACT

Severe acute respiratory syndrome Coronavirus-2 Main protease (SARS-CoV-2 M^{pro}) is a crucial enzyme having an essential role in facilitating both replication and transcription mechanism of the virus. Till now, the entire world is lacking any effective drugs or inhibitors to fight against the virus. Hence, it has been considered as a significant target site for discovery of the drug candidate. Kynostatin, a class of HIV^{pro} inhibitors (Kynostatin-764, Kynostatin-577, Kynostatin-1931, Kynostatin-227, Kynostatin-272) containing Allophenylnorstatine (APNS) are taken as targeted inhibitory molecules to check its potential against Coronavirus-2 M^{pro}. Applying molecular docking of all the above molecules with M^{pro}, Kynostatin-764 is found to have highest binding free energy -8.0 kcal/mol. Implementing Molecular Dynamic simulation and Poisson–Boltzmann surface area method (MM-PBSA), the binding free energy (ΔG_{Bind}) value of these five molecules are calculated as -28.31, -6.85, -21.59, -18.36, -15.69 (kcal/mol) respectively. By reason of an amplified promising van der Waals interactions and diminished solvation energies, Kynostatin-764 is found as an extremely active ($\Delta G_{\text{Bind}} = -28.31$ kcal/mol) molecule against SARS-CoV-2 M^{pro}. The interacting residues like Glutamic acid166 and Glycine143 of viral protease form Hydrogen bonds with Kynostatin-764 found from the Hydrogen bond analysis and which is verified from the studied data of LigPlot+ software. It seems quite an inspiring outcome rendering the pre-testified antiviral roles of Kynostatin-764. It is expected that the recent evaluation of binding effects of these APNS comprising Kynostatin molecules discloses some appreciated perceptions to enterprise the effectiveness of anti-SARS-CoV-2 M^{pro} drugs.

Keywords: SARS-CoV-2 M^{pro}, Kynostatin-764, Kynostatin-577, Kynostatin-1931, Kynostatin-227, Kynostatin-272, APNS.

ICABB_C111_Bis

Exploring the Therapeutic Ability and Possible Drug Resistance of PF-07321332 against SARS-CoV-2 M^{pro} through MD Simulations and Binding Free-Energy Estimation

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ABSTRACT

COVID-19 pandemic is devouring the world causing significant chaos due to the aetiological agent, Coronavirus-2 (SARS-CoV-2). The main protease M^{pro}, key enzyme of SARS-CoV-2 is the most fascinating molecular target for a pharmacological treatment and also liable for viral protein maturation and replication. For the antiviral therapy, no drugs have been approved clinically till date. Targeting the M^{pro} with a compound having inhibitory properties against it can hinder viral replication. In the current study, an orderly molecular docking, molecular dynamics (MD) simulation, and MM-GBSA based binding free energy calculations was being carried out to explore the therapeutic potency of antiviral compound PF-07321332 (PF) against the SARS-CoV-2 M^{pro}. PF, a covalent inhibitor, of which chemical structure has freshly been revealed, is a promising oral antiviral clinical aspirant with firm anti-SARS-CoV-2 activity *in vitro* and presently in phase III clinical trials. The drug was docked to the wild-type (WT) M^{pro} and two of its mutants (C145A & C145S). The protein-ligand (M^{pro}/PF) complexes were further examined through long MD simulations to check the possible drug resistance in the mutants. To understand the binding affinity, the MM-GBSA based binding free energy calculations for all the three M^{pro}/PF complexes were also implemented. Based on the predicted biological activities and the binding affinities of the compound PF to the WT and to the mutants (C145A & C145S) M^{pro}, it can be stipulated that, PF might have conventional potency to act as an anti-viral agent against the SARS-CoV-2 M^{pro} overcoming the possible mutation induced drug resistance.

Keywords: COVID-19; SARS-CoV-2 M^{pro}; PF-07321332; Drug resistance; Molecular Dynamics Simulation; MM-GBSA.

ICABB_C112_Sha

Screening and Identification of Small Molecules having the Potential to Inhibit an Important MVP enzyme of *Helicoverpa Armigera*

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ABSTRACT

Helicoverpa armigera is an insect pest that feeds on more than one hundred crops. It thus causes significant economic losses to farmers. This insect pest has developed resistance to a wide range of insecticides. Therefore, an insecticide with a new mechanism of action that is safer, more effective, and more environmentally friendly is urgently needed. Juvenile hormones play a significant role in the life cycle of insects, as they regulate both their morphogenetic and gonadotropic development. Mevalonate pathway (MVP) synthesizes precursors for juvenile hormone, and thus enzymes involved in MVP can be used in pesticide development. MVP is also involved in the production of several non-sterol isoprenoid metabolites that are crucial for protein prenylation as well as glycosylation. In the present study, homology modeling was used to create a 3-D model of one of the important MVP enzymes. Following that, a natural small molecule database library was chosen for virtual screening with software- PyRx version 0.8, then molecular docking using Autodock Vina was used to select molecules based on good binding affinities. The ADMET properties of the identified molecules were also analyzed using the pkCSM server, which revealed that they are non-toxic and follow Lipinski's rule of five. Furthermore, molecular simulation runs were carried out with GROMOS43a1 force field revealed that the identified compounds had a good binding affinity and formed a stable enzyme-inhibitor(s) complex. The identified natural compounds could be employed as MVP inhibitors, paving the way for designing eco-friendly insecticides for insect pest management.

Keywords: Mevalonate Pathway; Virtual Screening; Small Molecules Inhibitor; Docking; Molecular Dynamics Simulation.

ICABB_C113_Div

An in-silico Study of Driver Free Fatty Acid Receptor 3 Gene in Type 2 Diabetes Mellitus Therapy

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ABSTRACT

Type 2 diabetes mellitus is a cluster of diseases caused due to genetic, environmental, behavioral and other risk factors and characterized by hyperglycemia, insulin resistance (IR), and relative insulin deficiency. FFAR3 or GPR41 is a short chain fatty acid receptor reported to be expressed in pancreatic beta cells and inhibiting glucose-stimulated insulin secretion. It plays a vital role in energy homeostasis as studies revealed it regulates sympathetic activity by sensing the nutritional state. Herein, we propose the role of free fatty acid receptor 3 (FFAR3) involved in type 2 diabetes mellitus by carrying out differential gene expression analysis followed by their enrichment studies and pathways involved. Our set of analysis lists out the key driver genes involved in the type 2 diabetes mellitus involving the evident genes like IGF, IBP1 and our genes of interest i.e., FFAR3, SOCS1 and TNF. Enrichment studies of the shortlisted genes explains the biological significance and the pathways involved. We also predict the structure of FFAR3 as there is no 3D structure known for the receptor till date. Hence, by carrying out the following analysis, we suggest novelty by elaborative study of FFAR3 in type 2 diabetes mellitus therapy.

Keywords: FFAR3, Type 2 Diabetes Mellitus, In-Silico, Structure Prediction.

ICABB_C114_Sam

A Transcriptomic Based Meta-Analysis and Mutation Study Reveals Oncogenic Drivers and Regulatory Pathways in Pancreatic Adenocarcinoma

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ABSTRACT

Pancreatic ductal adenocarcinoma (PDAC) is one of the most lethal cancers. The absence of prominent biomarkers with a significant prognostic attribute is presently a major constraint. The study aims to determine driver genes with oncogenic mutation and their impact on the progression of the disease which can serve as molecular biomarkers for early detection. One of the most evident characteristics in pancreatic cancer revealed in the past two decades of research is that it's a disease of inherited and somatic mutations. Somatic alterations may hamper gene functions, such as, activation of oncogene and deactivation of tumor suppressor genes which disrupt and deregulate crucial pathways involved in the regulation of normal cell growth and pathways contributing to tumorigenesis. We performed a meta-analysis of PDAC samples using microarray data to identify differentially expressed genes. Screening of significantly expressed genes/proteins based on their interaction study was carried out. Enrichment and ontology analysis showed regulation of PI3K-Akt signaling pathway, focal adhesion, ECM-receptor interaction, AGE-RAGE signaling pathway in diabetic complications and activation of proteoglycans pathway in cancer. Based on these analyses, we discovered driver genes in PDAC and studied their somatic mutations using COSMIC database, such as, FN1 (Fibronectin 1) (p.P296L, p.C386F, p.2089H), IGF2BP3 (Insulin-like growth family member) (p.I54V, p.R81Q) and COL1A1 (p. V28=, p.M217L). An in-depth understanding and study of such driver genes can elucidate the establishment of substantially enhanced treatment strategies for PDAC.

Keywords: Pancreatic Ductal Adenocarcinoma, Somatic Mutation, Driver Genes, Microarray, Biomarkers, Meta-Analysis.

ICABB_C115_Him

Studying Key Regulatory Genes and Pathways Affecting Neurodegenerative Disorders Using Gene Expression Profiling Analysis

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ABSTRACT

Neurodegeneration is a condition where the irreversible loss of neurons takes place. It is one of the leading causes of disability-adjusted life-years affecting around 276 million people worldwide. These disorders include neurodegenerative disorders such as Parkinson's Disease (PD), Alzheimer's Disease (AD), Huntington's Disease (HD). While treatments are available to help relieve physical and mental symptoms linked with such diseases, there is still no way to slow down the progression of the disease. The current study explores the pathogenesis of neurodegenerative disorders through bioinformatics analysis. We performed an integrated approach to identify potential driver genes using gene expression profiling and network analysis. Differentially expressed genes (DEGs) were identified based on that a protein-protein interaction network was created. Enrichment and ontology analysis was conducted of identified driver genes showed their role in major pathways like pathways in cancer, pancreatic cancer, map-kinase cascade, Wnt-signaling pathway, Fanconi anemia pathway. Based on the analysis, we identified driver genes such as TP53BP1, NBN, BRCA2, PSMD13/PSMA8. Further analysis of these genes can serve in attaining a better understanding of the mechanisms involved in the onset and progression of neurodegenerative disorders.

Keywords: Neurodegenerative Disorders, Differential Gene Expression, Driver Genes, Pathways.

ICABB_C117_Piy

In-silico Screening of Phytocompounds Inhibiting Quorum Sensing System of *Acinetobacter Baumannii*

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ABSTRACT

Acinetobacter baumannii is a Gram-negative opportunistic bacterium which is increasingly being held responsible for nosocomial infections. *A. baumannii*, which is also a part of the WHO emphasized ESKAPE pathogens, has been implicated in respiratory infection/pneumonia, septicemia, and urinary tract infections. Pharmacological interventions based on neutralizing the virulence factors of pathogens facilitates a specific and effective protection. The cell density-dependent phenomenon which coordinates the virulent behavior of bacteria is called quorum sensing (QS). Generally, the quorum sensing circuit contains auto-inducer synthases, signal molecules (auto-inducers), transcription regulatory proteins and target genes. QS interference via quorum sensing inhibitors (QSIs) or using quorum quenching (QQ) enzymes, these have been developed to decrease the virulence of bacteria. Therefore, quorum sensing inhibitors or Quorum quenching enzymes, which mediate these activities, might possibly inhibit bacterial QS system and ultimately hinder biofilm formation. Indian medicinal plants are rich in diverse phytocompounds with anti-microbial potential: antibacterial as well as antifungal properties. In the present report we have prepared a natural compound library of phytocompounds from potent Indian medicinal plants such as amla, ginger, garlic, babchi, etc from IMPPAT database, characterized them on the drug likeness parameters and assessed their ability to interfere with key components of the quorum sensing system in *A.baumannii*. This study will help in identifying potential lead molecules of natural origin against this dreaded disease-causing pathogen.

Keywords: *Acinetobacter Baumannii*, Nosocomial Infection, Biofilm Formation, Quorum Sensing Inhibitors.

ICABB_C118_Ish

Computational Network Analysis Using Programming Language: Python

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ABSTRACT

Autism is one of the most common neurodevelopmental disorders. Till now no cure for autism spectrum disorder, intensive, early treatment can be effective. The medical treatments for the symptoms of this disorder patients are still lacking. Identification of the key target genes is one of the challenges. We used the methods in network biology to find the core gene which can be pathogenic of autism spectrum disorder. In this study, we constructed the Protein-Protein Interaction based on the genes associated with autism disorder. Further, to identify the hub proteins we used the Python programming language. The modules in the network were constructed using MCODE. The influence of hub protein in the modules were analysed using the in-house code written using Python programming language. It helps us understand the effect of key molecules i.e., hubs (*AKT1*, *ACTB*, *INS*, *CTNNA1* and *TNF*) in the autism network and provides a way to understand complex disorders such as autism. The computational code can be helpful in identifying the key regulators in any of the disease-based networks. It helps to quickly identify the pathogenic protein in complex disease networks. This study proposes a powerful code based on the network and also provides candidate proteins as a potential drug target for autism spectrum disorder. In the future, biochemical investigation of the observed hub-interacting partners could provide further understanding of the autism disorder.

Keywords: Network; Hub; Modules; Python.

ICABB_C119_Abh

Psychosomatic Disorder: Current Implications and Challenges

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ABSTRACT

Psychosomatic word is derived from the Greek word psyche means mind and soma means body. So, psychosomatic disorder can be defined as a disorder that involves both mind and body. These disorders can also be defined as psychophysiological disorders. Psychosomatic disorders become the main concern for the world in the manner of mental health. According to WHO one in every four men is suffering from a psychosomatic disorder. These disorders can affect any age group. Mostly, the rate of prevalence was found higher in females rather than that in males. Here a person can perceive physical symptoms like paralysis, blindness, or other diseases affecting the central nervous system of the body. Which leads to conversion disorders like mental disorders, emotional disturbance, and psychic disturbance. Studies also suggest that a person having psychosomatic disorder can also have heart disease, asthma, and many more. In 1978, Zegarelli et al., classified psychosomatic disorders into various types i.e. some disorders like personality disorder, psychophysiological disorder, psychoneurotic disorder, and psychotic disorder etc. In this article we are defining all different types of psychosomatic disorders, mechanisms and their effect on the body leading to progression of various diseases. Since it starts from mental illness and gradually negatively affects the whole system of the body. Currently the high precedence of psychosomatic disorder has necessitated the need for early diagnostic and better therapeutics for well-being, this may consequently be helpful to prevent, manage and treat properly. The large amount of omics data and soft computing-based technology has greater possibility to support the new biological data in modern medical science.

Keywords: Psychosomatic Disorder, Central Nervous System, Depression, Diagnosis, Mental Disorder.

ICABB_C120_Sha

System Biology Approach for Muscular Dystrophy

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ABSTRACT

Muscular dystrophy (MD) is one of the rare diseases which can be predominantly found in all age groups of people. MD are a group of more than 30 genetic diseases characterized by progressive weakness and degeneration of the skeletal muscles that control movement. Some forms of MD are seen in infancy or childhood, while others may not appear until middle age or later. Still the root cause of the number of genetically associated MD disease is not well known. The rate of progression of the disease depends upon the type of muscular dystrophy. DMD, the largest known human gene, provides instructions for making a protein called dystrophin. There are 79 exons present on dystrophin genes. Due to its largest size, DMD is more prone to mutations. There is no specific cure for MD, but various treatments are available on the basis of mutations occurring on a specific locus of a chromosome. People are not aware of muscular diseases occurring because of the phenotypic similarities of discrete types of MD that have been observed. The diagnosis of MD is still challenging. It's necessary to have awareness regarding MD among the population so that people can afford medical treatment of it before it turns into the worst form. In the first part of the chapter, we will introduce the foundational concept and key developments in MD and its various forms and the second part will touch upon the need to design a System Biology approach for MD.

Keywords: Muscular Dystrophy, Treatment, Mutation, Dystrophin, Systems Biology.

ICABB_C121_Shas

Prevalence of Rare Disease

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ABSTRACT

Rare disease affects less people among the population of specific areas. Rate of occurrence of rare disease is only one among 1000 of the population. In this review we focused on rare diseases, their most common types which can be found globally. According to the National Organization of Rare Disease (NORD) there are around 7000-8000 rare diseases found in the world. In the globe there are about 300 million people living with one of the rare diseases. There are about 70% of rare diseases which are genetically determined. Due to the low number of rare diseases found in the world, people have insufficient awareness. They are not even familiar with the fact that they are suffering from a rare disease. In most of the cases it has been observed that the longevity period of patients is very less, due to high rate of progression of disease. So, its need of an hour to escalate awareness among people, patients, and clinicians is must regarding the root cause of rare disease. Treatment of rare disease has become a challenge for the researchers due to less availability of patient's data. Thus, it's become a challenge to investigate, diagnosis of disease among cohort patients, accurate knowledge of root cause plus proper affordable medication to specific rare disease patients. Therefore, awareness towards rare diseases will make it easier to find more treatments and cures. It will result in a hope for millions of sufferers of rare diseases.

Keywords: Rare Disease, Rate of Progression, Longevity, Medication, Treatment.

ICABB_C123_Rupe

Role of Biological Networks to Understand the Diseases

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ABSTRACT

Networks, are complex collections of interactions or connections among different units, are frequently used to represent biological systems. From the molecular to the ecosystem level, every biological unit has connections with other biological entities, allowing us to describe biology using a variety of networks present in different human systems like neurological, metabolic. Previously studied multi omics required the development of more systematic data analysis approaches as well as a move away from a single gene/protein perspective. In this chapter, we highlighted the usage of network theory methods to analyse the different types of biological networks. We explained the topological and centrality properties of the networks that play an important role in identifying the key genes (hubs), functional modules, information flow, and strength of the network. The disease association analysis can be performed to understand the correlation between the key genes, module, and the disease.

Keywords: Networks; Biological Networks; Topological Properties; Centrality Measures; Nodes; Hub-Nodes.

ICABB_C124_Par

***In silico* Exploration of *Mesua ferrea* L. Phytoconstituents as Potential Inhibitors against SARS-CoV-2 Main Protease.**

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ABSTRACT

The SARS-CoV-2 (severe acute respiratory syndrome-2) is answerable for the wide-ranging global pandemic COVID-19. The consistency in the infection rate owing to the outbreak has been proven prominently hazardous across the world. *Mesua ferrea* Linn (Ceylon ironwood) is a rich source of phytoconstituents and is endowed with numerous remedial assets such as antioxidant, antimicrobial, antiviral, antitumor, immunomodulatory, and these are seen amply in Asian countries. Ten compounds of *Mesua ferrea* Linn i.e., Mesuol, Mammeisin, Mesuagin, Mammeigin, Mesuaferrol, Mesuaferrol-A, Mesuaferrol-B, Mesuaferrolone A, Mesuaferrolone B, Mesuanic acid were stipulated for virtual screening purposes against SARS-CoV-Mpro. All the phytoconstituents were percolated according to their docking score toxicity evaluation as well. Three phytoconstituents i.e. Mesuagin, Mesuol, Mesuaferrol-A were observed with topmost binding free energy; elicited finer interactions with the active site residues of SARS-CoV-2 main protease. The specified three compounds were even perceived with both non-toxic and non-carcinogenic values. The approximations reveal that Mesuol ($\Delta G_{\text{Bind}} = -33.32$ kcal/mol), is more viable in contrast to Mesuaferrol-A ($\Delta G_{\text{Bind}} = -25.13$ kcal/mol) & Mesuagin ($\Delta G_{\text{Bind}} = -25.13$ kcal/mol). It is prophesized that the current study on binding interactions of these inhibitors can hurl some valuable insights for blueprinting notably beneficial and efficacious anti-SARS-CoV-2 Mpro drugs.

Keywords: COVID-19; SARS-CoV-2 M^{pro}; *Mesua ferrea*; Drug Discovery; Phytoconstituents, Molecular Dynamics Simulation.

ICABB_C125_Anu

Virulence Factors as Drug targets in Candida Albicans

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ABSTRACT

The species of genus *Candida* are polymorphic fungi which are usually commensal but are known to cause opportunistic infections in immunocompromised hosts. *Candida* spp. infests at distinct sites of the human body having unique physiology, causing infections like vaginitis, oral candidiasis, candidemia etc. Candidemia is the most frequent hospital infection accounting for up to 15% of bloodstream infections, and *Candida* species are the main causative agents in 50–70% of systemic fungal infections. Pharmacological modulation of the proteins or traits of the pathogen which are necessary for the establishment of a disease in host. The present report is compilation of the virulence cascade of *Candida* spp. which can be exploited as potential drug targets namely: Phenotypic Switching (Y-M Shift), Adhesion, Biofilm Formation, Invasion, Hyphal Formation and Hydrolytic enzymes. We have also discussed the existing clinical regime against *Candida*, primarily comprising three cellular components - the endoplasmic reticulum, cell-wall and the cell-membrane. Five classes of established antifungal agents are handy against the invasive fungal infections viz. Azoles; Polyenes; Echinocandins; Allylamines; and Antimetabolites. These drugs act by inhibiting specific targets. By virtue of unceasing evolution, harmonious escalation in antifungal-resistance can be observed towards currently available antifungal drugs. We have also described the various reported resistance mechanisms observed to be on rise in *Candida* spp. The present review is warranted to facilitate the in-silico drug discovery initiatives against *Candida* spp. Hence, there is an urgent need to discover new drug targets and novel antifungal drugs.

Keywords: Candidemia, Virulence Factors, Antifungal Drugs, Drug Resistance.

ICABB_C126_Pari

Protein – Protein Interaction Network of Immune Inhibitory Proteins in Glioblastoma Multiforme

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ABSTRACT

Immunotherapy is an appealing treatment option due to encouraging preclinical outcomes but many potential immunotherapeutic techniques fail in clinical trials, and no immunotherapeutic medicines for GBM have been authorised to date. GBM has a lack of immunogenicity, few mutations, and a highly immunosuppressive tumour microenvironment, similar to many other difficult-to-treat diseases. Both tumour and immune cells, unfortunately, have been demonstrated to contribute to this immunosuppressive state. Furthermore, existing therapies worsen immunosuppression, which may explain why immunotherapy-based clinical trials in the GBM setting have failed. Understanding how these systems interact, as well as how to boost the anti-tumor immune response by treating local immunosuppression, will help immune-based treatments achieve better clinical outcomes. In this research work, the protein-protein interaction network of the immune inhibitory proteins that are secreted in the tumor microenvironment has been made using STRING database and visualized using CYTOSCAPE tool. Studying the PPI network helps us to identify the hub proteins and their interactions. The protein-protein interaction network of the immune inhibitory proteins of glioblastoma will help to better understand the biological pathways and mechanisms of the proteins and hence will assist in developing therapies for glioblastoma multiforme tumors

Keywords: Protein-Protein Interaction Network, CYTOSCAPE, STRING Database, Glioblastoma Multiforme.

ICABB_C127_Sri

Protein-Protein Interaction Network and Functional Characterization of Cyp450 genes in *Drosophila Melanogaster*

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ABSTRACT

Insecticide resistance has evolved in a number of insect species resulting in increasing application rates and even control failures. Understanding the genetic basis of insecticide resistance is critical for reducing its impact on agricultural yield and disease management. In insects, Cytochrome P450s genes have been linked to the development of insecticide resistance by degrading foreign chemicals into more soluble and less lethal versions. This is done either by increasing P450 expression or by altering the substrate profile or catalytic activity of the enzyme through structural modifications. Cytochrome P450 monooxygenases are multifunctional enzymes that have a role in growth, development, feeding, insecticide resistance, and plant toxicity tolerance. Protein–protein interactions (PPIs) are essential for many biological processes; therefore, constructing PPI networks gives several new insights into protein function. In the present study, the protein interaction network was built using *Drosophila melanogaster* as the model organism with abundant Cyp450 protein data, to study their functional relationship which can be serve as a reference for understanding molecular aspects of resistance mechanisms in other insects. Using literature mining and Uniprot database, we identified ~29 Cyp450 genes and their encoded proteins involved in the biological process of insecticide resistance in *D. melanogaster*. The PPI network was constructed by String (<https://string-db.org/>). Gene Ontology, Gene Coexpression and Topological properties of Cyp450 proteins were analyzed which may give a theoretical framework for researchers understanding the molecular mechanisms of insecticide resistance in controlling agricultural insect and pest species and promoting long term sustainable agricultural development.

Keywords: Insecticide Resistance, Cytochrome P450, PPI Network, *Drosophila Melanogaster*.

ICABB_C128_Kou

“Overview of the Computational Tools Used for Drug Repositioning for Covid-19”

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ABSTRACT

COVID-19 has posed an unparalleled threat to the global population, resulting in 280 million cases and around 5.4 million deaths reported as of 2021. Researchers are attempting to establish the most efficient feasible treatment lines and ways for expediting drug development and discovery procedures. As drug discovery and development is a cumbersome and expensive process, time-consuming that carries significant developmental risks, drug repositioning is an effective strategy to deal with this problem. In recent years, computational frameworks and tools have aided the drug repositioning strategy that has resulted in findings related to the repurposing of the drugs for therapeutic use, predicting similarities between FDA-approved drugs, and identifying possible drug candidates for COVID-19 treatment. These drug repurposing tools employ three distinct approaches namely, network-based, structure-based and AI-driven models that are used for increasing the accuracy and efficiency of repositioning. Though each of these approaches has its own set of challenges that restricts their implacability but nevertheless, this review focuses on the computational tools that have been developed for aiding the drug repositioning studies in COVID-19 treatment.

Keywords: COVID -19, Drug Repositioning, Computational Tools.

ICABB_C129_Var

Omics Data Analysis Using Computational Method

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ABSTRACT

Omics is a technology that includes exploring the roles, relationships, and actions of the different types of molecules that form the cells of an organism. These technologies give scientists the tools they need to analyze changes in DNA, RNA, proteins, and other biological components between species and between individuals and within a species. These molecular profiles can change in response to chemical or drug exposure in cells or tissues, and so have the potential to be used in toxicological assessments. Omics experiments are frequently carried out in high-throughput assays, which generate massive volumes of data on the functional and/or structural changes that occur within the cell. These novel approaches have helped us to make tremendous progress in our understanding of the molecular responses to cell and tissue injury, as well as disturbances in functional cellular systems. The stress resistance of sorghum and its resistance molecular mechanism, has a considerable significance in the research field. Sorghum also known as great millet is an ancient cereal grain belonging to the Poaceae family. It is naturally gluten free and is high in dietary fiber, proteins, minerals, antioxidants, vitamin B and phenolic components and has various applications. It is a model plant for proteomics and genomics research because of its natural drought tolerance qualities. Using an omics-driven technique, we used the source galaxy server to identify a list of genes associated with various conditions such as drought, stress tolerance, etc. of the medicinal plant *Sorghum bicolor*.

Keyword: Omics, Sequencing, Sorghum bicolor, Galaxy Server.

ICABB_C131_Shi

In-Silico Study of Selected Medicinal Phytocompounds for Their Mitocan Activity

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ABSTRACT

Mitochondria are potential targets for triggering death in cancer cells. Also, there is a diverse range of mitochondria targeting drugs known for their effectiveness and suggested to be used in anti-cancer therapies. The mechanism of action of mitochondrial-targeted anti-cancer drugs relies on their ability to disrupt the energy-producing systems of cancer cells, leading to increased ROS followed by activation of apoptosis pathways inside the cancer cells. The outcomes of various studies have led to the invention of “mitocans”, a category of drug known to precisely target the cancer cell’s mitochondria. Hexokinase II (HK2), a glycolytic enzyme is commonly overexpressed in most cancer types and located in the outer membrane of mitochondria. The overexpression of HK2 is reported to promote the survival of cancer cells by facilitating the constant ATP generation and protecting the cancer cell against apoptotic cell death. So, our research aims to explore the HK2 targeting potential of phytocompounds from the selected anticancer herbs. We selected phytocompounds such as zingerone, coumarin and withanolide E to assess their mitochondria targeting and/or HK2 targeting ability. Using Autodoc Vina, these compounds were docked against HK2 as well as their drug-likeness were also predicted. The findings show that by targeting HK2, all three natural chemicals studied might be potential natural mitocans. To verify the findings, more experimental research (*in vitro* and *in vivo*) are needed.

Keywords: Cancer, Mitochondria, Mitocan, Phytocompounds, Hexokinase II, ROS.

ICABB_C132_Rin

Molecular Analysis of dUTPase of *Helicobacter Pylori* for Identification of Novel Inhibitors using In Silico Approach

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ABSTRACT

Helicobacter pylori is the most common chronic bacterium, affecting nearly half of the world's population. Various gastrointestinal diseases, including gastritis, peptic ulcers and gastric cancer have been associated with *H. pylori* infection. Due to emergence of drug resistant strains of *Helicobacter*, there is an urgent need for development of novel therapeutics to combat the infection. A ubiquitous enzyme, Deoxyuridine 5-triphosphate nucleotidohydrolase (dUTPase), is considered as first line of defence against mis-incorporation of uracil into DNA, and essential for genome integrity. Absence of dUTPase triggers an elevated recombination frequency, DNA breaks and ultimately cell death. Hence, dUTPase can be considered as a promising target for designing of new lead molecules in *H. pylori* treatment. In this study, the three-dimensional model of the target protein was generated by comparative modelling and validated using various cheminformatics servers. Next, dUTPase inhibitors were identified through high throughput virtual screening and molecular docking approach using knowledge-based inhibitors and DrugBank database. Finally, top ten hits were scrutinised based on binding affinities, molecular interactions and protein-ligand fingerprint analyses. For second level of screening, the MM-GBSA binding free energy calculation of the docked complexes was performed. Different pharmacokinetics and drug-likeness parameters were also checked, favouring the drug potentiality of top candidates. Therefore, our screened molecules may be potential lead molecules for effective inhibition of *H. pylori* dUTPase protein.

Keywords: *Helicobacter pylori*, dUTPase, Molecular Docking, High throughput Virtual Screening, MM-GBSA.

ICABB_C133_Dece

Molecular Docking study to Investigate Interaction of Vasicine Molecule with TLR4

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ABSTRACT

Toll-like receptor 4 (TLR4), is an innate immune receptor which recognizes pathogen-associated molecular patterns (PAMPs) and has been considered as an important strategy for treating respiratory disorders. It has also been known to trigger the production of type I interferons and proinflammatory cytokines to combat infection. *Adhatoda vasica* is used in the indigenous system of medicine in India. The alkaloid Vasicine, isolated from extract of the leaves of *A. vasica*, is reported for bronchodilatory, respiratory stimulant effects. It is responsible for most of its antioxidant, anti-inflammatory and bronchodilatory activities of *A. vasica*. Overactivation of TLR4 leads to disruption of immune homeostasis and increases the risk for inflammatory disease. In the present study we looked into its anti-inflammatory properties and mechanisms in acute respiratory distress syndrome via molecular docking experiments where structure-based interactions between vasicine and TLR4 were investigated. The authors have discovered that vasicine could bind in the active site of TLR4 with a good binding affinity, indicating that it may be a potential inhibitor and may work as an anti-inflammatory agent to manage various diseases caused due to inflammatory pathways involving TLR4 receptor.

Keywords: TLR4, Vasicine, ARDS Molecular Docking.

ICABB_C134_Man

***In silico* Analysis to Investigate and Explore the Interaction of Ellagic Acid, a Potential Molecule for Anticancer Activity, with PI3 Kinase**

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ABSTRACT

Phosphoinositol-3-kinase has been widely reported to be a potent anti-cancer target when employed for cancer therapy. Ellagic acid is naturally occurring polyphenol found in fruits such as *Punica granatum*, *Prunus avium*, *Vaccinium sect. cyanococcus* etc. Prior research studies have clearly reported regulatory attributes associated with ellagic acid in regards to cell viability, cell cycle regulation and apoptosis. The structure-based interaction between ellagic acid and PI3K was investigated using active site molecular docking, which further highlighted the receptor-ligand binding profile along with 2D plots illustrating the biochemical interactions of the interacting residues. One of the most essential intracellular pathways, phosphoinositol-3-kinase (PI3K)/AKT/mammalian target of rapamycin (mTOR) signalling, is considered a master regulator for cancer. We discovered that ellagic acid binds at the active site of PI3K-with a good binding affinity, indicating that it may be an acceptable potential inhibitor for the enzyme and may be beneficial in dysregulation of pathways leading melanoma and non-melanoma skin tumours.

Keywords: Phosphoinositol-3-kinase, Ellagic acid, Skin cancer, Molecular docking, Binding Profile.

ICABB_C135_Chrr

***In-Silico* Molecular Docking and MD Simulation Analysis of Flavonoids as Potential Inhibitors of SARS CoV-2**

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ABSTRACT

The global pandemic that the world is currently witnessing, COVID-19, even with vaccines available, the test positivity rate (TPR) tends to remain highly threatening. This research focuses on identifying flavonoids, previously known for their broad-spectrum antiviral properties which can be potential drug candidates of the coronavirus. A total of 25 flavonoids (downloaded from PubChem database) are docked against 10 target proteins (downloaded from PDB database) of SARS Cov2 using PyRx docking platform which has inbuilt OpenBabel and Vina applications. The target proteins include NSP15 hydrolase, RDRp/RNA complex, main protease (Mpro), 3C-like protease, NSP 7, NSP 13, spike glycoprotein, ORF8 accessory protein, NSP 5, and NSP 9. They are screened according to their binding affinity values and the filtered phytochemicals are then subjected to various analyses including ADME properties (preADMET, swissADME), bioactivity score, and molecular properties (molinspiration), drug-likeness (preADMET), lipophilicity, water solubility, and pharmacokinetics (swissADME). The receptor-ligand interactions and the amino acid positions are obtained using Discovery Studio Visualiser. Molecular Dynamic Simulation analysis is performed to analyze the ligand stability of the screened compounds in target protein crystal structures. Density functional theory (DFT) analysis is performed to study the phytochemical reactivity properties and how efficiently they act when used against the target domains. Out of the 25, 3 compounds showed the best scores and more probability for drug action. The research herein provides new possibilities for *in vitro* and *in vivo* analyses of the proposed ligands to develop new drugs against coronavirus.

Keywords: NSP, ADME, Receptor-Ligand Interaction, Binding Site Pockets, MCDM.

ICABB_C136_Poo

In-Silico Investigation of Natural Allosteric Compounds towards Drug Efficacy Enhancement

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ABSTRACT

Allostery is one of the most direct and efficient techniques to control the functioning of biological macromolecules. Because of the few particular features of allosteric modulators, such as: excellent selectivity and low toxicity, allostery is gaining more attention in the field of drug development. The knowledge of various such features of allosteric entities (allosteric proteins and their allosteric sites), has made considerable gains due to the technological advancements in allosteric investigations. These characteristics are important in the development of the allosteric notion as well as in the prediction of allosteric interactions. In the present study, the authors wish to depict the role of allosteric modulators in increasing the efficacy of FDA approved anticancer drugs, so as to reduce the devastating side effects and to increase the efficacy of the drug molecules. Furthermore, the virtual screening along with pharmacophore modeling of the allosteric compounds may facilitate the insight of molecular interaction, having possibilities of dose optimisation of the drug molecule.

Keywords: Cancer, Allosteric Compound, Allosteric Sites, FDA approved Drug, Bioinformatic Tools.

ICABB_C137_Ron

In-silico Studies of Flavonoids as Potential Inhibitor of *Rhizopus Delemar*

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ABSTRACT

Fungal diseases are mostly neglected by man even though they cause a huge rate of death every year. Antifungal drugs are toxic and are known to have a lot of side effects. There are records of using herbal medicines to treat fungal disease in the Indian traditional Ayurvedic treatments. This research focuses on finding flavonoids which can be used as a potential drug candidate against *Rhizopus delemar* which causes black fungus disease. The phytochemicals are selected based on their previously known antifungal properties. A total of 25 flavonoids were docked against the target protein Lanosterol 14- α Demethylase of *Rhizopus delemar*. Flavonoids are screened according to their binding affinity values and then the filtered flavonoids are subjected to various analyses including toxicity, ADME properties (Pre ADMET, Swiss ADME), bioactivity score and molecular properties (molinspiration), drug-likeness (pre ADMET), lipophilicity, water, water solubility and pharmacokinetics (Swiss ADME). The receptor-ligand interactions and the amino acid positions are obtained using Discovery Studio Visualizer. Out of the 25, 3 compounds showed the best scores and more probability for drug action. The research herein provides new possibilities for *in vitro* and *in vivo* analyses of the proposed ligands to develop new drugs against *Rhizopus delemar*.

Keywords: Black fungus, flavonoids, Molecular docking, ADME.

ICABB_C138_Anam

Computational Screening of nsSNPs in Human Friedreich Ataxia Protein *frataxin*

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ABSTRACT

Friedreich ataxia (FA) is a rare inherited disease that causes progressive nervous system damage and movement problems. It usually begins in childhood and leads to impaired muscle coordination (ataxia) that worsens over time. It is due to the defect or mutation in FXN gene, which carries the genetic code for a protein called *frataxin*. This nuclear gene encodes a mitochondrial protein, which belongs to the FRATAXIN protein family. These proteins regulate the mitochondrial iron transport and respiration. The expansion of intronic trinucleotide repeat GAA from 8-33 repeats to >90 repeats results in Friedreich ataxia. The characteristic changes happening because of the genetic variations in *frataxin* is not well studied. Systematic *in-silico* approach investigated the role of 151 non-synonymous Single Nucleotide Polymorphism (nsSNPs) in *frataxin* and predicted its crucial pathogenic effect on the structure and function. Various sequence and structure-based servers like SIFT, PolyPhen-2, PANTHER, PhD-SNP, PROVEAN, PMut, SNAP-2, MutPred-2 and SuSPect analyzed 5% of nsSNPs as pathogenic. Further, these nsSNPs were investigated at structural level. These nine nsSNP (Y95C, Y95H, H177Y, D139Y, T133A, G170W, D139V, G138R, and V174A) substitutions were predicted as deleterious and crucial for protein function. Among these nine nsSNPs, **Y95C** and **Y95H** showed highest phenotypic effects to *frataxin* using SuSPect tool. These mutants could affect the mitochondrial ISC enzymes activities and mitochondria ultrastructure. This study identified **Y95C** and **Y95H** as key variations using various sequence and structure-based analysis that could affects the function of *frataxin*. Ensemble of structural conformation in *frataxin* due to mutation, which may contribute to the milder clinical phenotypes in the patients. Mutation causes misfolding of the native chain with consequent reduction of the protein concentration in the patient and possible mechanism of disease.

Keywords: Friedreich ataxia, Frataxin, nsSNPs, Deleterious, Phenotype.

ICABB_C139_Rup

The Current Genetics of Amyotrophic Lateral Sclerosis (ALS): Since 2015

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ABSTRACT

Amyotrophic lateral Sclerosis (ALS) is an incurable progressive neurodegenerative disease mainly observed and distinguished by the loss of motor neuron both upper and lower. It is of two types, familial and sporadic ALS with an occurrence of 1-5 for every 100,000. However major cases are sporadic ALS (sALS), but only 5-10% are associated with a genetic mutation which is inherited through family called familial ALS (fALS). In last decades, various research findings, provides understanding the importance of the diseases causing genes and their variants in ALS. Several mechanisms were suggested for the pathogenesis of ALS, including protein mutations, misfolding, aggregation, defects in transportation etc. ALS is notified to have a large number of potential genes considered as causative or disease modifying. Mainly SOD1, C9ORF72, FUS, and TARDBP were the most disease-causing variant in comparison with others minor involvement genes. There are many factors that may add to the missing heritability in ALS, limitations due to technical issues as well the inherently complex nature of the disease. In this review article, we are providing the information about novel genes reported since 2015; such as TBK1, C21ORF72, NEK1, CCNF, SCFD1, ANXA11, TIA1, KIF5A, LAGALS, GLT8D1, DNAJC7, ARPP21 were identified by genome-wide association studies, whole genome studies, or exome sequencing technologies. Each of the novel gene's/protein associated with one or more molecular pathways known to be involved in ALS. These genetic discoveries have identified key disease pathways that are therapeutically testable and could potentially lead to the development of better treatments for people with ALS.

Keywords: ALS, Genes, Pathophysiology, sALS, fALS.

ICABB_C141_Bisw

Structure-Based Virtual Screening and Molecular Dynamics Simulation Study Reveals Potent Multi-Target Inhibitors for the Treatment of SARS-CoV-2 Infection and Related Health Consequences

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ABSTRACT

Coronavirus 2019 (COVID-19) has triggered a worldwide pandemic with high mortality rates affecting almost every country on the planet. The absence of an effective vaccine or potentially hostile to viral medications against SARS-CoV-2, the causative agent, seriously impacted the reaction to this novel coronavirus. As a result, the availability of effective and new treatment medicines is urgently required. In this high-throughput virtual screening study including molecular docking, dynamics, and ADME properties analysis, we have screened natural compounds from the Natural Product Activity and Species Source (NPASS) database, FDA drugs, and phase-1 passed clinical trial drugs against therapeutic protein targets essential for the survival of SARS-CoV-2. The result showed multi-target natural and FDA-approved binders known for having antibacterial, antiviral, anti-inflammatory, antidiabetic, and cardioprotective properties, showing higher docking scores and binding energy with at least three or more therapeutic targets. Molecular dynamics simulation analysis showed stable interaction of the protein and inhibitor complexes inside the virtual biological environment and could effectively inhibit the SARS-CoV-2 infection. Further in-vitro, in-vivo, and clinical research will determine the optimal allocation of these medications to treat COVID-19.

Keywords: COVID-19, SARS-CoV-2, Multi-Targeting Compound, Molecular Docking, Molecular Dynamics.

ICABB_C142_Angn

Population Coverage-Based Analysis and Screening of Vaccine Candidates against *Salmonella Typhi* using Immunoinformatics Approach

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ABSTRACT

Typhoid fever is a public health problem caused by *Salmonella typhi* infect more than 22 million peoples every year that resulted into 500000 deaths annually. There are smaller numbers of antibiotic treatment available as drug-resistant typhoid bacteria have become more common in many regions of the world, including East and Southeast Asia, Africa, the Caribbean, and Central and South America. Current licensed vaccines against typhoid fever contain capsular polysaccharide of the *S. enterica* var. Typhi Vi antigen and live attenuated *S. enterica* var. Typhi strain Ty21a which are moderate in efficacy, provide protection of short period of time and unavailable to children below 5 years of age. Therefore, more effective novel typhoid fever vaccine is required that can provide global population coverage including multi-epitope-based vaccine due to its tailored immunogenicity, biodegradability and less adverse effect. The present study explored the immunoinformatics approach to select vaccine candidates against *S. typhi* based on predicted population coverage (PPC) of available epitopes from publically available immune epitope database IEDB (<https://www.iedb.org>). Initially, a total 122 HLA class I and 15 HLA class II restricted epitopes were retrieved from IEDB against 99 antigenic proteins of *S. typhi*. The IEDB based PPC tool found world population coverage 99.65%, 77.97% and 99.92% against the selected epitopes of individual MHC class I, MHC class II and combined (MHC class I+MHC class II), respectively. Finally, on the basis of more than 94% PPC values, 7 antigenic proteins viz. alternative bacteriophage tail fiber C-terminus (96.17%), Anaerobic sulfite reductase subunit A (94.23), conserved hypothetical protein (94.86%), hypothetical protein (94.11%), phage integrase (94.89%), putative exported protein (94.41%) and Putative ribonucleoside-diphosphate reductase alpha subunit (94.46%) were selected for further evaluation as vaccine candidates. In conclusion, immunoinformatics tools can be used as a cost-effective and convenient approach for screening of vaccine candidates against *S. typhi* to minimize the number of wet lab experiments needed in the developmental globally effective vaccine.

Keywords: Epitope, Immunoinformatics, Vaccine, Typhoid.

ICABB_C143_Pay

Endometrial Receptivity Deregulated Genes Corresponding to Recurrent Implantation Failure Implementing Machine Learning Methods

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ABSTRACT

Endometrial receptivity (ER) is the ability of the endometrium to accept and implant competent embryo to the uterus lining. One-third of implantation failures occur due to inadequate ER leading to recurrent implantation failure (RIF). Most of the couples are diagnosed with RIF as they experience infertility even with three high quality embryos transfer for IVF. However, non-receptive to receptive state transition and ER deregulated genes are poorly understood. Diagnostic tools like Endometrial receptivity array and rsERT have shown machine learning implementation remarkably improve pregnancy outcome. Therefore, machine learning applied on transcriptomics data can enhance our understanding of ER and elucidate the curial genes involved. Here, we have retrieved the CEL files from Gene Expression Omnibus (GEO) accession ID GSE26787 with 5 control and 5 RIF samples. The data was pre-processed and analyzed using gcRMA method and limma R package respectively. Differential gene expression (DGE) analysis was performed resulting in identification of 381 significant genes with p-value ≤ 0.05 and fold change ≥ 2 threshold. Here, we present a hybrid approach for identifying biomarkers by prioritizing and re-ranking the DEGs list using machine learning by implementing four distinct feature selection techniques namely Mutual information feature selection, ANOVA F-value (f_classif), SelectFromModel (LinearSVC) and Pearson correlation. The feature selection approaches resulted in identification of top 20 genes over-lapping in the four methods, further selected for gene ontology analysis using PANTHER to highlight their biological functions. Determination of the biomarkers and their function will help us diagnose and treat infertile couples more efficiently.

Keywords: Transcriptomics Analysis, Endometrial Receptivity, Recurrent Implantation Failure, Machine Learning, Women Infertility.

ICABB_C144_Jan

Sex-Specific Transcriptomic Differences in Pulmonary Tuberculosis Patients

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ABSTRACT

Tuberculosis is a leading Infectious Disease killer, claiming millions of lives every year. In most countries, more men develop active TB— there exists almost a 2:1 ratio of male-to-female patients. This difference could be attributed to either the contrasting physiological and genetic landscapes in men and women, non-uniform access to healthcare, or other lifestyle factors, such as nutrition, alcohol intake or smoking. Using transcriptomic datasets from different backgrounds, we investigated if there is a biological basis for these differences by determining whether or not sex influences gene expression in PTB patients using statistical approaches. We filtered samples from patients with active pulmonary tuberculosis (<6 months from the start of anti-tuberculosis therapy) and then looked at the differentially expressed genes in men versus women across cohorts. We found differences in several important pathways, including inflammatory responses and interferon signaling. Our results may have implications on the mechanistic understanding of Tuberculosis and the blood transcriptome-based tests currently under development for TB diagnosis.

Keywords: Blood Transcriptomics, Pulmonary Tuberculosis, Sex-specific Differences, TB Transcriptomics.

ICABB_C145_Bhum

SARS-CoV-2 and Emerging Variants of Concern in India

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ABSTRACT

Despite significant efforts by academics, physicians, pharmaceutical firms, and others from across the world in creating effective vaccines and treatments against the renegade virus, the SARS-CoV-2, the causal agent of coronavirus illness 2019 (COVID-19), remains uncontrolled. To better understand the evolution and spread of the SARS-CoV-2 virus, scientists from around the world are analysing its genetic mutations in real time. This approach has been proved to be very efficient during the Ebola virus epidemic in West Africa and the Zika virus spread in Brazil. Extensive surveillance and improved immunizations are essential in disarming these variations and stopping disease transmission. Detailed bioinformatic analysis of the sequence data helps to identify variants and to evaluate potential impacts on critical SARS-CoV-2 countermeasures, including vaccines, therapeutics, and diagnostics. Based on analysis these variants can be classified as Variants of concern, interest and variants being monitored. To apply such approach for investigating the evolution of SARS-CoV-2 researchers from different regions have collected sequences from the online databases such as GISAID and have analysed them by doing multiple sequence alignment and constructing phylogenetic tree using bioinformatic tools like MEGA, MAFFT and IQTREE. Monitoring the genomic diversity of SARS-CoV-2 using bioinformatic tools in these regions exposed the virus's circulating lineages, changes over time, and, in the case of substantial sampling, might be a viable tool to assess how interventions impact viral evolution. As a result, additional genome sequencing and analysis with linked clinical data are required to assess functional relevance and better forecast disease dynamics, which may aid in controlling the COVID-19 pandemic.

Keywords: SARS-CoV-2, COVID-19, Variants, Genomic Surveillance.

ICABB_C147_Sidh

Virtual Screening for Identification of Novel Drug for Parkinson's Disease

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ABSTRACT

Virtual screening using computational methods was used to identify new lead molecules against Parkinson's disease. Ligand based pharmacophore model was generated with a fitness score of 72.77. The 3 drug molecules used to generate the pharmacophore model were Droxidopa, Istradefylline and Apomorphine. The model was validated using an active set (10 compounds) and inactive set (49 compounds) of compounds. Further the model was screened against the Pubchem database to identify compounds with similar pharmacophore features. 35 compounds were obtained as hits after screening. These compounds were screened for their binding affinity in the protein targets like Dopamine receptors, Adrenergic receptors, Adenosine receptors using docking studies. The compounds which scored above -5KJ/mol were chosen and subjected to pharmacokinetic properties prediction including toxicity studies. The compounds with drug like properties and those which could cross the blood brain barrier were filtered. In order to validate the stability of the ligand-protein complexes they were undergone molecular dynamics simulation studies. The stability of the complexes was analysed using Root mean square value (RMSD) and Root mean square fluctuation value (RMSF).

Keywords: Apomorphine, RMSD, RMSF, Pharmacophore.

ICABB_C148_Divi

Docking Study for Identification of Potential Inhibitors from *Jasminum Grandiflorum* L Against Covid 19 Main Protease

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ABSTRACT

The spread of the worldwide COVID-19 pandemic and the absence of suitable treatment in this critical circumstance we need to find a permanent solution to cure this disease. In the current study, using molecular docking we found new probable inhibitors of COVID-19 by molecules from *Jasminum grandiflorum* L which is popular for its medicinal properties in South Asia, Arabian Peninsula, East and Northeast Africa, Yunnan and Sichuan regions of China. Many virus-based drug targets (targeting structural protein and non- structural protein) have been proposed by the scientists for preparing the antiviral drugs. The main protease's (Mpro) structure in COVID-19 gives an extraordinary chance to recognize potential drug candidate for the treatment because of its high specificity. Mpro has three domains that are domain I, domain II and domain III. The domain I and II are β barrel domains whereas the domain III shows a α -helical structure. Focusing on the main proteases present in COVs (3CLpro/ Mpro) (PDB ID 6LU7); docking of compounds from *Jasminum grandiflorum* L. was performed using the AutoDockTools 1.5.6rc3 software. Benzyl benzoate (-6.63 kcal/mol) gives score close to the synthetic drug Chloroquine (-6.88) and better than the synthetic drug favipiravir (-4.58 kcal/mol). Cis-3-Hexenyl Benzoate (-6.28 kcal/mol) gives score a lot better than the synthetic drug favipiravir (-4.58 kcal/mol). Other ligands like Benzyl acetate (-5.03 kcal/mol), Jasmine lactone (-5.60 kcal/mol), Indole (-4.83 kcal/mol), Trans-Jasmone (-5.12 kcal/mol), Cis- Jasmone (-5.61 kcal/mol) and Phenylethyl Acetate (-5.68 kcal/mol) also show better results than favipiravir (-4.58 kcal/mol). Benzyl benzoate gives the lowest energy that is -6.63 kcal/mol in comparison to the other docked ligands from *Jasminum grandiflorum* L. The present study identified plant-based compounds that can be further investigated to testify the medicinal use and to encourage preventive use against coronavirus infection.

Keywords: COVID-19, *Jasminum Grandiflorum* L, Docking.

ICABB_C149_Shub

Pre-Implantation Embryonic Development: Current Status and Future Prospects

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ABSTRACT

Due to the increase in the prevalence of infertility, several assisted reproductive technologies (ART) including IUI, dose administration to trigger ovulation, and IVF are becoming more popular. Moreover, there are a few challenges with IVF which are still unclear, such as the transfer of multiple embryos, the selection of apparently healthy embryos, the inadequate knowledge of embryonic development, which can lead to multiple pregnancies and associated complications or chromosomal anomalies. A variety of factors, which are inherited from parents, have altered embryonic development and affected translation and cytokinesis. Additionally, identifying epigenetic and genetic factors is essential because they can alter ploidy and gene expression. Usually, embryologists have preferred to use the pre-implantation genetic testing (PGT) invasive technique to minimize the risk of transferring chromosomally aberrant embryos and to detect aneuploidy in embryos. Although noninvasive techniques are considered to be safer than invasive, invasive removal of cells from preimplantation embryos may alter embryo development. As per recent research, variations in multiple factors such as gene expression patterns and occurrence of chromosomal mis-segregation among different species and developmental stages may serve as a barrier that prevents certain findings from being applied to embryo development. The main focus is to create a technique that would be faster, accurate, and noninvasive. The introduction of Artificial intelligence (AI) or machine learning in the field of IVF can be the new approach to automate embryo assessment and eradicate the complexities of manual techniques. In this review, we contribute to a better understanding of mammalian preimplantation embryos and explain how future studies and modern improvements can be leveraged to better pre-implantation embryos.

Keywords: ART (Assisted Reproductive Technologies); IVF (In-Vitro Fertilisation); Pre-Implantation Genetic Testing (PGT); Artificial Intelligence (AI); Chromosomal Anomalies.

ICABB_C150_Tanu

Laricitrin as a Potential Phytoconstituent for Drug Designing of Hypertension

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ABSTRACT

Hypertension or high blood pressure is a rising health concern since it is a major risk factor for cardiovascular disease and related complications, such as kidney damage and heart attack. Renin Angiotensin Aldosterone System (RAAS) plays integral role in regulating the blood pressure. Renin (RNE), Angiotensin converting enzyme (ACE), and Angiotensin –II receptor (ATR) are key proteins of RAAS. The study conducted *in silico* to analyze inhibitory activity of Phytoconstituents of *Lippia nodiflora*. The crystallography structure of the ACE, Renin and ATR were downloaded from rcsb.org in the .pdb format. Phytoconstituents of *L. noddiflora* were taken as ligand molecules. Structures of Ligands were obtained from PubChem Database. The molecular docking analysis was conducted in the PyRx tool with AutoDock vina scoring functions. Amongst the phytoconstituents of *L. nodiflora*, Laricitrin shows best binding energy of –12.1 Kcal/mol. The results indicate that Phytoconstituents of medicinal plants can prove to be a potential antagonist to cure hypertension.

Keywords: Laricitrin, Hypertension, RAAS.

SESSION II
Medical
and
Microbial Biotechnology

ICABB_M201_Arch

Mechanism of Telomerase Regulation in Response of Arsenic in Liver Cancer: A Promising Green Therapeutic Target in Liver Cancer Treatment

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ABSTRACT

Nowadays cancer is a matter of serious concern for this planet. Among them hepatocellular cancer (HCC) is the fifth most common cancer in the world with only 5-year survival rate of less than 5% despite of large number of treatment option available all around the world. The incidence of HCC is at least one million new patients per year. A hallmark of advanced malignancies is the ability for continuous cell divisions that almost universally correlates with the stabilization of telomere length by the reactivation of telomerase. Herbal compounds having broad-spectrum activity against several infectious diseases might even be evaluated for treating various types of cancer cells. Yes! Arsenic exposure has been associated with various deleterious endpoints including cancers, but neither of the mechanisms has been clearly understood. The main goal of this project is to analyze the effect of different doses of arsenic alone or in combination with selected natural compounds on cellular cytotoxicity as well as telomerase expression at different time interval. We found that, arsenic treatment resulted in cell death with its increase doses (i.e $\geq 10\mu\text{M}$) but at its lower dose (i.e $\leq 4\mu\text{M}$) along with natural counterpart showing a good anti-cancerous effect with least harm on normal liver cells, confirmed by microscopic examination, cytotoxicity assay as well as telomerase expression. Our study depicts that arsenic exert its effect by modulating Telomerase expression in certain types of cancer. The proposed research may be useful in determining the therapeutic potential of arsenic alone and in combination with natural compounds.

Keywords: Telomerase Inhibitors, HCC, Arsenic trioxide, Anticancer.

ICABB_M202_Bhaw

Neurological Comparison in Between Schizophrenia and Bipolar Disorder

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ABSTRACT

Schizophrenia has a variety of symptoms and epidemiological features. Schizophrenia is characterised with many structural and neuropsychological disability in the brain. Obstetric complications have been shown to increase the risk of schizophrenia but not bipolar disorder. This paper mentions some of the factors that differentiate these two. This includes white matter changes found in both, which have a neuro-biological basis and enable to interpret these disorders. A major goal is to identify brain functioning involved in chances of development of mental disorders. Another notion is distorted and excessive neural responses to reward are essential features of schizophrenia and bipolar disorder, respectively, as per the research. Along with Neurocognitive impairment that is thought to be on a severity scale across schizophrenia and Bipolar, possibly reflecting a gradient of neurodevelopmental load. The identification of brain anatomy shared by rationally identical individuals with bipolar and Schizophrenia may be crucial in understanding their shared neurobiological deficits. Other difficulties that people with Schizophrenia and Bipolar face include difficulties in self-evaluation of cognitive and functional performance. We would talk about how non-random mating in parents with bipolar disorder or schizophrenia raises population-level genetic diversity among the offspring generation and produces familial (threat) environments in children and adolescents. Due to common symptoms and identical familial patterns, neurological disorders are often misinterpreted based purely on clinical interviews. Until now, there's been no valid and objective measures used to detect and distinguish between neurological disorders.

Keywords: Schizophrenia; Bipolar Disorder; Neuropsychological Disability; Neurocognitive Impairment.

ICABB_M203_Hari

Role of p300, a Histone Acetyltransferase Enzyme in Osteoblast Differentiation

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ABSTRACT

Bone is a tough, vital and dynamic connective tissue which undergoes constant remodeling throughout an organism's life. Bone-forming osteoblasts respond to various hormones, cytokines, and growth factors and synthesize the extracellular matrix components. Runx2, a master transcription factor, is crucial for ossification by stimulating the activation of osteoblast differentiation marker genes, including type I collagen, alkaline phosphatase, and osteocalcin, to undergo expression. Coactivators like p300, CBP and PCAF, etc., tightly regulate osteoblast differentiation via Runx2. There is growing evidence indicating the role of p300, which possesses histone acetyltransferase activity (HAT), in regulating histones and transcription factors like Runx2 during osteoblast differentiation. In the current review, we aim to deliberate the role of p300 at the molecular level, emphasizing the importance of its HAT activity during osteoblast differentiation. Further, this review intends to highlight the regulation of p300 at multiple levels, including epigenetic, post-translational and by ncRNA's that might exert an indirect influence on bone formation.

Keywords: Osteoblasts, Differentiation, Runx2, p300, Epigenetics, Histone Acetyltransferase.

ICABB_M204_Apar

Telomere Independent Mitochondrial Functions of Human Telomerase (hTERT) in the Regulation of Cell Cycle and Redox Homeostasis

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ABSTRACT

Cancer is a common term for a large group of diseases that can affect any part of the body. It is a leading cause of death worldwide—accounting for nearly 10 million deaths in 2020 (WHO). The hallmark of cancer immortality is the limitless replicative potential. The end replication problem where the ends of linear DNA cannot be replicated entirely during lagging strand DNA synthesis is resolved due to the presence of telomere and the reverse transcriptase called telomerase. 85-90% of cancer cells have telomere length maintained by telomerase reactivation. Interestingly, recent studies have shown that the catalytic subunit of human telomerase, hTERT, is involved in various non- telomere related functions (non-canonical functions), including translocation to mitochondria upon stress. Even though several studies have identified the potential involvement of telomerase in the tumorigenesis process, complex diversifying mechanisms and the interacting partners that govern diverging functions such as cell cycle and cell death by hTERT is not well defined. It is unclear whether mitochondrial translocation is signalling for mitochondrial oxidation or permeabilisation or it is protective in nature. Usually, telomere length shortening is a slow process. A challenge in dissecting telomere dependent and independent cancer progression events is the lack of a model system that supports the long-time fate of the cell with respect to the telomere targeting. 10% of cancer cells are independent of telomerase for the telomere length maintenance; here, we use a telomere independent cell and overexpress hTERT to see the changes in the cell cycle and cell death. The real-time time analysis of mitochondrial oxidation and telomerase translocation have to be studied in cells after shRNA silencing and overexpression of telomerase.

Keywords: hTERT, Telomere, Translocation, Tumorigenesis.

ICABB_M205_Ursh

Stem Cell-Derived 3D Cerebral Organoids: A Potential Model for Alzheimer's Disease

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ABSTRACT

Alzheimer's disease (AD) is a neurodegenerative disorder that is currently incurable. The main pathological features of AD include extracellular accumulation of amyloid beta (A β) and intracellular accumulation of hyperphosphorylated tau proteins. A β and hyperphosphorylated tau proteins deposit in the neuronal cells as amyloid plaques and neurofibrillary tangles (NFTs), respectively. Several model systems such as animal models and monolayer cellular cultures have been extensively used in AD research. However, their limited application impedes our understanding of the pathophysiology of the disease and the subsequent drug discovery. With more than 55 million patients internationally, AD is considered a global health crisis that calls for a novel model system. Recently, three-dimensional (3D) cerebral organoids derived from human stem cells have emerged as a new tool to recapitulate AD pathogenesis. The present review discusses the advantages of 3D cerebral organoids over animal and two-dimensional (2D) cellular models, as well as elaborates on the use of AD cerebral organoids to model A β and tau pathology. In addition to the applications and future potential of this technology, possible solutions to certain limitations of cerebral organoids are also highlighted.

Keywords: Alzheimer's disease (AD), Cerebral Organoids, Disease Modelling, Stem Cells, Three-Dimensional (3D) Culture, Pathogenesis.

ICABB_M206_Priy

Telomeres and Telomerase Role in Heart Diseases, Aging and Regeneration

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ABSTRACT

Telomeres are G-rich tandem DNA sequences that are double-stranded (i.e., TTAGGG) found at the ends of eukaryotic chromosomes that gradually shrink with each cell division. Aging, inflammation, and oxidative stress, all of which have been associated with cardiovascular disease, accelerate shortening of telomeres and result in cellular senescence. Short leukocyte telomere length (LTL) has been associated to cardiovascular risk factors such as smoking, obesity, sedentary lifestyle, and hypertension in clinical investigations. Atherosclerosis is one of the most prevalent age-related cardiac diseases. In atherosclerotic plaques, reduced telomerase activity and short telomere length in leukocytes have been reported and linked to plaque instability, resulting in acute myocardial infarction. Telomerase prevents telomere shortening by conserving and lengthening telomeres. It consists of a catalytic telomerase reverse transcriptase (TERT) component and a telomerase RNA component (TERC) that serves as a template for the assembly of new telomeric DNA. Telomeric DNA shortening is thought to contribute to organismal aging by promoting genomic instability, replicative senescence, and cell death. The tissue regeneration potential of the aged myocardium is hindered by telomere shortening and senescent cell proliferation, which contributes to systolic or diastolic heart failure. TERT and telomerase have emerged as novel targets to treat cardiovascular aging and its accompanying inflammatory signaling, given that statin medication and endurance exercise both increase TA. Telomerase plays a significant role in heart regeneration. This review discusses the present state of knowledge about telomeres and telomerase in the process of aging, as well as its relationship to cardiovascular problems.

Keywords: Aging, Atherosclerosis, Leukocyte Telomere Length (LTL), Oxidative Stress, Telomeres, Telomerase.

ICABB_M207_Anam

Mesenchymal Stem Cell Therapy in The Treatment of Covid-19

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ABSTRACT

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) was discovered in December 2019 and is a highly transmissible and dangerous coronavirus. Fever, dyspnea, and respiratory issues are common symptoms of COVID-19. In extreme cases, it is characterized by a significant inflammatory reaction that does not respond to corticosteroid therapy. The ACE-2 receptor of epithelial type II cells/endothelial cells is the primary target of the SARS-CoV-2 virus, which promotes modulation of the immune response of host cells by triggering a cytokine storm, inflammation, and severe pneumonia symptoms, as well as secondary symptoms such as acute respiratory distress syndrome (ARDS). The affinity of S protein of SARS-CoV-2 for ACE2 is the key predictor of SARS-CoV-2's replication rate and the severity of COVID19 disease. Mesenchymal stem cells (MSCs) are capable of self-renewal, differentiation, homing, and immunomodulation, and are unaffected by the coronavirus due to the lack of ACE-2 receptors, implying that MSCs could be employed as a COVID-19 treatment. MSC transplantation improves immunological indicators (such as CD4 and lymphocytes) while lowering inflammatory markers (interleukin-6 and C-reactive protein). Despite the fact that MSC-based options are currently being considered due to a lack of data, various human clinical trials of MSCs have been launched to investigate their potential for COVID 19 treatment. The current review analyses and stresses how MSCs control the immune response, can heal the lungs from the virus's impact, and other aspects of MSCs as a COVID-19 remedial source.

Keywords: Acute Respiratory Distress Syndrome (ARDS), ACE2, Mesenchymal Stem Cells (MSCs), SARS-CoV-2.

ICABB_M208_Vai

ORF-Selected Genome Fragment Libraries as Innovative Tools to Study Proteomes

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ABSTRACT

Microbes are one of the oldest inhabitants on earth and continue to evolve with their human hosts. The interactions of microbes with human hosts are central to health necessitating their in-depth study. Genome-scale expression libraries can serve as key tools to study microbial genes, understanding protein-protein interaction networks, and identification of immunodominant epitopes. The available strategies employed for the construction of DNA fragment libraries involve random fragmentation of genomic DNA due to which the majority of clones are off-frame (only 1 in 18 is in-frame) reducing the usefulness of such libraries. Our work describes a simple one-step selection system for enrichment of clones encoding Open Reading Frames (ORFs). The system is based on an E. coli enzyme TEM-1 beta-lactamase, which confers resistance against beta-lactam drugs such as ampicillin. The enzyme can be divided into two protein fragments, namely Alpha (24-195 aa) and Omega (196-286 aa) that re-constitute the enzyme activity when brought together by a mediator such as an in-frame protein inserted between the two fragments. Thus, an in-frame clone allows translation of full-length functional beta-lactamase making it resistant to ampicillin. On the contrary, an off-frame clone results in incomplete translation of beta-lactamase protein making it sensitive to ampicillin. Hence, selection of clones on appropriate concentrations of ampicillin can be used to enrich clones that encode ORF. In this work, we have demonstrated the usefulness of the system by construction of a large ORF-selected M. tuberculosis library. This study is expected to facilitate generation of ORF-selected DNA fragment libraries.

Keywords: Open Reading Frame, Microbes, Beta-lactamase, M. tuberculosis.

ICABB_M209_Rak

Expression, Purification and In-Silico Characterization of *Mycobacterium smegmatis* Alternative Sigma Factor SigB

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ABSTRACT

Sigma factor B (SigB), an alternative sigma factor (ASF) is very similar to primary sigma factor SigA (σ^{70}) but dispensable for growth in both *Mycobacterium smegmatis* (Msmeg) and *Mycobacterium tuberculosis* (Mtb). It is involved in general stress responses including heat, oxidative, surface, starvation stress and macrophage infections. Despite having an extremely short half-life, SigB tends to operate downstream of at least three stress-responsive Extra Cytoplasmic Function (ECF) sigma factors (SigH, SigE, SigL) and SigF involved in multiple signalling pathways. There is very little information available regarding the regulation of SigB sigma factor and its interacting protein partners. Hence, we cloned the SigB gene into pET28a vector and optimized its expression in three different strains of *E. coli*, viz; (BL21(DE3), C41(DE3) and CodonPlus (DE3)). We also optimized several other parameters for the expression of recombinant SigB including IPTG concentration, temperature, and time-duration. We achieved the maximum expression of SigB at 25 °C in the soluble fraction of the cell which was purified by affinity chromatography using Ni-NTA and further confirmed by Western blotting. Further, structural characterization demonstrates the instability of SigB in comparison to SigA is carried out using homology modelling and structure function relationship. We have done protein-protein docking of RNA polymerase (RNAP) of *Mycobacterium smegmatis* (Msmeg) and sigB. This effort provides a platform for pulldown assay, structural and other studies with the recombinant protein to deduce the SigB interacting proteins, which might pave the way to study its signalling networks along with its regulation.

Keyword: Alternative Sigma Factor, Recombinant SigB, Mycobacterium, Stress-Responsive, ECF.

ICABB_M210_Anu

Determination of Antibiofilm Potency of Methanolic Leaf Extract of *Murraya koenigii* against Environmental Isolates of *Enterobacteriaceae* Family

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ABSTRACT

Phytochemicals are the oldest therapeutic means being used for multiple healing and recovery purposes. Present study explores the antibiofilm activity of leaf extract of *Murraya koenigii* against the isolates of Enterobacteriaceae family isolated from surface water source and names as EB1 and EB2. Improved crystal violet assay was used to evaluate their biofilm making potential. It was found that EB1 and EB2. EB2 was observed as a moderate biofilm producer whereas EB1 was found to produce biofilm at lower abilities. Kirby Bauer's method was used to determine the drug resistance using discs of ampicillin, gentamicin, nalidixic acid, imipenem and doripenem as the representative antibiotics of various classes. The crude extract had shown inhibitory effects on the biofilms of both the isolates. There was 60% decrease in the biofilm formation ability of EB1 at the concentration of 10 mg/mL whereas EB2 biofilm was successfully decreased by 75% at the crude extract concentration of 25 mg/mL. The results demonstrated the antibiofilm ability of *M. koenigii*.

Keywords: *Murraya koenigii*, Enterobacteriaceae, Biofilm, Antibiotic Resistance.

ICABB_M211_Anmm

Therapeutic Peptides for Antimicrobial Resistance

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ABSTRACT

Antimicrobial resistance (AMR) has posed a severe danger to worldwide public health, necessitating urgent, ideally long-term, action. More and more antibiotics have become ineffective as the bacteria are becoming resistant to drugs, and the attention is now turning towards the alternate medicines for the treatment of infections. Even though various natural alternatives are available, there is a need to investigate, analyse and put them into therapeutic usage. Synthetic chemistry, genetic engineering, and biotechnology advancements have opened up new pathways for the hunt for antibiotic-replacement medicines. Current medication treatments have failed to combat this threat due to microorganisms' capacity to bypass the processes through which the function of drugs occurs. The common method involves isolating and purifying antimicrobial peptides, followed by screening them on microbial cultures. Recent trends show an increase in the utilisation of peptides as therapeutic candidates, owing to their significant benefits over small molecules. Moreover, these peptides can also be employed as anti-biofilm agents.

Keywords: Antimicrobial Resistance, Peptides, Therapeutic, Biofilm.

ICABB_M212_Sha

Cervical Cancer Care & Management: A Conquerable Malignancy

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ABSTRACT

Cervical cancer is an oncovirus driven cancer, a second leading cause of death in women after breast cancer claiming one life in every 2 minutes across the globe. The incidence and mortality rate by cervical cancer covers around 85% of the women from developing countries however, the disease have higher possibility of elimination with various prevention, screening and treatment strategies when dealt effectively with advanced monitoring. In recent years, systematic efforts by the leading health organizations like WHO has been initiated at the global level which aims at total culmination of the screening and preventing practices to curb cervical cancer by the next century 2120. Besides, the development at the regional level with enhanced awareness of the issue is an added advantage that is providing a promising output of target achievement with multiple therapeutic strategies. By 2045, around 50 % of the population from developing region is expected to receive cervical cancer treatment albeit a long and challenging road for a conquerable malignancy. Thus, based on current scenario the present review briefly apprises the readers about preventive and therapeutic aspects of combating cervical cancer and how far we have come close to the target keeping in mind of various factors affecting the cervical cancer prevalence.

Keywords: Cervical Cancer, World Health Organization, Prevention, Elimination, Immunity, Vaccines, Apoptosis, Standard Therapies, Phytoterapeutics, Pallative Care, Socio-economic, Transtioning Countries.

ICABB_M213_Lav

Heterologous Expression, Purification and Structural Characterization of Ribonuclease E, a Key Player in RNA Metabolism of *Mycobacterium smegmatis*

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ABSTRACT

Ribonuclease E (RNase E) an essential endoribonuclease gene in *Mycobacterium* species is the key mediator in most reactions of RNA metabolism like mRNA, rRNA and tRNA processing as well as their degradation qualifying it as an important drug-target. Here, we first report the cloning of full-length *Mycobacterium smegmatis* mc²155 RNase E [MSMEG_4626] and its expression with IPTG in *Escherichia coli* as a GST fusion protein. The expression of the recombinant protein was optimized in different *E. coli* strains followed by optimization of temperature, IPTG-concentration and time-points of induction. Significant amount of recombinant protein expression was seen after 3 hours of induction with 0.1 mM IPTG at 37°C. Although regulatory genes are highly unstable in nature, therefore instead the use of protease inhibitors we observed low molecular mass proteolytic fragments along with full-length recombinant protein. We successfully standardized the protocol for the maximum expression of soluble recombinant GST fusion protein with minimum degradation. Which was further purified by affinity chromatography using glutathione agarose beads. The recombinant protein was further confirmed by immunoblotting technique using anti-GST antibody. Further, functional characterization was done by using insilico techniques like homology modelling, docking and multiple sequence alignment studies revealed four amino acid residues; Asp613, Phe657, Ile662, Glu688 in the catalytic domain of RNase E that are totally conserved in both *E.coli* and *Mycobacterium* species and are also involved in RNA binding. These identified residues might act as candidate drug-targets to combat the growing number of antibiotic-resistant mycobacterial diseases. Also, the recombinant GST-RNase E protein can unravel the mechanism of RNA degradation/processing through protein-protein interaction studies.

Keywords: Ribonuclease E · *Mycobacterium* · RNA Metabolism · GST fusion protein · Drug-Target.

ICABB_M214_Pla

Study Activity Level, Energy Expenditure and Meal Pattern in Female University Students as a Function of Body Mass Index

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ABSTRACT

The rest-activity rhythm and meal pattern are the energy related behavior whose imbalance causes weight gain or obesity. Females of young age group engaged in higher study have generally shown to have sedentary life and higher risk of weight gain. However, there is lack of such reports from developing states like Chhattisgarh, south-east India. Therefore, the current study was conducted with the aim to assess the rest-activity and energy expenditure in young age group (18-30 years) university female students with normal weight and overweight (classified according to BMI) from Raipur and nearby areas. The rest-activity and energy expenditure were monitored using Actical accelerometer for 5-7 days. The circadian rhythm in activity count (AC) and energy expenditure (EE) were analyzed using the Cosinor rhythmometry. A significant rest-activity and energy expenditure rhythm in both normal and overweight with peak activity and energy expenditure was observed during afternoon to evening hours, irrespective of their BMI. A significant wide eating time window and meal frequency was recorded in overweight compared to normal weight female group. It could be concluded that robust circadian rhythm exists in rest-activity and energy expenditure of the females. However, the odd time activity peak along with the wide eating window and higher meal frequency could cause trouble. This study helps to understand the altered lifestyle through rest-activity, energy expenditure as well meal pattern behavior in young age group females undergoing higher education and thus weight management.

Keywords: Rest Activity Rhythm, Energy Expenditure, Activity Count, Cosinor Rhythmometry, Eating Window.

ICABB_M215_Sne

Therapeutic and Clinical Propositions of Mesenchymal Stem Cells (MSCs) Focusing on Recent Trial Updates

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ABSTRACT

The mesenchymal stroma harbors considerable population of stem cell-like cells with differentiation and self-renewal abilities that originate from several sources like amniotic fluid, Wharton's jelly, umbilical cord etc. Mesenchymal Stem Cells (MSCs) are most commonly found in the perivascular niche. This multipotent progenitor cells have the ability to differentiate into mesodermal cell types such as adipocytes, chondrocytes and osteocytes. MSCs can also exert significant immunosuppressive and anti-inflammatory effects by interacting with lymphocytes from both innate and adaptive immune system. MSCs of fetal origins can go through same processes as MSCs derived from elsewhere. Before senescence, they make more cell divisions than adult MSCs of bone marrow or adipose tissue. The propitious properties of mesenchymal stem cells (MSCs), such as their ability to differentiate into diverse cell lineages and their regenerative properties, have intrigued researchers, whose work has provided fascinating perspectives on cell-based therapies for wide range of diseases. MSCs have a high potential for replication in vitro. International Society for Cellular Therapy (ISCT)-based MSC isolation has resulted in heterogeneous, nonclonal stromal cell cultures containing stem cells with various multipotent characteristics, committed progenitors, and differentiated cells. Nonclonal stromal cultures which are derived from bone marrow and other tissues are presently used as sources of putative MSCs for therapeutic aims. Also, MSCs have potential to endogenously repair as well as reduce the inflammatory responses that may lead to decreased morbidity and mortality rate of COVID-19. Herein, the MSC-based clinical prospects, clarifies, the recent clinical findings, therapeutic effects of MSC and clinical trials.

Keywords: Wharton's Jelly, Senescence, Cell-Based Therapies, COVID-19, Mesodermal Cell.

ICABB_M216_San

Genetic Variation of Glutathione-S-Transferases M1 and Cardiovascular Disease Risk in Diabetes Mellitus

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ABSTRACT

Background: Oxidative stress and lipid abnormalities play a vital role in development of cardiovascular disease (CVD) in patients with diabetes mellitus (DM). GSTM1 (Glutathione S-transferases Mu 1) is widely studied in various disease pathophysiological status with regard to the homozygous deletion of the gene. There is no substantial evidence on the association of GSTM1 in CVD development in DM patients has been investigated in the present study. Blood samples were collected from patients in 4 groups (n=96 each) of Control, DM, CVD and DM with CVD. PCR was performed to analyse the association of GSTM1 null polymorphism and gene frequency, lipid profile, oxidative stress statistically. The frequency of null genotype was higher among CVD (0.63%) compared to DM/CVD and DM groups (0.54%, 0.58% respectively). GSTM1 null conferred increased risk in DM (OR: 1.74), DM/CVD (OR: 1.50) and CVD (OR: 1.21) but not statistically significant. Even though GSTM1 did not show significant association, they were associated with increased concentration of LDL in CVD demonstrating the role of lipid in CVD development. The antioxidant status was seen to be decreased in CVD followed by DM/CVD and then in DM indicating the role of oxidative stress in CVD development in DM patients. The results suggest that lipid profile, oxidative status with reduced antioxidant capacity and GSTM1 genetic variations may modify CVD development among DM patients. This study is limited by sample size and hence further longitudinal studies with large sample size are required to confirm the association.

Keywords: Antioxidant, CVD, DM, GSTM1, Lipid Profile, Oxidative Stress.

ICABB_M217_Sri

Understanding Krabbe's Disease and Its Recent Advancements

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ABSTRACT

Neurodegenerative diseases are characterized by the progressive degeneration of both the central and peripheral nervous systems. They are incurable and pose a major threat to human health. Krabbe disease is one among those, which is a rare hereditary degenerative disease affecting both central and peripheral nervous systems. It is marked by the presence of globoid cells (cells with multiple nuclei), the destruction of the protective myelin layer of nerves and of brain cells. Krabbe disease belongs to a group of hereditary diseases called 'leukodystrophy' a rare lysosomal storage disorder (LSD). In the absence of GALC, galactosylceramide lyso-derivative galactosyl sphingosine (psychosin) accumulates toxically in oligodendrocytes and Schwann cells, causing demyelination of the central and peripheral nervous systems, respectively. Treatment strategies such as enzyme replacement therapy, AAV gene therapy, enzyme chaperon, and gene therapy show the potential of LSD. Unfortunately, Krabbe disease was relatively refractory to most monotherapy interventions. Currently, there is no cure for Krabbe disease, however, *in silico* studies can provide important insights in selecting the target domain through analyzing the proteomics and genomics data generated from clinical samples. Various hypothesis has been put forward regarding how such a small molecule of psychosine can cause such adverse effects. This review describes and emphasizes the importance of the new insights gained from these studies including the recent advancements in Krabbe's disease and the PLX200 and FDX- 101 drug which has been approved by the FDA recently.

Keywords: Krabbe Disease, Therapeutic Interventions, GALC, Psychosine, *In Silico* Studies.

ICABB_M218_Riz

Tumor Tissue-Associated Microbiome Pattern in North Indian Patients Diagnosed with Colorectal Cancer

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ABSTRACT

Colorectal cancer (CRC) is one of the most regular cancers, it ranks second in mortality and third in incidence and among all types of cancers globally. The dysbiosis of gut microbiota is involved in CRC formation, progression and its response to treatment, thus a pilot study was undertaken with the objective to find the CRC-tumor-associated microbiota using NGS. 16s rDNA sequences of bacterial DNA isolated from flash-frozen tissue samples was analysed. Libraries were created of 2 hypervariable regions (V3-V4) amplicon and bar-coded for sequencing using Ion Torrent platform. Higher species abundance was observed among the CRC tissue samples than adjacent normal tissues. Alpha diversity showed the richness and evenness of species were similar in both tumor tissues and their adjacent area. Further, beta diversity showed distinct bacterial family composition. Diversity and rarefaction analysis showed 66 species were significantly different in CRC patients ($p \leq 0.05$). Our data suggest presence of distinct tumor-specific microbiome that colonize within tumor. The pathogenic phylum Proteobacteria and fusobacterium abundant in CRC. Tumor-targeting and tumor-killing facultative anaerobic (*Clostridium*, *Bifidobacterium*, *Escherchia coli*) species were abundant in the CRC tissue samples. Additionally, species like *Fusobacterium*, *Bacteroides fragilis* and *Prevotella copri*, *parainfluenzae* were significantly abundant in CRC-tissue samples. Such specific bacterial colonization can selectively utilize for overcoming the drug penetration challenge due to their interaction with tumor-microenvironment.

Keywords: CRC, Microbiome, Next-Generation Sequencing (NGS), 16s rRNA, Microbial Species, Dysbiosis.

ICABB_M219_Aru

Nitric Oxide (NO) as a Potential Biomarker In LPS-Induced Sepsis-Associated ARDS in A549 Cell Lines

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ABSTRACT

Nitric oxide (NO) is synthesised from L-arginine, where the latter is converted by an enzyme called nitric oxide synthase (NOS), and L-citrulline is obtained as a by-product. NO possesses a critical role in regulating physiological and pathophysiological processes including, inflammatory responses, blood flow, vascular integrity, and cell death. While it serves a protective role in the lungs to prevent any injury, it also harms them beyond a limit. Its function is further associated with its three isoforms, namely nNOS (neuronal nitric oxide synthase/NOS1), iNOS (inducible nitric oxide synthase/NOS2), and eNOS (endothelial nitric oxide synthase/NOS3). NOS1 is involved in neurotransmission, NOS2 lowers the blood pressure associated with septic shock, and NOS3 is responsible for smooth muscle relaxation and vasodilation. It is observed that eNOS and iNOS, isoforms of NO, play an essential role in promoting sepsis if not controlled beyond the threshold as it shows deleterious effects on the cell line. An increase in iNOS will increase NO production, leading to the formation of reactive oxygen species (ROS), producing free radicals responsible for the development of various diseases, including ARDS. On the other hand, the reduction in eNOS and its uncoupling is associated with the low availability of L-arginine, promoting lung injury and sepsis due to hindrance in physiologic regulatory events involved in eNOS-derived NO. In this piece of work, the role of NO has been analysed as a biomarker in LPS-induced sepsis-associated ARDS, by exploring the literature available. Further wet-lab experiments are required to validate the hypothesis.

Keywords: Nitric Oxide, Acute Respiratory Distress Syndrome, Lipopolysaccharide, Reactive Oxygen Species, L-citrulline, L-arginine.

ICABB_M220_Ana

Neuro Imaging Using Synthetic Bioluminescence

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ABSTRACT

The timeline for Neuroimaging techniques starts as early as the 1800s and is still very active with several conventional but highly popular techniques. Bioluminescence imaging utilizes native light emission from one of several organisms which show bioluminescence by the production of luciferase enzyme like North American firefly, the sea pansy, and bacteria like *Photobacterium luminescens*, etc. In a systematic order the procedure involves obtaining the enzyme from a luminescent species, genetically modifying it to a sensor molecule, hijacking a virus infecting the neurons, attaching it to their sensor molecule to attach the sensors onto the cell's interior. A reddish light is produced when an artificial luciferin called AkaLumine-HCl is in a position to penetrate the barrier. The modified and altered AkaLuc protein was found to be a more effective substrate catalyst as well as more abundantly produced by cells. To test the sensor's compatibility with a larger number of neurons, it was implanted into mouse hippocampus brain slices and flooded with a higher concentration of potassium ions, which caused the cells' ion channels to open, resulting in a 1000-fold stronger signal from the natural luciferase-luciferin reaction. This shows that there is a lot of potential for a strategy like this to be stable and long-lasting.

Keywords: Bioluminescent, Luciferase Enzyme, AkaLumine-HCl.

ICABB_M221_Ham

Eskape Pathogens and Potential Target Gene Families Virulence

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ABSTRACT

ESKAPE pathogens (*Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and *Enterobacter* species) are the most common source of nosocomial infections worldwide. The majority of them have exhibited resistance to multiple drugs, which is one of the most difficult problems to deal with in clinical practice. Multidrug resistance is one of the top three risks to global public health, and it is typically exacerbated by the overuse or prescribing of drugs, inadequate antimicrobial use, and substandard pharmaceuticals. Understanding the pathways of tolerance in these bacteria is critical for the discovery of new antimicrobial agents or other alternative tools to combat public health issues. In-depth literature survey and an in-silico analysis was carried out to identify the key gene families responsible for defensive mechanisms. A list of non-homologous essential gene targets of these pathogens has been documented. They can be targeted and pave way for anti-microbial therapy.

Keywords: Antibiotic Resistance; ESKAPE Pathogens; MDR; Nosocomial Infection.

ICABB_M222_Pan

KRAS Mediated Signaling Pathways in Lung Cancer

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ABSTRACT

Lung cancer is accountable for the largest number of cancer related deaths globally. The somatic activating mutations of every member of RAS group-KRAS, HRAS & NRAS have been observed in a wide range of human cancers. In patients with lung cancer KRAS has been recorded as the most common mutated gene belonging to RAS family. The mutation of KRAS mostly occurs in lung adenocarcinoma which is the most orthodox form of non-small cell lung cancer (NSCLC). These mutations shown in KRAS are found at the codon 12 and sometimes at codon 13 and codon 61. The presence of KRAS mutation is associated with lack of EGFR inhibitors response in NSCLC. These genes are highly conserved and encode the GTPases that are responsible for cycling between active and inactive states in an event of extracellular stimuli. Mutated KRAS contributes to oncogenicity by activating the mitogen activated protein kinase (MAPK) and extra cellular regulated (ERK) pathways. KRAS goes through alternate splicing which results in formation of two proteins- KRAS4A and KRAS4B. KRAS4B is developmentally essential with specific functions that cannot be compensated by other RAS family members. The specific type of KRAS mutations may be helpful in providing information with respect to disease aggressiveness and drug sensitivity. Research studies suggest that KRAS status plays an important role as a marker for therapeutic response. This review article aims to study the mutations of KRAS and its associated genes in different types of lung cancer and signaling pathways involved in the pathogenesis of these mutations.

Keywords: KRAS, RAS Family, Lung Cancer, NSCLC, Signaling Pathways.

ICABB_M223_Deb

Manifestations in COVID-19 Patients Related to Cardiovascular Diseases

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ABSTRACT

Coronavirus disease 2019 (COVID-19) of Wuhan in Hubei Province, Central China, and has rapidly spread to 72 nations. This global pandemic caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has affected billions of lives worldwide causing severe health and financial crises at an alarming rate. Recently, amongst 416 hospitalized COVID-19 patients, 19.7 per cent were found to have a cardiac injury. In addition, 23.0% of 191 patients admitted for COVID-19 suffered from heart failure. These observations show a strong co-relation between COVID-19 and associated heart complications, making it important to understand their relation for better management and treatment. ACE-2 receptor plays a crucial role within the RAAS system and has been often seen expressed widely in cardiac fibroblasts, cardiomyocytes, and coronary endothelial cells, which also serves as the regulators within the functioning of the heart. It has also been discovered as the functional receptor for the entry of coronaviruses, specifically for infection with SARS-CoV-2 into the host cells. Different manifestations of heart diseases observed in COVID-19 include myocardial injury, arrhythmia, acute coronary syndrome and venous thromboembolism. This review discusses the COVID-19 induced cardiac complications and also the effect of COVID-19 medications on the heart. Along with this, we will be looking into present medications and also into future prospects.

Keywords: SARS-CoV-2, Heart, ACE2, Disease, Mechanism.

ICABB_M224_Man

Role of CDKN2A gene in Melanoma

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ABSTRACT

Melanoma is a malignant cancer of melanocytes, the cells that provide colour to skin. Melanoma not only occurs on the exposed skin, but it can also occur on areas like inner cheek, throat, eyes, etc. The exact cause of melanoma is still unknown, but it is observed that the skin exposed to Ultraviolet Radiations from sunlight or tanning lamps have a great effect on its occurrence. CDKN2A gene, is a tumour suppressor gene. This gene in humans is located at chromosome 9 on band p21.3. It is expressed in many tissues and cell types. This gene gives instructions to form p16 and p14 proteins, which keeps the cells from growing and dividing too rapidly, thus acting as a tumour suppressant. These two protein kinases: CDK4 and CDK6, help in controlling cell division and modulates transcription. They do so by activating retinoblastoma (Rb) family of proteins. This protein family causes blockage in traversal from G1 to S-phase, resulting in inhibition of synthesis of DNA. The CDKN2A gene in fact plays a very vital role in many types of cancer. It is associated with familial melanoma, glioblastoma and pancreatic cancer, as well. In the present article the role of the CDKN2A gene has been reviewed in connection with: melanoma in terms of the mutations found in the gene and application of this knowledge for treating melanoma.

Keywords: Melanoma, CDKN2A, CDK4, CDK6, Retinoblastoma.

ICABB_M225_Kaj

Rhodiola Rosea: A Multidimensional Adaptogenic Herb

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ABSTRACT

Rhodiola rosea is a naturally growing revered adaptogenic plant in some wild Arctic regions of the world and belongs to the family Crassulaceae. The herb has been demonstrated to amplify body's nonspecific resistance, ameliorate stress related decline in work performance, reduce fatigue, enhance cognition and prevent high altitude illness. Different model systems have been used to study and reveal the pharmacological effects of *Rhodiola rosea* which includes its potential to boost immune system, relieve stress, cancer prevention, reduce depression and enhance brain functions, allowing the human and animal body to overcome the unfavorable internal and external stressors. Most of these cellular and systemic benefits are ascribed to *Rhodiola rosea* extracts such as rosavins, p-tyrosol and salidroside which showed their ergogenic effects by the mechanism of free radical mitigation. Several clinical studies have demonstrated the mechanism of action of *Rhodiola rosea* extracts in the cerebral cortex and brainstem which slows the breakdown of serotonin and dopamine acting as a mood stabilizer and helps in increasing motivation. It also increases the availability of epinephrine and norepinephrine to drive energy. The adaptogenic properties of *R. rosea* are contributed by its capacity to manipulate the amount and function of monoamines and opioid short chain peptides like beta-endorphins. *R. rosea* has been described to avert both catecholamine release and ensuing cyclic adenosine monophosphate upgradation in the myocardium, and the exhaustion of adrenal catecholamines persuaded by acute stress. The discussed benefits of *R.rosea* thus pave the way for its investigation as an intervention in multiple pathological settings and support its role as an adaptogenic plant.

Keywords: Salidroside, Adaptogen, *Rhodiola rosea*, Ergogenic Effect, Monoamine, Neurotransmitters, Beta-Endorphins.

ICABB_M226_Kan

Positron Emission Tomography in Multiple Myeloma

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ABSTRACT

Multiple Myeloma (MM) is a heterogeneous disease of plasma cells (a type of white blood cells); monoclonal plasma cells grow uncontrollably in the bone marrow and excess production of non-functional immunoglobulins takes place. Cyclin D proteins (D1, D2 and, D3) are dysregulated which occurs due to trisomies, translocations, specific cyclin D gene amplifications and other cytogenetic events that occur during different stages of the disease leading to MM. In later stages of MM, alterations in DNA methylation and acetylation are observed. The growth and survival of myeloma cells are greatly affected by bone marrow microenvironment. The bone marrow stromal cells adhere to MM cells resulting in the activation of NF-κB pathway along with supporting proliferation of tumor cells, these also provide drug resistance and the anti-apoptotic proteins are expressed. Complete Blood Count (CBC) is one of the most common diagnostic methods for MM, bone marrow biopsy, urine studies, radiologic evaluation are other methods for the same. Positron emission tomography (PET)/CT scans are widely being used due to its ability to detect extramedullary diseases. There are two staging systems for MM (Durie Salmon system and International Staging System (ISS)), out of which ISS is preferred as it has better prognostic value for all forms of therapy. Although there is continuous improvement in response rates to treatment, MM remains the second most common hematologic malignancy, which was earlier considered to be fatal in almost all the cases. With increased understanding of the neighboring microenvironment and genetic landscape of MM, there is a scope for improvement in diagnosis and response to treatment by development of more effective drugs for targeting the disease. The review will provide a brief insight about Positron emission tomography (PET)/CT used in the diagnosis of multiple myeloma.

Keywords: Multiple Myeloma, Bone Marrow Stromal Cells, Microenvironment, PET/ CT Scan, Staging.

ICABB_M227_Abh

Bacteriophages as Therapeutics

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ABSTRACT

Water is the fundamental need of all living organisms on Earth. Due to human activities, water pollution due to the presence of pathogenic bacteria (*E. coli*, *Pseudomonas* and *Salmonella* etc.) results in gastro-intestinal illness, skin, ear, respiratory, eye, neurologic and wound infections. With evolution of bacterial strains, efficacy of antibiotics has been decreasing due to antibiotic resistance. Notably, literature surveys carried out suggest that phage therapy can be an alternative method to target pathogenic microorganisms. Continuous efforts are being carried out to understand the science behind phage therapy as a therapeutic tool. In the current study, genomic sequences of coliphages have been mined from literature, compared for similarities using various phylogenetic tools and analysed.

Keywords: Water, Bacteriophage, Antibiotics, Phage Therapy, Phylogenetic Analysis.

ICABB_M228_Har

Telomeres and Telomerase in Ageing

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ABSTRACT

Telomeres are the repetitive DNA on the ends of linear chromosomes, which is a part of the multimeric protein shelterin complex dedicated to protecting the chromosomal ends. Telomere attrition or shortening is a key hallmark of ageing cells. Telomere shortening due to incomplete lagging strand DNA synthesis, sequence modifications due to oxidative damage and other accumulating anomalies such as compromised epigenetics/proteostasis is observed to push the cell into cellular senescence. The telomeric DNA is synthesized using telomerase, a reverse transcriptase that synthesizes the repetitive DNA ends of telomeres on the template telomerase RNA component (TERC). Besides the primary function of protecting the DNA ends, they have also been shown to exhibit transcriptional silencing via a phenomena known as telomere position effects (TPE), endorsing the idea of epigenetic regulation of gene expression via mammalian telomeres. The literature evaluating the role of telomere biology in ageing indicates that ageing can be a result of unprotected telomeres resulting in DNA damage signals or another equally plausible model is that progressive telomere shortening leads to changes in the expression of genes away from the telomeres plausibly initiating age-related pathological imbalance of gene expression. Herein, we discuss telomere attrition as a hallmark of aging along with the emerging evidence for its epigenetic implications.

Keywords: Telomere, Telomerase, Ageing, TERC, Telomere Position Effects, Epigenetic.

ICABB_M229_Iqn

Virtual Screening of Phytochemical Compounds from *Berberis Vulgaris* as Potent Inhibitors of *H. Pylori* Infections: An *In Silico* Approach

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ABSTRACT

Helicobacter pylori infection is known to be the most common prevalent bacterial infections in humans, which is further associated with development of gastrointestinal ulcers, chronic gastritis, ulcerative colitis and enterocolitis. Treatment of *H. Pylori* infections using the current medical regime is often very costly and has some adverse side effects too. Recent advances in research have explored several natural inhibitors of *H. Pylori* infections. *Berberis vulgaris* is known to have a bioactive compound, Berberine, with reported antimicrobial activity against bacterial infections. This present study focuses on virtual screening of bioactive phytochemical compounds from *Berberis vulgaris*, which largely conformed to drug likeliness criteria and ADMET properties. Moreover, the selected compounds showed lesser mutagenic, hepatotoxic effects and higher absorption rates in the human intestine. The best drug-like compounds were further subjected to molecular docking studies. The docking results revealed the promising inhibitory potential of bioactive compounds against Shikimate dehydrogenase, a key enzyme in the infection cycle of *H. Pylori*. Data gathered from this study will support the future research in development of potential medicaments using natural bioactive compounds in management of *H. Pylori* infections.

Keywords: *H. Pylori*, Berberine, ADMET, Molecular Docking, Phytochemicals.

ICABB_M230_Shr

Plant-Based Vaccine for COVID-19

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ABSTRACT

Plant-based vaccines are the ones in which the gene encoding the desired antigen protein is integrated into the plant genome via recombinant DNA technology. Developing safe, low- cost oral vaccines can be made from transgenic plant-derived antigens. Many advancements in this area have resulted in benefits like improved protein antigen expression for using plants for vaccine productions and eased immunogenicity assessments of candidate vaccines. Antigen protection inside the hostile intestinal environment is a benefit of oral delivery of plant-based vaccines. A recent work shows the production of such a vaccine targeting SARS- CoV-2 Receptor Binding Domain (RBD) being produced via *Agrobacterium*-mediated agroinfiltration and expression in *Nicotiana benthamiana*. This work summarizes the state- of-art in the field of plant-based vaccines as an alternative to conventional methods of production.

Keywords: Plant-based Vaccines, SARS-CoV-2 Receptor Binding Domain (RBD), Human Angiotensin-converting enzyme-2 receptor (ACE2), Fc region of IgG1, *Agrobacterium Tumefaciens*.

ICABB_M231_Riy

HAEMOCHROMATOSIS

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ABSTRACT

Iron is an important component of the Earth's crust which has very much importance in our life. The exchanging electrons in aerobic conditions makes iron essential for fundamental cell functions, such as DNA synthesis, transport of oxygen and electrons, and cell respiration in its appropriate level. On the other hand, as humans have no means to control iron excretion, excess iron, regardless of the way of entry, accumulates in parenchymal organs and threatens cell viability. Haemochromatosis is a common systematic recessive genetic disorder characterized by progressive iron overload or caused by a reduction in the concentration of the iron regulatory hormone hepcidin, or a reduction in hepcidin-ferroportin binding. Hepcidin is a protein that regulates the activity of ferroportin, which is the only identified cellular iron exporter. This type of disease is very much common in populations of northern European origin. HLA-H is a recently reported candidate gene for this condition. The most common form of haemochromatosis is due to homozygous mutations (specifically, the C282Y mutation) in HFE, which encodes hereditary haemochromatosis protein. Avoid the intake of food and drinks which contain high vitamin C content as it increases the iron absorption which can worsen the haemochromatosis level. Diagnosis of this haemochromatosis is non-invasive and includes clinical examination, liver biopsy, MRI scanning, imaging and genetic testing. Iron removal therapy is an effective lifesaving strategy that includes phlebotomy, although iron chelation can be used in some patients. Patients display mutations in the gene coding for HFE, a protein that normally acts as an inhibitor of transepithelial iron transport. These control sites may be influenced by gene therapeutic approaches; one general therapy for hemochromatosis of different etiologies is the inhibition of DMT1 synthesis by antisense-generating genes, which inhibit apical iron uptake by intestinal epithelial cells. Also Hepcidin supplementation might be an innovative future approach too.

Keywords: Hepcidin, Ferroportin, Iron Overload, HFE.

ICABB_M232_Som

Viral Infection and Glioblastoma

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ABSTRACT

Adult malignant gliomas are the most prevalent type of primary brain tumour. Glioblastoma has a high incidence and mortality rate, which is matched by a lack of effective treatments. Previous research has found a link between viral infection and the development of gliomas. The genome and associated proteins of the human cytomegalovirus (HCMV) have been found in a large number of malignant gliomas. In 2002, researchers discovered a high incidence of the HCMV in glioblastomas. Literature was curated and several databases were studied to understand the link between glioma and HCMV infection, as well as the likely mechanism by which HCMV contributes to malignant glioma. These findings imply that HCMV is highly frequent in glioblastomas, which were found using advanced immunohistochemical techniques. Here pp65 was used as the biomarker that was found in the glioma sample of the patients with HCMV positive glioblastoma. It was found that there was 65.8% positive immunoreactivity for pp65. Hence there is an elevated expression of HCMV pp65 in glioma samples. This study provided us a different connection, which when targeted can help us work further into designing a suitable treatment plan.

Keywords: Glioblastoma, Human Cytomegalovirus, pp65, Immunoreactivity.

ICABB_M233_Par

Mouse Models for Glioblastoma

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ABSTRACT

Glioblastoma multiforme is a type of glioma that is classified as grade 4 and is one of the most commonly occurring malignant brain tumors. Even with intensive therapies, the prognosis is very poor. Hence it is essential to develop new treatments and therapies to effectively treat glioblastoma. Understanding the biology of tumors, finding new treatment targets, and analyzing the efficacy of novel therapeutic methods all require development of preclinical mouse models. There are two types of preclinical glioblastoma models now available: xenograft models and genetically modified mice models. Glioblastoma cell-line and patient derived xenografts are the two types of xenograft models. Glioblastoma cell-line xenografts have the advantage of high engraftment rates as well as high growth rates, however it is debatable whether they accurately reflect the underlying biological basis of glioblastoma. Patient-derived xenografts are considered to be ideal preclinical models in glioblastoma research as they preserve both the genetic and histological properties of the parent tumor. However, they are unable to adequately represent the host's antitumor immunity. Each model provides important insights into the mechanisms of tumor developments. This review discusses the advantages and limitations of each model.

Keywords: Glioblastoma Multiforme, Glioblastoma Cell Line Xenografts, Patient – derived Xenografts.

ICABB_M234_Jyo

Molecular Cloning, Expression, Purification and Immunological Characterization of Binding Domain from BoNT/A

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ABSTRACT

Clostridium botulinum produces seven different types (A-G) of toxins, and it's listed as the most toxic substance to human. The disease which is caused by botulinum neurotoxin is termed as 'Botulism'. Due to its high toxicity, Centre for Disease Control (CDC) categorizes BoNT as category 'A' biowarfare agent. BoNTs are 150 kDa proteins that have three key domains: a light chain (LC), a translocation domain (HN), and a binding domain (HC). The HC directs the BoNT to the membrane of neuronal cells, and each serotype has evolved to interact to different target receptors in distinct manners. In the present study, the heavy chain binding domain (HC) was amplified by PCR, cloned in pET28 b+ vector and transformed in BL21DE3 expression host. The recombinant plasmid confirmed by colony PCR as well as restriction digestion. The recombinant BoNT/A HC protein expression conditions such as IPTG concentration, time, media and temperature were optimized. The expressed recombinant BoNT/A HC protein was purified through Ni-NTA affinity chromatography and further confirmed by Western blot. Polyclonal antibodies were raised in mice and rabbit against rBoNT/A HC and the antibody titers were estimated via indirect ELISA. Antibody titers of rabbit and mice sera were ~1:128000 and 1:32000 respectively. Further, the IgG was purified and used for the development of sandwich ELISA having sensitivity of ~31.25ng/ml.

Keywords: Botulism, BoNT Neurotoxin, Biowarfare agents, His-Tagged Protein.

ICABB_M235_Ris

Application of CAR T-cell in Cancer Therapy

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ABSTRACT

CARs (chimeric antigen receptors) are synthetic receptors that allow T lymphocytes to identify tumour-associated antigens (TAAs) without the use of the major histocompatibility complex (MHC). Although cancer cells have different lineages and heterogeneity, they all share target antigens like CD19, CD20, CD22 that allow CAR T cells to detect tumour cells regardless of the cell origin. In treating resistant B cell malignancies, CAR-T cells targeting the B-cell marker CD19 have exhibited exceptional response rates. As a result, more precise target antigens produced by tumour cells have been added to this approach in recent years. The optimization of each of the four primary components of a CAR-extracellular antigen-sensing domain, extracellular hinge or spacer domain, a transmembrane domain, and intracellular signalling domain has improved the efficiency of CAR-T cell treatment. New studies of CAR T cell treatment that discriminate against conventional CAR T cells that potentially promote tumour cell death are highlighted in this review. NK-CAR and clustered regularly interspaced short palindromic repeats (CRISPR)-CAR treatment are both in clinical trials. Patients can also benefit from stem cell transplantation, using CAR T cells, since they can live a normal life without the chance of relapse. As a result, CAR T cell treatment is known as a "living medication."

Keywords: CD19, CARs, Cancer, CRISPR, NK-CAR. Tumour-associated Antigen, TCR.

ICABB_M236_Har

The Implication of Pleiotropic Hyaluronan Binding Protein 1 in Regulating Apoptosis and Tumorigenesis

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ABSTRACT

Hyaluronic Acid Binding Protein 1(HABP1/p32/C1QBP) is a multi-compartmental, multi-functional protein belonging to the family of hyaladherins and binds with Hyaluronic acid, a negatively charged polysaccharide having high molecular weight, found in the extracellular matrix (inside as well as on the surface of the cell). Several studies have reported the physiological role of HABP1 in cell-cell adhesion, signal transduction, mammalian reproduction, tumorigenesis, etc. In mammalian cells, the functioning of HABP1 is stringently regulated and even minor alterations in its level can lead to perturbed cell growth. Abnormal expression of HABP1 also leads to generation of excess reactive oxygen species (ROS) in the fibroblasts, that creates an intrinsic mitochondrial dysfunction and ultimately causes apoptosis. Loss of HABP1 from skin papilloma also suggests its involvement in initiating and promoting tumor formation. Apart from these, HABP1 is overexpressed in malignant gliomas and also on tumor cell surfaces, making it an attractive target for development of biomarker and treatment of gliomas. This study attempts to compile available information on relevance of HABP1 to apoptosis or cancer progression that can be employed in achieving novel biomarkers and drugs for therapeutic interventions.

Keywords: HABP1, Hyaluronic Acid/Hyaluronan, Apoptosis, Reactive Oxygen Species, Fibroblasts, Skin Papilloma, Glioma.

ICABB_M237_Div

Role of CRISPR-Cas9 Gene-Editing Technique in Neuro-Degenerative Diseases (NDDs)

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ABSTRACT

Neurodegenerative diseases have risen to alarming numbers in recent times and have been categorized amongst one of the greatest public health challenges. It not only lacks disease-modifying treatments, but the existing treatments are also not efficacious. One of the chief rationales culminating in the lack of efficacious therapeutic alternatives is due to the limited understanding of the complex etiology associated with its genetic origin. Further, many of the neuronal functional activities are regulated and controlled by the genetic along with factors such as DNA methylation & histone modeling. Any kind of alterations in these mechanisms that regulate may affect the cerebral development and mechanism causing neurodegenerative diseases (NDDs). Therefore, understanding these genomic-associated genetic variants is of utmost essential to translate this understanding into therapies. This study explores the benefits of lately developed CRISPR/Cas 9 based functional genomics approach for treating CNS disorders, specifically the NDDs. CRISPR gene therapy technology has revolutionized the various genome and epigenome manipulation targets. Furthermore, it also explores the possibilities of employing CRISPR/Cas 9 tools for several cellular signaling in NDDs as an effective therapeutic intervention in overcoming NDDs which is caused due to certain abnormalities.

Keywords: Genetic Variants, Epigenetic Causes, Glucocorticoids (GR), Mineralocorticoids (MR), Hypothalamic Pituitary Adrenal (HPA) Axis, Neurodegenerative Disorders.

ICABB_M238_Men

Screening of Hydrolytic Enzymes Production by Plant Growth Promoting Bacterial Isolates

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ABSTRACT

Soil harbors heterogeneous group of beneficial bacteria, plant growth promoting rhizobacteria, which colonize in the plant roots and improves the plant growth. They improve soil fertility and foster the plant growth through nutrients mobilization, phytohormone production, alleviating stress and suppressing phytopathogens. Plant Growth Promoting Rhizobacteria (PGPR) suppress phytopathogens through various hydrolytic enzymes such as urease, esterase, protease, lipase, cellulase, pectinase, amylase and chitinase by deformation of their cell wall and act as biocontrol agent. This is an important mechanism of PGPR for controlling the soil-borne phytopathogens and improves the plant growth in the form of sustainable plant disease management. The present study involves the screening of various extracellular hydrolytic enzymes like urease, esterase, protease, amylase, cellulase, pectinase of best 14 bacterial isolates (MA4, MA5, MA6, MA9, RP9, T-1, T-2, E-2, O-2, R-1, TC4, TC11, TG2, and TM9) which were already characterized as PGPR in-vitro in previous study. Out of 14 isolates, 3 isolates (TC4, E-2 and R-1) showed positive for urease test, RP9, TC11, TM9 exhibited positive for cellulase test, while only RP9 isolate showed positive for amylase and pectinase test. RP9, MA4, MA6, MA9 and TM9 isolates revealed positive for protease test whereas O-2, R-1, TC4, TC11, MA6, MA9 and MA4 showed positive for esterase test. The screening of lipase and chitinase test is still in progress. These enzymes are also used for various industrial purposes like pulp industry, food industry, detergent industry, agricultural industry etc. Besides, these isolates can be used singly or consortium as biofertilizers as well as for controlling the soil-borne phytopathogens to improve plant growth in sustainable manner.

Keywords: Phytopathogens, Chitinase, PGPR, Hydrolytic Enzymes.

ICABB_M239_San

Biology and Applications of a Psychrophilic Fungus with Special Reference to *Pseudogymnoascus Roseus*

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ABSTRACT

Psychrophilic (cold-loving) organisms are those that do not show or show defective growth above 20°C. They inhabit various cold environments across the Globe including polar regions, high mountains, glaciers, ocean deeps, the upper atmosphere, refrigerated temperatures. To overcome the low temperature related adversaries, they develop certain special morpho-physiological characteristics. For examples, they have elevated level of intracellular trehalose, polyol and unsaturated membrane lipids, and exhibit secretion of antifreeze proteins and cold-active enzymes. Most of these molecules find applications in biotechnology and pharmaceuticals. *Pseudogymnoascus roseus* BPF6 isolated from Baramullah (J&K) soil produces cold active cellulases that can hydrolyse cellulose at 20- 30°C. Conclusion: - *Pseudogymnoascus roseus* BPF6 produces cold active cellulases that can hydrolyse cellulose at 20-30°C, which is also the favourable temperature range for *Saccharomyces cerevisiae* to produce ethanol by fermenting carbohydrate. Thus, cellulases from this fungus have potential application in simultaneous saccharification and fermentation.

Keywords: Psychrophilic Fungus, *Pseudogymnoascus roseus*, Cold-Active Cellulases.

ICABB_M240_Dar

Detection of a Notorious Pathogen Sorbitol Non-Fermenting, β -glucuronidase-negative *Escherichia Coli* O157:H7 from Different Sample Sources

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ABSTRACT

Specific *Escherichia coli* strain producing Shiga toxin (STEC) O157:H7, represent a hazardous public health problem worldwide ever since identified as a foodborne pathogen in 1982. STEC O157:H7 infection in humans mainly occurs through consuming contaminated food causing various human gastrointestinal tract diseases, including watery or bloody diarrhea and might develop a life-threatening disease, such as haemorrhagic colitis, Thrombotic Thrombocytopenic Purpura and Haemolytic Uraemic Syndrome. The later is characterized by thrombocytopenia, microangiopathic haemolytic anaemia and acute renal failure. Standard microbiological procedure was done to isolate and identify the *E.coli* strain from various sample sources like clinical stool and environmental like water, food etc. All the *E.coli* isolates were subjected to STEC O157:H7 detection and was tested by sorbitol fermentability and β -glucuronidase activity using 4-Methyl-Umbelliferyl β -D glucuronide *E.coli* (MUG EC) broth medium, Sorbitol MacConkeys (SMAC) Agar and combined MUG-SMAC medium. A total of 149 *E.coli* isolates consisting of 62 clinical stools and 87 environmental samples isolates were used for this study. Amongst them 26 were Sorbitol non-fermenting (SNF), of the total 26 SNF 23 were negative for β -glucuronidase activity. The sensitivity of MUG-SMAC plating reported is 82.5% and not every laboratory has sufficient resources to incorporate the serotyping, toxin or PCR assays. Taking into account the clinical significance of STEC O157:H7 make us in need to use rapid and accurate methods for their detection and to establish appropriate control measures to get rid of such organisms. Our study suggests methodical safety assessment and adding up to the use of MUG-SMAC test in laboratories.

Keywords: *E.coli* , STEC O157:H7, Sorbitol Non-Fermenting, β -glucuronidase Activity.

ICABB_M241_Aks

A Systematic Review of Techniques Used for Surveillance of Antibiotic Resistance

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ABSTRACT

World is facing high mortality rate due to infections caused by various microorganisms. The effects of these infections have been reduced by the introduction of a wide range of antibiotics to the market. But infections are still top cause of mortality worldwide, because of mutation of antibiotic-resistance genes. Misuse of Antibiotics is a major reason which influence the selection of resistance. In spite of the problem of antibiotic resistance in microorganisms, we are able to gather very few information regarding the diversity, distribution and origins of resistance genes, especially for the unculturable majority of environmental bacteria. To fight against this problem, we need to clearly understand the different resistance genes that allow bacteria to resist antibiotics. Therefore, many techniques have been developed worldwide and are used to infer mechanistic insights into functioning of these antibiotic resistance genes. However, no “ideal” methodology exists as every technique has some advantage or drawback over the others restricting its implacability but nevertheless, this review focusses on comparing these techniques and elaborating limitations attached to them.

Keywords: *Antibiotic Resistance, Mortality, Antibiotics.*

ICABB_M242_Somy

Covid-19 and Glioblastoma

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ABSTRACT

Background: Glioblastoma (GBM) is the most common and aggressive primary brain tumor in adults whereas the mortality rate of COVID-19 is as high as 61.5%. Both of these diseases are equally devastating but when you put them together it becomes something unstoppable. There have been researches that show that people with GBM are more susceptible to COVID-19. Protein like ACE2, ACTB, MAP2K, etc. is upregulated in Glioblastoma. These are the protein that acts as the receptor for the COVID-19 spike protein, through which the virus gains entry to host cells making Glioblastoma patients easier target for COVID. Here we curated papers to find different proteins that were upregulated/downregulated in COVID and GBM. Then we used Cytoscape and MCODE analysis to analyze the protein-protein network to extract COVID-glioblastoma markers. Proteins like ACTB, CCNB1 and CDK1 have been introduced as a hub – bottleneck. Therefore, it can be concluded that these proteins play important roles in the pathology. Whereas KIF11, RPL35, CD4, LCP2, POLR2E and TNC are proteins that involved in protein networks of COVID-19 in glioblastoma and have been determined as seeds. Hence these are the proteins to targeted for the development of drugs target discovery. The strategy is to target the proteins that are actively involved in the COVID-19 and glioblastoma cells and inhibited or modified them in such a way that the glioma cell die due to triggering of the apoptotic pathway. For this, understanding the molecular mechanisms and involved pathway of these identified seed proteins is required and it may lead to the development of drugs target discovery.

Keywords: Glioblastoma, COVID-19, Cytoscape, MCODE, Hub – Bottleneck Protein, Seed Protein.

ICABB_M243_Amr

Escalating Occurrence of Rickettsial Infection in The Patient of Fever of Unknown Origin (FUO)

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ABSTRACT

Rickettsioses, a zoonotic disease, is the most frequently reported infections in both urban and rural communities worldwide. It is one of most emerging vectors borne infections. Rickettsial diseases may pose a serious threat to public health if not diagnosed or misdiagnosed as it has shares symptoms with other febrile diseases like: malaria, dengue, chikungunya and typhoid etc. Rickettsial infections remain under-diagnosed due to lack of diagnostic facilities in the developing world. Serological assays are the core of febrile illness diagnosis. In developing countries like India, rickettsial diseases are tested by serology-the Weil Felix test. The present study was performed to document the prevalence of rickettsial diseases in patients with fever in the Surat region, part of south Gujarat by serological method Weil felix test. Total 202 clinical blood samples from patients with fever and 25 healthy volunteers' blood samples were collected, processed, preserved and evaluated prospectively. All samples were tested by Weil Felix test for rickettsial diseases. Out of 227 serologically tested samples total 109 shows rickettsioses positive, 65 by OXK suggestive of scrub typhus, 66 by OX19 for typhus group and 35 by OX2 for spotted fever. Occurrence of rickettsioses is significantly high 53.96% in our study region. The lack of geographical distribution data, low index of suspicion and delayed diagnosis poses a challenge to the physician. This disease should be included in differential diagnosis of PUO.

Keywords: Rickettsial Infection, *Scrub Typhus*, Weil Felix Test, Typhus Group Fever, Spotted Fever.

ICABB_M244_Arus

Exploring microRNAs as Therapeutic Targets in Patients with ARDS

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ABSTRACT

Acute Respiratory Distress Syndrome (ARDS) is a severe form of ALI (acute lung injury) and is characterised by three pathophysiological conditions such as: reduction in the ability to eliminate CO₂, hypoxemia, and reduction in lung volume and compliance. Despite its high mortality rate, mechanical ventilation is considered as the main clinical therapeutic strategy in improving the lung volume and gas exchange, to increase the survival rate. In recent years, various investigations performed via high-throughput screening studies have revealed that microRNAs (miRNAs) can serve as therapeutic targets for ARDS. miRNAs are a class of highly conserved, small non-coding RNA molecules that are single-stranded and 18-24 nucleotides long. They regulate the expression of the desired gene by inhibiting the translation of target mRNA or by early degradation of the complementary miRNA. As miRNA expression is a characteristic of a cell and/or tissue type, it makes miRNAs the favourable therapeutic targets. Additionally, since ARDS does not have a standardized laboratory diagnosis, miRNA may be implied to use them for diagnosis as well. It has been demonstrated that microRNAs play both the roles: protective and detrimental, in the pathophysiology of ARDS, starting from regulation of the release of cytokines, till recovering from lung injury and cell survival. Some of the protective microRNAs are: miR-126, miR-146a and miR-150, etc. In the present piece of work, upregulation or downregulation of ARDS-associated microRNAs is being discussed as therapeutic targets for ARDS.

Keywords: ARDS, ALI, miRNA, miR-126, miR-146a and miR-150.

ICABB_M245_San

Prevalence and Geographical Burden of *Scrub Typhus* Disease in MP, Central India

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ABSTRACT

Scrub typhus, a vector-borne zoonotic disease caused by bacteria *Orientia tsutsugamushi*, is a potentially lethal emerging infectious disease in India. Scrub typhus produces severe multiorgan failure and has a circumstance fatality rate of up to 70%, if not treated properly. Scrub typhus epidemiology varies due to Climate conditions, etiological agents and arthropod vectors involved in transmission. The geographical burden of the disease remains unclear in this region. Our goal is to present a thorough review of the geographical burden of scrub typhus in MP India, and management of scrub typhus in both long standing endemic regions and newly identified infectious foci. The information about this is collected from published literature on scrub typhus and google trends. We conducted a systematic narrative synthesis to summarize included studies. It was noticed during the study that Scrub typhus has a unique epidemiology in Madhya Pradesh (M.P.), India and its regional distribution were found to be varied in this study, with the highest proportion of cases recorded (67.2%) in 2018 Malwa region, (45%) in 2019, (26%) in 2020 and (75%) 2021 in Vindhya region. This might be due to lack of awareness about the condition and diagnostic facilities in M.P. as, 81.7 % higher cases were reported from rural areas, than the other regions. The occurrence of the cases was reported to be in the monsoon and post-monsoon seasons, between July to January and could be related with an increase in the frequency of scrub typhus cases. Our study revealed an increasing trend of scrub typhus in MP, India, indicating a worsening condition since 2018 to 2021. Morbidity and mortality of this disease can be reduced if diagnosed early through RDT, ELISA, PCR and treated appropriately.

Keywords: Scrub Typhus Disease, MP, *Orientia tsutsugamushi*.

ICABB_M246_Aay

Senescent Cells in Ageing

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ABSTRACT

As we age we accumulate more and more cells that have stopped dividing and have stopped functioning normally, but are still metabolically active and having an adverse effect on the surrounding cells, and these cells are called senescent cells. Cellular senescence was first described by Hayflick and Moorfield using *in vitro* cell culture studies in 1961. It has been historically viewed as a mechanism to protect against cancer but emerging evidence proved that the physiological relevance of cellular senescence is beyond that, its complex biological mechanism can be utilized as an amelioration of tissue repair and ageing disorders. One of the most exciting areas of the research into longevity is the studies being done on cellular senescence. Although the senescent cells can no longer replicate, they remain metabolically active and typically provoke an immune response through the secretion of pro-inflammatory factors including a bunch of substances like cytokines and chemokines and extracellular matrix metalloproteinases (MMPs), and these substances form SASP (senescence associated secretory phenotype). This review describes the phenomena of cellular senescence and its' manifestation mechanisms in three possible biological scenarios of senescence derived ageing; first, excess cellular senescence results in stem cell exhaustion. Second, uncontrolled cell senescence leads to deregulated nutrient sensing and third is SASP including potent inflammatory cytokines secretion by senescent cells.

Keywords: Ageing; Cell Senescence; Proinflammatory Cytokines; SASP; MMPs; Deregulated Nutrient Sensing; Stem Cell Exhaustion.

ICABB_M247_Vai

Role of Cytokines in Covid-19

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ABSTRACT

Outbreak of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) baffled the world. Lack of information about Covid-19 and its symptoms created a havoc throughout the world. We were already familiar with other strains of SARS, SARS-CoV-2 is the deadliest of them all. SARS-CoV and MERS-CoV reveal 80% and 50% similarities with SARS-CoV-2 respectively. As the striking death rate increased around the globe, many scientists were challenged to find some remedies to cure this virus. This pandemic questioned the practice of health workers. This virus is seen to have great influence over inflammatory cells, hence triggering the cytokine storm. Sudden accumulation of inflammatory cells caused serious multi organ damage. Angiotensin Converting Enzyme Receptor (ACE2) is the receptor through which the virus enters. These receptors are found in the lungs, small intestine and many other organs. It was found that this virus causes Acute Respiratory Distress Syndrome (ARDS) which affects both upper and lower respiratory tract. Cytokine storm is considered as the major reason for the surplus increase in the death ratio. Cytokines unleash destruction with the invulnerable framework betraying itself in immune system infections. These proinflammatory cytokines cause tissue damage. The receptor led to the entry of the viral genome in the cells. and triggers cytokine storms and different cytokines fluctuate in this situation. Targeting cytokines helps pharma companies to design the vaccines and drugs required to cure and control the COVID infection and patient management.

Keywords: COVID-19, Cytokine, ACE2, Target-Receptor.

ICABB_M248_Aays

Modelling Ageing

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ABSTRACT

It is predicted that by 2050 nearly 20% of the global population will be above the age of 60y. The increased elderly population will have compromised physiological and functional capacity along with an increased susceptibility to multiple chronic diseases. Thus, there is an imperative need to study aging, its underlying mechanisms and develop interventions that facilitate healthy ageing. Modeling human ageing has been facilitated by diverse model systems and strategies. Broadly the models reported in literature can be classified into cellular and animal models. The studied cellular models include primary cultures derived from elderly humans or animals, secondary cell lines of animal or human origin treated with chemicals to accelerate ageing hallmarks such as peroxide, d-galactose or gene knockouts/silencing of critical life span governing genes. *S. cerevisiae* or the yeast is also an important eukaryotic unicellular model endorsed by several researchers for studying ageing and is used to simulate replicative ageing as well as chronological ageing. The multicellular or animal models to simulate and study ageing comprises of aged *C.elegans*, *D.melanogaster*, *Mus musculus*, *R.norvegicus* as well as primates. However, the prime reason these conventional model organisms rose to popularity was that they had shorter lifespans. Thus, there is an emerging literature endorsing the use of long-lived animals as more favorable models for ageing and longevity studies. For example - bats, turtles, and reptiles are finding ever increasing support for examining the longevity pathways. Lastly, direct indications of human lifespan governing mechanisms are also gleaned from studying octogenarian, nonagenarian and centenarians. Blue zones are regions around the world where people have higher than usual lifespan, five such zones have been identified globally - Okinawa (Japan), Sardinia (Italy), Nicoya (Costa Rica), Icaria (Greece), Loma Linda (USA), and investigations on the biology, lifestyle and diet of the populations in these regions is being investigated to better understand ageing. The present study discusses the above-mentioned models in terms of utility and applicability to ageing research.

Keywords: Ageing; Cell Lines; *S. cerevisiae*; *C. elegans*; *D. melanogaster*; *Mus musculus*; Health Span; Life Span.

ICABB_M249_Sma

Role of Biotechnology and its Diagnostic Implications in Management and Treatment of Head and Neck Infection

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ABSTRACT

Biotechnology studies genetic materials of infection causing pathogens to determine particular disease-producing agents. Its techniques assess the role of microbial agents and genetic factors which contribute to human diseases. Head and neck infection is the most common infection in human body managed by otorhinolaryngology specialists. The proliferation of infection could be moderate in its chronic stage. Microbiological identification of head and neck infection for confirmation of pathogens, direct sequencing for finding the variants, whole-genome sequencing for detecting structural variants, polymerase chain reaction (PCR) for amplification, post-amplification analysis, recombinant DNA technology helps to detect molecular defects as well as acquired infectious diseases. Such types of diagnostic techniques are used to detect and differentiate numerous microbial pathogens and its antibiotic/antifungal resistant mechanisms. It is very cost-effective and produces more accurate results than basic conventional techniques. Molecular biology has developed with rapid and confirmatory diagnosis. Sometimes the primary conventional methods are unable to diagnose the concerned pathogens of head and neck infection. Molecular and microbiological techniques along with their applications in microbial characterization, a review of previously standardized techniques, sample acceptance and rejection criteria for commonly encountered illnesses and severe infections are all focused. Future gene based diagnostic methods are considered for faster characterization of infectious agents and the discovery of new antibiotic/antifungal agents. Biotechnological processes are being utilized for rapid detection and diagnosis of head and neck infection to create better future treatments.

Keywords: Head and Neck Infection, Pathogens, Biotechnology, Diagnostics, Treatment.

ICABB_M250_Ish

Pathogenic Co-Infection is Critical Risk Factors for the Severity of COVID-19

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ABSTRACT

Microbes, often known as microorganisms, are microscopic unicellular creatures that can only be seen using a microscope and are undetectable to the naked eye. They account for more than 60% of all living creatures on the planet and may be both useful and dangerous. Some bacteria are capable of causing serious illnesses and infections, as well as contaminating food and other items. Many, on the other hand, serve an important role in maintaining the environment's equilibrium. A plethora of microbial domains, such as viruses, bacteria, archaea, and fungi, have coevolved and interact in complex molecular pathogenesis. Millions of individuals have been impacted by the pandemic coronavirus illness 2019 (COVID-19), which is caused by the Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2). Co-infection is thought to be a major risk factor for the severity and fatality rates of COVID-19. Some people may die as a result of co-infection rather than the virus itself. This chapter is divided into two sections: the first is about microbial pathogens, which mostly focusses on the functionality of the genes, and the other one is human arising pathogen, SARS-CoV-2, which emphasis on the pathogenicity of SARS, transgenic model organisms for infection, prevention, and progression in vaccine unravelling and antiviral therapeutics. The information gained is still useful in comprehending pathogenic co-infection with SARS-CoV-2. However, the participation of various microbial co-pathogens, as well as the underlying molecular pathways leading to exorbitant illness in critically sick COVID-19 patients, has yet to be thoroughly investigated.

Keywords: Microbes; Pathogens; Infectious diseases; SARS-CoV-2; Co-infection.

ICABB_M251_Aish

Role of MGB Axis in Onset of Depressive Behaviour

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ABSTRACT

According to the WHO report (2017), the global prevalence of Depression accounts for around 322 million people. It has been reported that MDD is associated with dysbiosis of gut microbiota composition in both human and animal depressive models. A healthy gut with diverse microbes is vital for normal brain functions and emotional behaviour; the CNS controls most aspects of GI physiology. The MGB axis represents the interkingdom communication between the brain and the gut microbiota. Changes in the bidirectional relationships between the GIT and CNS are linked with the pathogenesis of neurological disorders; therefore, the microbiota/gut-and-brain axis is an emerging and widely accepted concept. Studies of germ-free (GF) murine models have shown that murines having abnormal gut-microbiome show significant changes in their brains, especially in regions corresponding to stress. Another study, conducted on cynomolgus macaques displaying naturally occurring depressive-like (DL) behaviours showed that they have characteristic disturbances of the phylum Firmicutes in their microbial composition. This is further strengthened by the fact that MDD patients have also shown increased *Bacteroidetes*, *Proteobacteria*, and *Actinobacteria*, and less *Firmicutes*. Another randomized human trial showed that *Bifidobacterium* and *Lactobacilli* sp. have variable impacts on cognitive and emotional behaviours. The intricate and bidirectional molecular relationship between the gut microbiome and the CNS ensures gut homeostasis and correct digestion. Overall, it is clear that the gut microbiome playing a facilitating role between stress response, and depression has been emerging. Challenges in the form of heterogeneous nature of gut microbiota composition and depressive symptoms in the clinical setting warrant further investigations.

Keywords: Gut Microbiota, MGB Axis, Major Depressive Disorder, Firmicutes, *Lactobacillus*.

ICABB_M253_Arc

Use of Stem Cells in Curing Human Diseases

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ABSTRACT

Specialized cells in the human body are called Stem Cells. They are able to differentiate themselves from any living cell and have the ability to regenerate themselves. The goal of any stem cell therapy is to repair damaged tissue that can heal itself. Ongoing research on stem cell therapy offers hope to patients who often would not receive treatment to cure their illness but simply to alleviate the symptoms of their chronic illness. Diseases such as Leukaemia, Autism and Diabetes are just a few of the incurable diseases that we have studied extensively and found to be effective in stem cell therapy. Stem cell therapy is used in a clinical setting, more research is needed to understand the behaviour of stem cells during transplantation and the mechanisms of interaction of stem cell with a diseased / damaged microenvironment. Medical researchers expect elderly and embryonic stem cells to treat cancer, Type 1 diabetes, Parkinson's disease, Huntington's disease, Celiac disease, heart failure, muscle and nerve damage, and many others. Stem-cell therapy is the use of stem cells to treat or prevent a disease or condition. In summary, it is usually one month until you begin to see the gradual effects of stem cell treatment and you may notice changes in your medical condition for 6 months or more.

Keywords: Microenvironment, Neurological, Stem Cell Therapy, Stem Cells.

ICABB_M254_Mar

Preliminary Evaluation of Antibacterial Efficacy of a Polyherbal Formulation on Antibiotic Resistant Pathogens

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ABSTRACT

Context: Antimicrobial resistance (AMR) is one of the world's most urgent public health problems. Current strategy of antibiotic development is based on single target-single compound approach. This makes easy for the bacteria to become antibiotic resistant very fast, but in the case of traditional polyherbal formulations, the drug works on the principle of synergy. Development of bacterial resistance to such synergistic combinations will be much slower than those for single drug therapy (antibiotics). The research work proposes the application of a polyherbal drug formulation against multidrug resistant (MDR) clinical bacterial isolates. The formulation was prepared as per the Ayurveda formulary of India. The formulation is a combination of *Tinospora cordifolia*, *Terminalia chebula* and *Zingiber officinale*. Phytochemical screening showed the presence of alkaloids, phenols, saponins and carbohydrates. Agar well diffusion assay was carried out on 14 antibiotic resistant bacterial clinical isolates from respiratory tract under standard conditions as per CLSI guidelines. The MDR isolates include *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* and *Acinetobacter baumannii*. The results showed highly promising antimicrobial activity of the formulation on MDR pathogens compared to standard antibiotics. Polyherbal formulations can easily inhibit the growth of antibiotic resistant pathogens. Researchers have to explore the antibacterial potential of various Ayurvedic formulations as an alternative strategy to combat antibiotic resistance.

Keywords: Antimicrobial Resistance, Polyherbal Formulation, *Terminalia chebula* and *Zingiber officinale*.

ICABB_M255_Vive

Detection of Parkinson Disease related Extracellular Vesicle's Surface Protein Using Aptamers

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ABSTRACT

Parkinson's Disease (PD) is the most recurrent and progressive neurological disorder that affects body movements, and still, there is no effective treatment for PD. The diagnosis relies on the motor symptoms that developed too late for disease-modifying interventions. Extracellular vesicles (EVs) are the secreted membrane particles involved in cell-to-cell communication. So far, many studies have found EVs associated with neurodegeneration disorders, and surface protein on the EVs can be an act as a biomarker that shows potential for diagnosis and prognosis. For detecting surface protein on the EVs, an antibody is commonly used. However, it is found that antibodies are not thermally stable and give false-positive results when the sample is highly complex. Nowadays, nucleic acid called aptamers has been widely used in biochemical assays. Aptamers are highly specific, thermally stable, and have a high affinity compared to antibodies. We hypothesized an aptamer-based method to detect surface protein on EVs associated with PD. We will combine the robustness of aptamer in binding specificity with the signal amplification ability of CRISPR-Cas13/Cas12 trans-cleavage activity. This may provide a new detection strategy to detect surface protein on EVs in a rapid, sensitive, and cost-effective, showing high potential towards early diagnosis and treatment.

Keywords: Parkinson Disease, Extracellular Vesicles, Aptamer, CRISPR.

ICABB_M256_Riya

Use of Biodegradable Polymers and Hydrogels for Developing Artificial Skin

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ABSTRACT

Skin is the largest and most crucial organ of the body and every year or every minute people suffer from severe injuries leading to loss or causing damage to skin tissues. Now, this damage might occur due to burns, skin cancer, accidents, severe scarring. So, due to deep wounds, the body's natural wound-healing system may fail, requiring the need of external or artificial assistance. The existing grafts are quite expensive making them unaffordable for several individuals and the development requires a lot of time which delays the healing process and it also has other drawbacks such biodegradability, immuno-rejection, etc. So, because of these challenges' studies are conducted to create artificial skin. Different polymers, or a combination of them and cultivated skin cells, can be employed in the development of artificial skin; these materials allow the area to be sealed to prevent dehydration and bacterial infection, the most important aspects for curing. Now, artificial skin has another important aspect that is it can also be used for cosmetic and medical testing. So, this report aims to briefly describe all the Biomaterials, the importance of hydrogels, different fabrication techniques and stem cells required to develop an artificial skin and it also focuses on the drawbacks of existing strategies.

Keywords: Artificial Skin, Skin Grafts, Stem Cells, Biomaterials, Hydrogels, Fabrication Techniques.

ICABB_M257_Vedi

Gut Microbiota & Alzheimer's Disease: Correlation Explored

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ABSTRACT

The intestinal flora is composed of a complex community of microbial species found in the gastrointestinal ecosystem, the changes not only to various intestinal diseases, but also to central nervous system diseases such as Alzheimer's disease (AD). Also has an effect. AD, the most common form of dementia, is a neurodegenerative disease associated with cognitive impairment and the accumulation of amyloid β peptide ($A\beta$) in the brain. Most notably, the microbiota gut hornochse is a two-way communication system that is not yet fully understood, but includes neural, immune, endocrine, and metabolic pathways. Studies in germ-free animals and animals exposed to pathogenic microbial infections, antibiotics, probiotics, or fecal microflora transplants suggest a role for gut microbiota in host recognition or AD-related etiology. Increased intestinal and blood-brain barrier permeability induced by microbiota dysbiosis can mediate or affect the etiology of AD and other neurodegenerative diseases, especially age-related diseases. In addition, bacteria that colonize the gut flora can secrete large amounts of amyloid and lipopolysaccharide, which regulate signaling pathways and produce inflammatory cytokines associated with the etiology of AD. In addition, gut microbiota imbalance can cause inflammation, which is associated with the etiology of downregulated pathogenic clearance, disruption in the signaling processes of the gut brain axis and greater accumulation of beta-amyloid fibrils in the central nervous system. The purpose of this review is to summarize and discuss current findings that may elucidate the role of the gut flora in the development of AD. Understanding the underlying mechanism can provide new insights into new treatment strategies for AD.

Keywords: Alzheimer's Disease, Gut Microbiota, Dysbiosis, Amyloid, Microbiota-Gut-Brain Axis, Inflammation.

ICABB_M258_Medh

Probiotic Supplementation in Chicken Feed

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ABSTRACT

Presently, the increased bacterial resistance is the reason behind elimination of sub-therapeutic use of growth antibiotics as growth promoters in poultry. An alternative to sub-therapeutic antibiotics in poultry, is the use of probiotic microorganisms or synbiotic combinations of prebiotics and probiotics. Feed supplementation by probiotics aid as promoters of early development in chicken. Probiotics, when administered in adequate amounts confer a health benefit on the host. They can be fungi, yeast and bacteria. Most common probiotic is Lactic acid bacteria, especially *Lactobacillus* and they are considered for use in the feed industry lately. They are desirable members as they affect the intestinal micro-flora positively and help improve the health of the host. Probiotics can also be administered as a mixture of microorganisms thereby improving the gut micro-flora by displacing harmful bacteria which are detrimental to the sustenance of living beings. Usually, live non pathogenic bacterial strains that belong to genus *Lactobacillus*, *Streptococcus* or *Enterococcus*, are used in livestock and poultry. A probiotic is good when it exhibits a few qualities such as being, non-pathogenic, non-toxic, symbiont, and most importantly the capability to resist the adverse environment of the GI tract. *Lactobacilli*, isolated from chicken gastrointestinal tract, were examined and its potential probiotic properties were studied. These strains also exhibit inhibitory activity against enteropathogenic bacteria like *Clostridium Perfringes*, *Salmonella* and *E.coli*. Digestive enzymes like amylase, protease and lipase, found in th. *Lactobacillus* spp collected from birds, enhance the digestion and absorption of carbohydrates, proteins and fats, respectively, and thereby improving the feed conversion efficiency.

Keywords: Chicken Feed, Probiotics, Digestive enzymes, Enteropathogenic, Gastrointestinal Tract.

ICABB_M259_Aan

Progerin: Next Generation Anti-Aging Target

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ABSTRACT

Aging is an unavoidable phase in our lives. Ongoing studies to understand the causes and physiological processes associated with aging, point out that one of the causes of natural aging is nuclear DNA damage which is associated with telomere shortening which leads to cell death. Further, loss of epigenetic structure, increased DNA methylation, altered post translational modifications, damage by reactive oxygen species (ROS) oxidizing lipids, proteins and DNA mutation also adds up to the aging process. One of the biomarkers used in these studies is Progerin, which is a mutant form (C-terminal short by 50 amino acids) of Lamin A, which is fibrillar or filamentous in nature and is one of the isoforms of the *LMNA* gene product. It is now established that the natural process of aging is similar to Hutchinson-Gilford progeria syndrome (HGPS), a genetic disorder which occurs due to the mutation in exon 11 of the *LMNA* gene. The underlying cause of premature aging in HGPS is lapse in cleavage of mutant Lamin A from nuclear due to presence of farnesylated group, leading it to be permanently attached to the nuclear envelope and cause abnormalities. Treatment strategies for HGPS include inhibiting the farnesylation of progerin and it is envisaged that Farnesylation and methylation inhibitors may be promising approaches for delaying natural process Aging.

Keywords: Progeria, Progerin, Lamin A, Aging.

ICABB_M260_Jyot

Gut Microbiota Brain Axis: A Bidirectional Communication

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ABSTRACT

The human gut-microbiota and brain could be a bidirectional communication that integrates the central systema nervosum and also the enteric system, that links the brain with the channel. It's essential in maintaining homeostasis of the gastrointestinal, central systema nervosum and microbial systems of animals. Microbiota make neuroactive compounds which has 90% of our neurotransmitter serotonin which successively helps in emotion regulation then send signals via brain to the digestive system. Several research evidences show that the gut microbiota brain axis is crucial for brain development and performance. The metabolism of gut microbiota is modulated by the physiology of the host brain through the gut- brain axis. Discovery shows the connections between the gut microbiota, neurotransmitters and brain function are using direct and indirect methods for communication. With the rise amount of HSHF (High Sugar High Fat Diet) which was directly linked with Gut Microbiota. The Gut Microbiota, in turn, uses TMAO (Tri-Methyl-Amine Oxide) to regulate choline levels, forming a relationship between the Microbiota, Brain circRNAs and Metabolism. The information was gathered utilizing a variety of technical approaches, including germ-free animal models, probiotics, antibiotics, and infection studies. The link of dysbiosis with CNS illnesses (i.e., autism, anxiety-depressive behaviors) and functional gastrointestinal disorders validates microbiota-gut microbiota axis interactions. The association between dysbiosis and disease, with a special emphasis on functional bowel disorders and their link to psychological stress. Information on the interlinking of the microbiota and brain axis to aid in the identification of prospective therapeutic markers and mechanistic solutions to various diseases can be found in pathology, toxicology, diet, and nutritional studies.

Keywords: Gut Microbiota, Nervous System, Bidirectional, Stress, Gut-Brain Axis.

ICABB_M261_Many

Cardiac Regeneration: Recent Advancements and Future Prospects

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ABSTRACT

As the prevalence of cardiovascular disease (CVD) increases, invasive treatment methods including coronary reperfusion therapy, coronary artery bypass, and angioplasty have become more popular. These treatments are primarily used to relieve acute symptoms instead of promoting heart repair and regeneration. According to the WHO, majority of the population is suffering from myocardial infarction or ischemic strokes, as compare to other CVDs. Furthermore, despite significant progress in research and numerous discoveries, there are still a few obstacles and clinical complications in developing better diagnosis and treatment strategies for CVDs. The evolution of biomedical engineering and regenerative medicine offers new perspectives and led to the development of novel cardiac regenerative approaches and cardiac reprogramming by targeting some key signaling molecules. In recent studies, exosomes, miRNAs, nanoparticles, and patient-specific cardiomyocytes (CMs) have all been used to promote regeneration efficacy and overcome limitations in the field of cardiac regeneration. In this review, we will summarize the CVDs, limitations in the domain of cardiovascular research, breakthroughs in regenerative medicine, and the application of biomedical engineering in the development of innovative therapeutic strategies.

Keywords: CVD (Cardiovascular Disease), Coroary Aretry Bypass, Coronory Reperfusion Therapy, Exosomes, miRNA.

iCABB_M262_Priya

Development of Quality Standards for rDNA Therapeutics

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ABSTRACT

Indian Pharmacopoeia Commission (IPC) is a standard setting organization under Ministry of Health & Family Welfare, Government of India. Indian Pharmacopoeia (IP) is published by the IPC as the official book of standards for the drugs being manufactured and/or marketed in India in fulfillment of the requirements of the Drugs and Cosmetics Act, 1940 and Rules 1945. IP contains a collection of authoritative procedures of analysis and specifications of drugs for their identity, purity and strength. IP also publishes standards for biotherapeutic such as Vaccines and Immunosera for Human and veterinary Use, Blood and Blood Related Products and Biotechnology Derived Therapeutic Products etc. These standards are developed with the detailed consultation and discussion with experts and stakeholders including manufacturers, regulatory bodies, research and academic institutions. IP prescribes standards for identity, purity and strength of drugs essentially required from health care perspective of human beings and animals

Keywords: Indian Pharmacopoeia (IP); Quality Standards; Biologicals; recombinant DNA Therapeutics.

SESSION III
Food, Agriculture
and
Natural Products

ICABB_F301_Bhup

Anti-arthritic Activity of Snow Mountain Garlic Against Complete Freund's Adjuvant-Induced Arthritis in Rats

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ABSTRACT

In the Indian traditional medicine system, Snow Mountain Garlic (*Allium ampeloprasum* L.) (SMG) has been described to possess immunity booster, anti-inflammatory, and antioxidant activities. It is a perennial herbaceous plant cultivated at an altitude of ~6000 feet above mean sea level in the territory of Jammu and Kashmir. Although the natives of the aforesaid region use this high mountain wild variety of garlic to treat rheumatic conditions, yet no scientific explanation is available to endorse the pharmacological activity. Therefore, in the present investigation antiarthritic potential of SMG was evaluated by Freund's adjuvant-induced arthritis in rats. The results indicate that at dose 500 mg/Kg, SMG produced a significant reduction in arthritis index, paw volume, joint stiffness, and paw diameter. SMG extract has shown better protection against bodyweight alterations and ameliorated altered hematological parameters in comparison with common garlic. Further, the pre-clinical serum markers of inflammation and arthritis viz rheumatoid factor, erythrocyte sedimentation rate, C-reactive protein also normalized to 34 ± 5.7 IU/ml, 3.4 ± 0.9 mm/hr, and 76.5 ± 5.7 µg/L respectively, in the SMG (500 mg/Kg) treated arthritic rat. Taken together, the presented study results support the traditional use of SMG as an antiarthritic agent. In conclusion, the present study substantiates the ethnomedicinal use of SMG in the treatment of inflammatory ailment. However, additional clinical investigations are much needed to prove the potency of SMG in the treatment of rheumatoid arthritis.

Keywords: Snow Mountain Garlic, CFA, Anti-Inflammatory, *Allium*, Antiarthritis.

ICABB_F302_Jat

Ficus Religiosa* a Potential Source of Therapeutics for *Herpes Simplex Virus-I

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ABSTRACT

Herpes Simplex Virus-I (HSV1) infects around 67% of the population, under the age of 50 (WHO). A person once affected with the virus has to carry the infection lifelong. Symptoms for this infection are severe as these are not only immensely painful but also, open the gateways for other diseases such as Multiple Sclerosis, Graves' Disease and many others. No medication is yet available for the disease except that the symptomatic relief can be obtained, up to some extent, by some drugs available in the market. We have been getting therapeutics for old and emerging diseases, from the Nature, since ancient time. One of such sources of medicines is the tree *Ficus religiosa*, which is commonly known as “Peepal tree”. This tree carries many medicinal properties such as: antimicrobial, antibacterial, antiviral and is also used to cure diabetes. In the present study, various bioinformatics tools such as: AutoDock, Vina and Ligplot+ and databases were used to explore various phytoactives of this tree, such as: piperine, piper longumine, kaemferol, to dock with gB, gC, & gD proteins from HSV-1. Analyzing the results, these compounds are proposed to be the potential candidates against *Herpes Simplex Virus -1*. Further in vitro and in vivo experiments would be required to validate these results in real life.

Keywords: *Herpes Simplex Virus-1, Ficus Religiosa, Antimicrobial, Antiviral, Piperine, Kaemferol.*

ICABB_F303_Sop

Computational Identification and Function Annotation of *Pseudomonas syringae* pv. Tomato (strain B13-200) miRNAs and Prediction of Their Target Genes in the Tomato Genome

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ABSTRACT

MicroRNAs (miRNAs) are post-transcriptional regulators of gene expression. It is a well-studied subject of non-coding RNAs that have been identified in the genomes of plants, animals, bacteria, and viruses. In this work, we examined the whole genome sequence of *Pseudomonas syringae* pv. tomato strain B13-200 (PSTB13) in order to identify non-coding RNAs. Two mature miRNA sequences were predicted from the genome of PSTB13 using the CID-miRNA and maturebytes software. The identified putative miRNAs were 22 nucleotides in length, which is in the range of previously reported for animal and plant miRNAs. We found 16 possible target mRNAs in tomato for the two miRNAs discovered in PSTB13. Most of the identified targets are transcription factors involved in tomato development, such as stress response, structural components, development, and metabolism. The DAVID web service was used for gene ontology (GO) analysis. In this study, fourteen GO terms were discovered to be highly enriched with seven target genes (eight GO terms for biological process, four GO terms for cellular component, and one GO term for molecular function). Pathway annotation of target genes showed that two predicted PSTB13 miRNAs are involved in the glyoxylate and dicarboxylate metabolic pathways. Further, our findings will help to understand the role of miRNAs in *S. lycopersicum* and will serve as the foundation for future research into PSTB13 miRNAs. Overall, this research will provide useful insights into the role of miRNA in controlling the growth and development of the important food tomato.

Keyword: CID-miRNA; MicroRNA; *Pseudomonas syringae* pv. tomato strain B13-200; psRNATarget; Tomato.

ICABB_F304_Vis

Plant Growth Promoting Activities of *Klebsiella* SL17 Isolated from Carcass of Caterpillar

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ABSTRACT

Klebsiella sp. belongs to Enterobacteriaceae family of Gammaproteobacteria. The aim of the present study was isolation, characterization and screening of plant growth promoting (PGP) activities of *Klebsiella* SL17 isolated from carcass of *Spodoptera litura*. *Klebsiella* SL17 was identified on the basis of 16S rRNA sequencing and biochemical characterization. The organism produces large quantities of exopolysaccharide and produces creamish white gummy colonies on Nutrient agar medium. The cultures of *Klebsiella* produced plant growth hormone Indole Acetic Acid (100 µg/ml) after 5 days incubation in Luria Broth supplemented with 200 µg/ml Tryptophan in static condition at 37°C. IAA was extracted from the cultures and separated and identified by Thin Layer Chromatography. *Klebsiella* also solubilized phosphate on Pikovskaya's agar medium within 24 h. Static cultures of *Klebsiella* growing in Pikovskaya's medium solubilized 6.25 ± 0.019 µg/ml in 24 h at 37°C. The organism is highly susceptible to Cephalosporin, Quinolones, Chloramphenicol, less sensitive against Penicillin, and not susceptible to Lincosamides and Cefixime. The organism can be useful in the production of IAA and also as biofertilizer in Agroindustry.

Keywords: Agroindustry, Biofertilizers, Indole Acetic Acid, *Klebsiella*, Plant Growth Promoting Activities (PGP), *Spodoptera litura*.

ICABB_F305_Bho

Probiotic Characteristics and Antioxidant Activities of *Lactobacillus Plantarum* FDS2 from Fermented Food

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ABSTRACT

Probiotic Lactic acid bacteria exhibiting free radical scavenging antioxidant activity have been used in fermented foods and food supplements. *Lactobacillus plantarum* FDS2 isolated from fermented spices possessed probiotic properties viz. (i) tolerance to pH 2, bile salt 4%, phenol 0.6%, and NaCl 6% (ii) Viability of *L. plantarum* during transition from oral cavity (simulated saliva) 8.22 log cfu/ml to gastro-intestinal tract (simulated gastro-intestinal fluids 7.98-7.84 log cfu/ml), (iii) *L. plantarum* showed a broad-spectrum antimicrobial activity against food spoilage organisms and food-borne pathogens. *L. plantarum* whole cell, cell free culture and intracellular cell free extract exhibited free radical scavenging activity evaluated using DPPH (2,2-Diphenyl-1-picrylhydrazyl), ABTS (2,20-Azinobis(3-ethylbenzothiazoline-6-sulfonate) and iron chelating assay. ABTS (410 mg/ml trolox equivalent activity) and iron chelating activities (62.87%) were higher with whole cells. Cell Free Culture fluid exhibited higher DPPH scavenging activity (63%). The results demonstrate the probiotic potential and Antioxidative activities of *L. plantarum* FDS2 strain.

Keywords: ABTS, Antioxidant, DPPH, *Lactobacillus Plantarum*, Probiotic.

ICABB_F306_Pri

Exploring the Role of Linalool Synthase Promoter in *Ocimum basilicum*

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ABSTRACT

Ocimum basilicum belonging to the family Lamiaceae, has a high monoterpene content. Many of the monoterpenes are aromatic compounds and have a large market in the cosmetic and perfumery business. Monoterpene synthases have received little attention despite their economic importance. Furthermore, neither the functional nor molecular aspects of these genes in *Ocimum* have been well investigated. *O. basilicum* variety CIM-Surabhi, created by CSIR-CIMAP utilizing half-sib family selection, was found to be high in linalool, a monoterpene, according to GC-MS analysis. Linalool synthase (LiS) produces linalool, which is stored in *O. basilicum* glandular trichomes. Real-time expression and GC-MS analysis of LiS gene in root, stem, leaf, trichome, and inflorescence showed the highest expression in trichome followed by leaf suggesting this gene to be trichome-specific. In the present study, the promoter region of the LiS gene was identified from the genomic data of *O. basilicum*. The ~2kb upstream promoter sequence was cloned in pGEM-T cloning vector and sequenced. The LiS gene promoter was cloned in the vector pCambia 1304, coupled with transcriptional fusion to the chimeric reporter gene GFP-enhanced: -glucuronidase (GUS). We investigated the expression of LiS promoter transiently in *O. basilicum* variety CIM-Surabhi. Understanding the spatio-temporal expression and gene regulatory patterns of the target gene will be greatly aided by studying the promoter expression pattern. The LiS gene promoter study will aid in the discovery of novel transcription factors, giving a possible target for determining the mechanism of differential linalool accumulation in plants.

Keywords: *Ocimum basilicum*, Promoter, Linalool Synthase, Monoterpene.

ICABB_F307_Pea

Studies on the Microbial Potential of Fermentation Broth in Enhancing the Aroma of Agarwood Essential Oil

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ABSTRACT

In Northeast India, particularly Assam, agarwood (*Aquilaria malaccensis*) is a major aromatic plant which is also famous globally. Extraction of fragrant agarwood oil is carried out by hydro-distillation in commercial units called “Dega” located mostly in Upper Assam. However, prior to distillation, agarwood chips are soaked in water for a period of 45-90 days. This step has a significant role in the quality of the agarwood oil but scientific studies to understand the exact role of this microbial interaction on agarwood oil quality are very few. The study of the microbiome of agarwood fermentation basin is therefore the first logical step to understand the role of the microbes in determining the quality of aroma as well as quantity of agarwood oil. In this study, fermentation basins of different commercial “Deg” located at Namti in Sivasagar, Nahoroni in Golaghat and Fauzdaripatty in Nagaon of Assam were selected where agarwood chips had been soaked in water for different durations. Identification and characterisation of the isolates, was carried out by standard microbiological and molecular techniques of samples of fermentation broth collected from the basin. A total of 20 bacterial and 14 fungal isolates were obtained. The microorganisms were screened for the fermentative potential by various enzyme assays such as for cellulase, xylanase, lipase. The organisms so screened can be used in fermentative analysis either alone or in consortia to improve and enhance the fragrant potential of agarwood.

Keywords: *Aquilaria*, Enzymes, Microorganism, Fragrance.

ICABB_F308_Ush

Oleosin Gene Family of *Carthamus Tinctorius*: Uncovering of Natural Allelic Variants Associated with High Oil Content Through Sequence-Based Allele Mining

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ABSTRACT

Oleosins are oil body structural proteins that play an important role in lipid storage in the oil seed crops. In safflower, about 90% of the released varieties and hybrids in India are of low oil content; therefore, there is a need to improve the oil yield which is one of the major limiting factors affecting safflower productivity. In present research work, we were interested in determining whether there are any allelic differences in the Oleosin genes which are associated with high oil content in safflower. Eleven Oleosin genes, namely CtOleosin 1 to CtOleosin 11) were predicted through gene annotation from genome assembly of safflower. All the Oleosin genes showed conserved oleosin domain ((PFO1277) and ‘proline knot’ motif. Further bioinformatics analysis revealed the size of their CDS range from 400 to 675 bp, encoding 137 to 227 aa polypeptides with molecular weights of 14.812 to 22.155 kDa. The transmembrane domains and Putative conserved motifs were predicted. Allele mining of these genes in 20 each low and high oil content genotypes of safflower for nucleotide variation revealed two distinct haplotypes with CtOleosin2, CtOleosin4, CtOleosin5 and CtOleosin9. CtOleosin 4, 5, 9 showed nucleotide change in the coding region in high oil lines leading to the change in the amino acid composition from methionine to lysine, threonine to serine and serine to glycine respectively. Whereas, CtOleosin2 showed nucleotide change in the 3’ UTR region without aminoacid change. A total of 100 germplasm lines representing a wide range of oil content, were used for association analysis between SNPs and high oil and confirmed the mutations was associated with high oil content. The natural variation in the tested Oleosin candidate genes provides a significant asset for further improving oil content in safflower.

Keywords: Oleosin, Genes, Oil Content, Allele Mining.

ICABB_F309_Amr

***In-Vitro* and *In-Silico* investigations of Anti-oxidant and Anti-Proliferative Potential of *Abrus precatorius* Seed Extracts in Cervical Cancer**

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ABSTRACT

Abrus precatorius is a medicinal herb with a variety of therapeutic benefits, however the potential of its seed extract in cervical cancer (CaCx) still haven't been explored. In this study, we explored the antiproliferative efficacy of *A. precatorius* seed extracts (ethyl acetate and 70% ethanol) obtained from distinct extraction methods (Soxhlet and maceration) in Hep2C cells. Through our HPLC analysis, we identified phytochemicals such as tannic acid, rutin and piperine. APE (mac) showed the most significant antiproliferative activity against Hep2C cells. In addition, the APA(Mac) extract exhibits the highest SOD and GST activity, whereas the APE(Mac) extract showed the highest catalase activity and GSH content. Additionally, APE(Mac) extracts showed the lowest MDA content. Finally, we looked into the significance of receptors such as Glucocorticoids, Her2, and HEXB in cervical cancer growth. In comparison to doxorubicin (standard), our molecular docking investigations revealed that tannic acid and Her2 receptor have the highest binding energy. In conclusion, this research shows that *A. precatorius* seed extracts contain intriguing bioactive components that are likely anticancer agents against CaCx and could be used as a herbal treatment to inhibit growth of cancer cells.

Keywords: *Abrus precatorius*; Antiproliferative; Seed; Receptors; Cervical Cancer.

ICABB_F310_Sne

Contributions of Plant-Derived Polyphenols as Efficacious Envoys Against SARS-COV-2 Virus: A Review

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ABSTRACT

Polyphenols are the most important class of bioactive compounds of nature, showcasing numerous health effects primarily based on their direct antioxidant properties and function in modulation of intracellular signalling. Several natural compounds isolated from plants (polyphenols) provide a start line for research regarding use of plant extracts for viral treatment and prevention. This group of natural substances (betulinic acid, indigo, aloemodine, luteolin, and quinomethyl triterpenoids, anthraquinone, tannins, gallates or quercetin and flavonoids) is a potential key for designing antiviral treatment protocols for inhibiting viral proteases. Worldwide pandemic of COVID-19 is spawned by Severe Acute Respiratory Syndrome Coronavirus-2 (SARS-CoV-2). Therapies against SARS-CoV-2 target either virus or immune system. However, therapies supported by specific antibodies, like monoclonal antibodies and vaccines, may be ineffective enough as this virus randomly changes its antigenicity due to various mutations. There are currently numerous clinical trials investigating consequences of polyphenols in prophylaxis and therefore treatment of COVID-19, from symptomatic, via moderate and severe COVID-19 treatment, to anti-fibrotic treatment in discharged COVID-19 patients. Antiviral properties of polyphenols and their influence on immune system modulation may serve as a solid premise for originating polyphenol-based natural approaches to treat COVID-19. These antiviral polyphenolic medications may palliate enzymes of SARS-CoV-2, which are requisite for viral duplication and subsequent infection. Already known pharmacophore constitutions of bioactive substances are nifty in the intricacy of anti-Covid-19 articulations. Advantages of utilising mixtures made of polyphenols is correlated to the high-safety portrait without prominent side-effects. Therefore, polyphenols may be considered as promising tools for effective treatment of SARS-CoV-2 infection.

Keywords: Bioactive Compounds, Immune System, Antiviral Therapies, Pharmacophore Structures.

ICABB_F311_Jat

Screening of Bio-actives from Religiously Important Indian Trees, Against SARS - COV2

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ABSTRACT

Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV2) was discovered in Dec 2019 in China affecting over 25.6 core people and took over 51.3 lacs human lives so far. Several old and new drug molecules have been tried by the Doctors and Scientists to inhibit coronavirus but, no drug has been approved by WHO till date. As, most of these drugs are synthetically prepared, they carry many side effects. In India, many herbs and trees are preserved religiously, which are ultimately found to have environmental or health benefits. Many old researches have shown that Peepal has many phytochemicals that show antiviral and antibacterial properties. In the present study, the researchers focus on naturally-derived compound from the Peepal (*Ficus religiosa*). In this paper, the authors have used different bioinformatics tools like: AutoDock, Vina and LigPlot+, etc, and checked if, the phytochemicals of *Ficus* could interact with the target protein of virus or not. The results for interactions were analyzed and the ligands which were successfully interacting were identified. These ligands can further be tested in vitro to further verify their potential to inhibit SARS COV2 virus. The present research is expected to find naturally therapeutics for the treatment for COVID19 that could be more easily accessible to all patients with fewer side effects.

Keywords: SARS-COV-2, *Ficus religiosa*, Cow Urine, Goat Milk, AutoDock, Ligplot+.

ICABB_F312_Shr

Treatment of Diabetes Type 2 By Natural Products, Targeting AMPK Signaling Pathway

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ABSTRACT

Type 2 diabetes is a chronic disease that affects a huge amount of the population worldwide, causing an average of 1.6 million deaths since 2015 (WHO). There are no treatments available for diabetes and it can be “managed only” by some drugs, currently available in the market. Almost all these drugs have some kind of adverse effects on the health of the patient which can include things from weight gain to hypoglycemia. Hence, there is a need to develop new therapeutics that can help in the management of diabetes in a better way. 5’ Adenosine monophosphate-activated protein kinase (AMPK) pathway is one such target that can be used in this case and is targeted by modern day medicine. AMPK activation in several studies has been shown to have enhanced glucose uptake and inhibition of intracellular glucose creation. Many studies have suggested that improper function of AMPK activity might be responsible for diabetes. Using this pathway many drugs are under trial like C13 (Glaxuride) and AICAR (5-aminoimidazole-4-carboxamide-1-β-D-ribofuranoside). Besides these drugs, natural products like resveratrol, berberine, quercetin, can be potential candidates as therapeutics for diabetes, as they have also shown potential in regulating the AMPK pathway and therefore, can be useful in managing diabetes mellitus. In-silico experimentation and molecular dynamic simulations done on the target proteins (IP6K1 and 2) with selected compounds have provided a hope that these compounds may work as a better therapeutic solution over the synthetic products. These results should further be verified by wet lab experiments.

Keywords: AMP, AMPK, Berberine, Diabetes, Natural Products.

ICABB_F313_Har

Analysing Bioactive Isoflavones and Phytosterols for Their Potential in Target-Specific Treatment of Sepsis-Associated ARDS

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ABSTRACT

Acute Respiratory Distress Syndrome (ARDS) is a fatal condition having hypoxia and inflammatory causes leading to non-cardiogenic pulmonary oedema. Patients marked with this condition are deemed critically ill and might require mechanical ventilation, yet the mortality rates due to this condition have been alarmingly high. This condition might arise due to faulty gaseous exchange and upregulation of pro-inflammatory factors leading to Acute Lung Injury (ALI). ALI manifests itself as ARDS in later stages. Progression in pathogenic diseases like pneumonia, non-infectious sepsis, teratogens, smoking or environmental pollutants has been reviewed over the years for their role in the manifestation of this condition. Several natural products have been exploited over the years for their anti-microbial and anti-inflammatory potential. Isoflavones and phytosterols are two such bioactive compounds found in red clover and soybean oil that have been explored for their medicinal potential in the past. In this piece of work, we focus on the target-specific action of these bioactive compounds for their potential role in the treatment of ARDS. Several structural databases and molecular docking platforms have been used to study their action on target molecules and more than satisfactory results have been obtained. Genistein, Equol and Stigmasterol are the compounds that exhibited the highest binding affinity for the target protein. Further wet-lab experimentation employing these ligands would be required for solidifying the research findings.

Keywords: ARDS, Inflammation, Sepsis, Isoflavones, Phytosterols, Molecular Docking.

ICABB_F314_Shu

***In Silico* Study on Edible Seeds Derived Anticholesterolemic Bioactive Compounds Against HMG - CoA Reductase Target**

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ABSTRACT

Hypercholesterolemia is one of the most prevalent health concerns amongst humans, which is further associated with incidence of other heart related problems. Recent medical treatment for hypercholesterolemia is often very costly and has some adverse side effects too. Advances in research have explored bioactive compounds from various sources in managing the conditions of hypercholesterolemia. Edible seeds are reported as a miniscule pack of bioactive compounds having various health benefits. This current study employs an in-silico approach to gain insights into the binding interactions of the bioactive compounds which are reportedly present in Edible seeds, against the protein HMG-CoA reductase, which plays a crucial role in cholesterol metabolism. Phytochemical compounds were virtually screened and selected which largely conformed to drug likeness criteria and ADME properties. The best selected compounds were subjected to molecular docking and molecular dynamics simulations. The docking results revealed the strong binding interactions of the phytochemical compounds with target protein. Moreover, dynamics simulation study data suggested that the docked complexes showed stable interactions with minimum energy loss under the simulated conditions. Findings from this study will further support the future research in development of potential medicaments from other natural sources for management of hypercholesterolemia.

Keywords: Phytochemicals, Simulations, HMG CoA reductase, Molecular Docking, Hypercholesterolemia.

ICABB_F315_Ris

Analysis of Chamomile Tea for Its Potential Health Benefits

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ABSTRACT

Chamomile is an official drug listed in pharmacopoeias of many countries especially for inflammatory disease and spasms. Herbal teas prepared from Chamomile, or tisanes, are increasingly gaining the attention of scientific activity. It can be easily prepared by brewing the dried flower heads of chamomile and has been known for its medicinal properties. References of this herb can be found in many ancient medical texts such as Roman and Egyptian civilisation. Many bioactive properties of chamomile are now also being increasingly reported in scientific literature. The main bioactive components of the flowers include several phenolic compounds and flavonoids such as patuletin, quercetin, apigenin luteolin, and their glucosides. Chamomile is also shown to have potential antimicrobial, antioxidant, anti-inflammatory, antimutagenic, cholesterol-lowering activities, and *in-vitro* antiplatelet activity. Antispasmodic and anxiolytic effects are also shown in animal models. However, human trials are still very limited with some studies suggesting its positive role in anxiety, dyspnea and diabetes mellitus management.

Keywords: Chamomile Tea, Antioxidant, Chamazulene, Herbal Teas.

ICABB_F316_Man

Technologies for Zinc Based Nutraceuticals

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ABSTRACT

Zinc is a trace mineral that is required by the human body in very small amounts and yet it takes part in a number of important functions in the human body. Four main types of zinc products were prepared in this study, namely, air-dried and lyophilized zinc microspheres, zinc drops and liquids, zinc lozenges, and zinc jelly. The technique of ICP-AES analysis was used to analyze the zinc content and to check whether these products meet the daily requirement of zinc. Two different types of zinc salts that is zinc sulphate and zinc gluconate were used to study which is better and more advantageous among the two. It was found out that zinc gluconate has more advantages as it is well absorbed and better in taste than zinc sulphate. However, due to its high molecular weight, it could not be used in making zinc lozenges, jellies, and drops as a lot of the salt are required to meet the RDA. So, in these cases, zinc sulphate can be used as it is cheaper and required in less amount. The release study of lyophilized zinc microspheres and zinc lozenge was also performed in vitro to study the release kinetics of zinc inside the body. However, the novel dosage form of zinc was explored and various nutraceuticals of zinc were prepared that met the daily requirement of zinc so as to treat zinc deficiency and provide the health benefits of zinc when taken as a supplement.

Keywords: Nutraceuticals, Microsphere, Zinc Supplements, ICP-AES.

ICABB_F317_Nik

Comparative Analysis of Phytoconstituents in *Curcuma caesia* and *Curcuma amada* from Western, Central and Northern Region of India

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ABSTRACT

Curcuma caesia and *Curcuma amada* are rhizomatous perennial plants in the Zingiberaceae family with a wide range of ethno-medicinal use. In the present study, sampling of these two herbs was done from Jabalpur, Madhya Pradesh of Central India and phyto component screening of Ethanol and Methanol extract was performed. The qualitative analysis result was compared with the samples from other two eco-geographical regions, i.e., Western and North-East India. The phytochemical screening result of *C. caesia* methanolic extract shows the presence of alkaloids, phenols, flavonoids and tannins in all three samples collected from North-East, West and Central India, however, saponin was only reported in the sample of North-East India. In ethanolic extract, all phytochemicals screened are found to be present in all samples. In case of *C. amada*, the phytochemical screening of methanolic extract shows the presence of alkaloids, terpenoids, phenols, flavonoids, tannins, saponins, anthraquinones from North-East and Western region but alkaloids, saponins and anthraquinones was absent in sample from Central India. Phenols, flavonoids, tannins and terpenes are found to be present in ethanolic extract of *C. amada* in all three samples. Although the presence of alkaloids and saponins is detected in *C. caesia*, they are absent in *C. amada* sampled from these three geographic regions of India. From this study, it is clearly evidenced that the presence or absence of phytoconstituents depends on different climatic conditions. As the phytoconstituents of medicinal plants have been playing a key role in treating various diseases, it is crucial to explore the source while screening secondary metabolites in the pharmaceutical industry.

Keywords: Phytoconstituents, Eco-geographical region, *Curcuma caesia*, *Curcuma amada*, India.

ICABB_F318_Priy

Skin Microbiome: Current Target for Cosmeceuticals

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ABSTRACT

Skin acts as a barrier to the external environment and perform various functions like maintaining internal homeostasis, sensations to touch based stimuli, vitamin D production and defence against foreign pathogens, prevent dehydration. Skin has its own diverse microbiota like bacteria, virus, fungi that is collectively called as skin microbiome. Skin is considered as neuroendocrine organ which interact with both external environment and microbiome. This endocrine system of the skin helps in maintaining skin integrity, homeostasis, functionality. Skin microbiome balance is disturbed (condition called dysbiosis) by both internal and external factors which lead to skin problems like acne, psoriasis, dandruff. It is important to maintain the healthy skin ecosystem. Cosmeceuticals i.e., combination of cosmetic and pharmaceuticals, is a recent trend in the skin care industry where we add extract or bioactive compounds in the form of lotions, creams, mists to increase the supply of nutrition to the skin. Being hybrids of cosmetics and pharmaceuticals, they are applied topically as cosmetics but also contain the ingredients that influence the biological functions of the skin. Prebiotics (to stimulate the growth of favourable bacteria), Probiotics (good bacteria to skin) and Postbiotics (adding by-products of bacteria) are added into the product to enhance the skin flora. Bioactive compounds like phytochemicals (polyphenols), microbial metabolites (e.g., Lactic acid, hyaluronic acid) and minerals/vitamins (e.g., selenium, Vitamin E), peptides are used as an ingredient in cosmeceuticals. They act as antioxidants, anti-hyperpigmentation, anti-inflammatory, anti-ageing, anti-wrinkles, and UV protection. Developing product that can improve the healthy eco-system of skin is a new trend in dermatological products which are the future generation skin care products.

Keywords: Skin Microbiome, Cosmeceuticals, Prebiotics, Probiotics, Postbiotics, Bioactive Compounds.

ICABB_F319_Kar

Replacing Synthetic Ingredients by Sustainable Natural Alternatives: Application to The Cosmetic Industry

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ABSTRACT

Natural products contain various bioactive chemicals that show many pharmacological activities such as: antimicrobial, anti-cancerogenic, anti-viral, anti-inflammatory, and antioxidant properties, in addition to supplying necessary nutrients for humans and other organisms. These bioactive chemicals have been the key point of interest to the cosmetic industry for their usage in nutricosmetic and cosmeceutical products. These products are being designed to minimize skin-aging, skin-irritation, and giving UV protection etc. Tea leaf extracts are the most commonly used plant-based cosmetics due to its antioxidant property. It is also a rich source of vitamin B, vitamin E, caffeine, tannin, folate, potassium, manganese, and magnesium. These substances help to prevent and delay the indications of aging while also improving the skin's appearance. Vitamin E helps cells regenerate, hydrate, and replenish themselves. Tannins regulate sebum production and aid in the treatment of oily skin. Because of the above said benefits, tea extract is commonly used as an active ingredient in skin care products. According to 2018 statistics, the global tea-based skincare market was worth \$168.2 million, and it is expected to grow at a Compound Annual Growth Rate of 7.5% in the next 5 years. Furthermore, rising awareness of vegan beauty products, as a result of growing socio-economic concerns about animal welfare, will propel the market forward. Due to low toxicity of tea extracts and their synergistic actions with antioxidants in this study we reviewed the use of tea extract in a variety of cosmetic formulations.

Keywords: Bioactive Compounds, Antioxidant, Anti-aging, Cosmetic Industry, Natural Products.

ICABB_F320_Sim

Occurrence and Distribution Pattern of Microsatellites in *Camelina* (*Camelina sativa* L.)

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ABSTRACT

Microsatellites, also known as SSRs (Simple Sequence Repeats), are 1-6 nucleotide long motifs tandemly repeated in almost all the genomes. These sequences have been assigned different regulatory, structural, and functional roles in diverse biological systems. Therefore, understanding the occurrence and divergence of microsatellites has become an area of interest recently. In this study, we have mined microsatellites in *Camelina sativa* L., an oilseed plant of Brassicaceae, employing a microsatellite search tool, MISA. In total, 356083 microsatellites were mined from 641.35 mb of the genome. The microsatellite density was found to be 555.20 microsatellite per mb. Most abundant repeats were mononucleotides followed by di-, tri-, tetra-, penta-, and hexa-nucleotides. The coding regions constituted 21% of the *Camelina sativa* genome and harbored 13835 microsatellites representing 39% of the total microsatellites. Trinucleotide repeats were most abundant in the coding regions followed by di-, mono-, hexa-, tetra-, and penta-nucleotides. The analysis of microsatellite motifs in the coding regions revealed that among mononucleotide repeats A/T repeats were predominant, whereas among dinucleotide repeats AG/CT repeats were predominant. Surprisingly, no CG/GC repeats were observed in the coding regions of this species. Among trinucleotide repeat AAG/CTT were predominant followed by ATC/ATG>AGG/CCT>AAC/GTT>ACC/GGT. The underrepresentation of poly(C) and CG repeats might have played some role in the instability of the genome. Variation in the microsatellite dynamics in the coding regions is known to generate aberrant proteins affecting their functions. Functional characterization of microsatellite enriched genes will further help in revealing the regulation of various biological activities in this plant species.

Keywords: Microsatellites, Relative Abundance, Microsatellite Motifs, SSR, Coding Regions, *Camelina*.

ICABB_F321_Neh

Effects of Various Processing Methods on Antioxidant and Anti-Microbial Properties of *Triticum aestivum*

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ABSTRACT

Triticum aestivum (common wheat) is one of India's most cultivated and consumed crops and many parts of the world. It contains all the micronutrients, rich in vitamins (thiamine and vitamin-B), minerals (zinc, iron), a rich source of fiber and antioxidants as well. Wheat is widely used for making wheat flour, bread, chapatti, refined forms of it, Dalia, and many more. Wheatgrass is one of the well-known rich sources of antioxidants. This study analyses and compares the variation in antioxidant and anti-microbial properties in different processed stages of *Triticum aestivum*. The various samples were extracted in different solvents and further estimated for antioxidant and antimicrobial activity. The antioxidants were estimated by determining the total Phenolics and DPPH of the samples. The results showed that there was a substantial reduction in the antioxidant property of bread and chapatti samples as compared to wheat flour extracts. The antimicrobial activity was determined by plating bacterial and fungal strains and applying different extracts to calculate the zone of inhibition. Antioxidants help our body to neutralize oxides present or produced within the body because of various metabolic activities. The presence of antioxidants also increases the life span of food items. The significant effect on the antioxidant and antimicrobial property due to procedures like heating, grinding, and baking to change the form of wheat into another product impacts its antioxidant properties inside and outside.

Keywords: *Triticum aestivum*, DPPH, Anti-Microbial, Antioxidant.

ICABB_F322_De

Deep Insights in Identifying Various Drug Targets for Acute Respiratory Distress Syndrome

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ABSTRACT

Acute respiratory distress syndrome (ARDS) is life threatening lung injury which is characterized by the critical onset of pulmonary edema and severe hypoxemia because of failure in pulmonary gas exchange. It was first recognized in the 1960s. severe hypoxemia due to pulmonary gas exchange failure and was first recognized in the 1960s. ARDS arises utmost often in the patients suffering from sepsis, aspiration of gastric contents, pneumonia or severe trauma and is currently in approximately 10% of intensive care units patients worldwide. High- throughput gene profiling has been reported as a powerful tool in revealing several chief pathways linked with pathogenesis of ARDS such as: MyD88-dependent pathway, TNF signalling pathway and MAPK signalling pathway. There are certain proteins which are specifically expressed during ARDS. Among many of them, few of the primary biomarkers for ARDS such as: ICAM-1, TLR-4, TNF- α , and IL-8 have been closely associated with pathogenesis of ARDS. Distinct expression of these proteins has been observed in the MyD88-dependent pathway, TNF signalling pathway and MAPK signalling pathway which explicitly facilitate the pathogenesis of ARDS in human subjects. This review article mainly focuses on information of the overexpression of these biomarker proteins in the lungs that lead to ARDS mediated inflammation.

Keywords: ARDS, Inflammation, Drug Targets, Pathway.

ICABB_F323_Mah

Fermentation Characteristics of an Ancient Rice Variety - Kalanamak

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ABSTRACT

Kalanamak is one of India's highest-quality fragrant rices. Black husk (kala = black; the suffix 'namak' implies salt) is the source of its name. In every quality attribute except grain length, Kalanamak rice outperforms Basmati rice, which is considered the highest-grade rice in international trade. Cooked fermented rice water has been shown to have anti-ageing properties and have potential to be employed as a raw material in skincare products. In vitro biological antioxidant activity and elastase inhibitory effect were found in Kalanamak fermented rice water, in earlier studies. In the present study, this ancient rice variety is being studied for its fermentation-induced microbial diversity profile. Standardization of the fermentation process for ratio of rice vs water, cooking time and fermentation time is being done. The cultivable microbial profile, antioxidant activity and antimicrobial properties will be presented.

Keywords: Kalanamak Rice, Cultivation, Rice Water, Basmati Rice.

ICABB_F324_Nik

Advancements in Food Packaging

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ABSTRACT

Increased knowledge of consumer towards the degradation of food products due to food packaging leads to a need for innovation of existing food packaging system to the next level. This will ensure good quality food products and healthy life style. Active, bioactive, and intelligent packaging's are some of the emerging innovative solutions for improving the safety and shelf life of the food product. These packaging directly impact consumer's health as they hold willful interaction with the food and its surroundings. Thermal stability, mechanical strength and barrier performance are some of the novel progresses which has boost characteristics of food packaging. Aroma emitters, ripeness indicator, prevention of moisture infusion, retardation in oxidation, biosensors, prevention of microbial attack and hindrances in respiratory process are some of the indifferent food packaging technologies. The objective of this study is to give necessary awareness of different innovation in food packaging techniques and their layoff of strength, preservative action and appropriateness in different variety of foods.

Keywords: Active Packaging, Intelligent Packaging, Food Safety, Nano Technology.

ICABB_F325_Sri

Therapeutic Potential of Phyto-Constituent in Management of Pesticide-Induced Neurotoxicity

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ABSTRACT

Agricultural development is accompanied by the adoption of modern technologies, as well as the widespread use of agrochemicals, which has become a worldwide environmental and public health problem. Human exposure to pesticide and consumption of their residues, has been linked to various neurodegenerative diseases such as Parkinson's, Alzheimer's and Huntington's diseases as well as seizures, cognitive and sleep disorders. Phytoconstituents derived from medicinal plants influence the function of receptors for the primary inhibitory neurotransmitters, which helps to maintain the brain's chemical balance. Phytochemicals found in plants as secondary metabolites, including terpenoids, alkaloids, phenylpropanoid, phenolic acids, flavonoids, and tannins, have been linked to a wide range of biological characteristics, including biomedical ones like antioxidant, anti-inflammatory, and antibacterial activity. Several model systems are being employed to study the impact of chemical-induced toxicity and the therapeutic/preventive functions of various plant-derived compounds. Traditional medicinal plants with natural components may be proven to be of high therapeutic potential and beneficial in the long term due to minimal side effects and cost effectiveness. In this review, the protective effect of phyto-constituents against the pesticide -induced neurodegenerative diseases will be studied.

Keyword: Neurodegenerative Diseases, Pesticide exposure, Phytoconstituents, Therapeutic Potential.

ICABB_F326_Mans

Tumor Oncogenes and Suppressor Genes Involved in Skin Cancer

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ABSTRACT

Skin cancers are of many types of which the most commonly diagnosed is the non-melanoma skin cancer whereas melanoma is the life-threatening form which is least diagnosed. The exact mechanism of skin carcinogenesis is yet unknown. However, different studies and research have been carried out in order to gain a better understanding of the process. The genetic basis of cancers is a relatively new approach to gather knowledge about some of its mechanisms. Mutations of genes such as CYLD, P53, patched (ptc) gene, Ras oncogenes etc are expounded to be the most common genetic abnormality identified in skin cancer. These are basically classified as the tumor suppressor genes and oncogenes that are involved in the regulation of a variety of signalling pathways such as NFkB pathway, mTOR pathways, MC1R pathways AKT pathway etc. These genes and the involved genetic pathways are associated to tumor cell proliferation, apoptosis regulators. In the present study, new treatment guidelines, based on current knowledge of these genes are discussed. Here we review the major Tumor Suppressor Genes (TSGs) and Oncogenes implicated in cell cycle events which may lead to skin cancer and examine recent data exploring the signalling during the development and progression of these types of human tumors.

Keywords: Skin Cancer, Tumor Suppressor Genes, Oncogenes, Signalling Pathways.

ICABB_F327_Deb

Dependency of Ultimate Inherent Glycemic Potential of Pearl Millet upon the Intrinsic Parameters: Microstructure, Matrix Composition, Molecular Structure

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ABSTRACT

Inherent glycemic potential is an index of starch bioavailability in terms of eliciting postprandial glycemic response of staple cereals which leads to chronic hyperglycemia such as type 2 diabetes mellitus, cardiovascular diseases and their sequelae. Directed investigation in this direction is thus required to understand the role of explanatory variables governing IGP as well as to develop a model system for limiting high blood glucose of staple cereals. Therefore, in the present study, we have addressed a few basic questions to share a comprehensive understanding on various illustrative variables possessing roles like: does inherent indices like microstructure, matrix compositions/ interactions and molecular configurations affect starch digestibility and ultimate IGP? This study inscribes these questions by considering two starch sources of varying inherent matrix composition as pearl-millet and rice. The *in-vitro* simulation model mimicking oral-gastrointestinal digestion showed low IGP for PM with 63.71% as compared to rice with 65.89 % and it was well correlated with microstructural parameters [pericarp thickness ($22.71 \pm 0.20 \mu\text{m}$), granule size ($2.16 \pm 0.12 \mu\text{m}$), endodermal surface area ($1199.64 \pm 2.86 \mu\text{m}^2$)]. Further, dense food matrix components as well as visualization of higher S-L complexation through CLSM directly assigned to the superior matrix interactions which hinders permeability of carbolytic enzymes. Moreover, FTIR & XRD molecular patterns also showed synergistic effects through higher longer-range (CD % 21.73 %) & shorter-range ($R_{1047/1022}$: 0.80) crystalline structures in this direction. Henceforth, this study focuses on the inherent parameters like microstructure, matrix composition/ interactions, molecular structural hallmarks responsible for low glycemic profile of pearl millet.

Keywords: Inherent Glycemic Potential, Pearl Millet, Food Matrix Interactions, Molecular Crystallinity.

ICABB_F328_Zak

The Inhibitory Effect of Sunset Yellow on Thermally induced Human Serum Albumin Aggregates: Possible Role in Naturopathy

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ABSTRACT

Protein aggregation and amyloid formation are the major causes of various neurodegenerative diseases nowadays. There are various factors that results in the misfolding or unfolding of the protein and thereby gradual formation of aggregates that badly affect the functionality of the protein. High temperature, pressure, pH, detergents etc are various factors that can cause protein aggregation. Experiments were performed on Human Serum Albumin (HSA) because it is one of the important proteins that plays crucial role in the normal functioning of the body. It is a carrier protein that carries small molecules and drugs to various parts of the body. Anti-amyloidogenic potential of Sunset Yellow (SY) dye on HSA was studied using various biophysical and microscopic techniques like Rayleigh Light Scattering (RLS) measurement, ThT binding assay, Congo Red (CR), ANS binding assay that shows gradual decrease in fluorescence intensity with the increasing concentration of the sunset yellow. Circular Dichroism (CD) spectroscopic measurement was performed for the study of structural changes and modifications of the protein. Similarly, Transmission Electron Microscopy (TEM) and SDS-PAGE were also performed to study the conformational changes in the protein. Thus, all the results show that the sunset yellow (SY) dye is the potential inhibitor of the protein aggregation.

Keywords: Protein Aggregation; Anti aggregation; Human Serum Albumin; Sunset Yellow; Inhibition; Amyloid Fibrils; Neurodegenerative Diseases.

ICABB_F329_Pus

Performance of Non-Targeted Effect of Neonicotinoid Insecticide - Imidacloprid Residues on Phyllospheric Bacteria and its Impact on Fruit Quality in Grape

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ABSTRACT

Grape is an important fruit crop of India, consisting phyllosphere microbiota playing a vital role in its quality. In this study, we report the effect of imidacloprid residues on culturable phyllosphere bacteria and its impact on quality in Cabernet Sauvignon. The formulation was applied at recommended (RD) and 10 times of RD (10RD) doses. The berry and leaf samples were collected at 0,1,3,5,7,10,15,21,30 days and assessed for its dissipation kinetics. The samples were extracted by QuEChERS method and analysed by LC-MS/MS. The berries showed residues of 0.45, 0.23, 0.12 mg kg⁻¹ for RD at day 1, 15, and 30 days, respectively. The leaves showed residue @ 12.5, 1.8, 0.6 mg kg⁻¹ at RD in 0, 15, and 30 days, respectively. The bacteria were isolated from berry and leaf suspension in NA. The CFU count was high in control at day 1, @15th day, CFU count was high for SD and 10RD, indicated impact of residues on count. The 30 isolates were studied for pesticide tolerance by disc diffusion, screened for degradation, 5 isolates exhibited more than 50% degradation on 7th day with LC-MS/MS. The harvested grapes showed phenols, flavonoid, anthocyanin content to be the highest in control such as, 1.18 mg g⁻¹, 42.3 mg g⁻¹, 719.3 mg L⁻¹ compared to 10RD as 0.5 mg g⁻¹, 28.3 mg g⁻¹, 498.5 mg L⁻¹, resp. The one-way ANOVA with p-value < 0.05, depicted the control and 10 RD are significantly different. The study suggested, the pesticide residue had significant impact on microbiome and berry quality.

Keywords: LC-MS/MS, Residue, Grape, CFU, Phyllosphere, Dissipation.

ICABB_F330_Push

Investigation on Non-Targeted Effect of Triazole Fungicide - Hexaconazole Residues on Phyllospheric Bacteria and its Impact on Fruit Quality in Grape

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ABSTRACT

Grape is an important fruit crop of India, consisting phyllosphere microbiota playing a vital role in its quality. In this study, we report the effect of hexaconazole residues on culturable phyllosphere bacteria and its impact on quality in Cabernet Sauvignon. The formulation was applied at recommended (RD) and 10 times of RD (10 RD) doses. The samples were collected at 0,1,3,5,7,10,15,21,30 days and assessed for its dissipation kinetics. The samples were extracted by QuEChERS method and analysed by LC-MS/MS. The berry samples showed residues of 0.52, 0.07, 0.057 mg kg⁻¹ for RD. The leaves showed residue @ 14.17, 5.97, 1.02 mg kg⁻¹ at RD in 0, 15, 30 days, respectively. The bacteria were isolated from berry and leaf suspension in NA. The CFU count was high in control at day 1, while on 30th day it was high in 10 RD, indicating the impact of residues on count. From this, 24 isolates were studied for pesticide tolerance by disc diffusion. Out of 24 isolates screened for residue degradation, 4 isolates exhibited more than 50% degradation on 7th day with LC-MS/MS. The harvested grapes were evaluated, revealed that phenols and anthocyanin content were highest in control as 1.18 mg g⁻¹, 359 mg L⁻¹ as compared to 10 RD as 0.31 mg g⁻¹, 28.33 mg g⁻¹, and 498.5 mg L⁻¹, respectively. The one-way ANOVA with p-value <0.05, depicted that the control and 10 RD are significantly different. The study suggested that the pesticide residue had significant impact on microbiome and berry quality.

Keywords: LC-MS/MS, Residue, Grape, CFU, Phyllosphere, Dissipation.

ICABB_F331_Shai

Bioprospecting Genomes of *Lactiplantibacillus plantarum* Isolates from Different Niches Unveiled the Diverse Repertoire of Bacteriocins and Probiotic Genetic Traits

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ABSTRACT

Bacteriocins are the natural bioactive antimicrobial peptide (AMP) compounds, synthesized by several microbes as an array of defence mechanism against other bacteria. Such AMP producing bacteria can serve as a valuable source of antibacterial and bio preservative. Identification of bacteriocin producing strains by traditional biochemical characterization is more tedious and cumbersome that can be overcome by molecular methods based on DNA of the microbe that can allow rapid identification of bacteriocin properties of strains. The present study reports the bioprospection of 100 *Lactiplantibacillus plantarum* (LP) genomes obtained from varied sources like kimchi, milk, pickles, juice, vegetables, meat, kefir, cheese, gastrointestinal tract, etc. Whole Genome sequence analyses found PLANTARICIN as the most predominant bacteriocin across LP genomes (n=98). We observed a set of LP strains (n=36) harbouring genes encoding multiple bacteriocins (pediocin, sactipeptide, mutacin, enterolysin, bovicin, and enterocin) in different combinations. Further investigation of the genetic features of the selected LP genomes (n=10) unveiled variation in the presence of probiotic genes (*dnaK*, *groEL*, *rmlB*, *ldh*, *eno*, *bsaA*, *fol A/B/ D*, *dltA/D*, *gadB*, *fbp*, *nox*, *clpP*, *hslV*, *trxA*, *trxB*, *tpx*, *nrdH*, *kat*, *npr*) emphasizing the fact that genome characterization is a crucial step to guide appropriate selection of strains for industrial purpose. Overall, genome-based characterization of LP strains allowed valuable insight into strain specific variations in bacteriocinogenic and probiotic genetic features of LP strains. This type of genetic profile can assist and facilitate the selective use of LP strains or its extracted bacteriocins as nutraceutical/ bio preservatives or antimicrobial in the clinics.

Keywords: *Lactiplantibacillus plantarum*, Whole Genome Sequence, Bacteriocins, Probiotic Genes.

ICABB-F332-Div

Potential Indian Medicinal Plants for treating Neuro-Degenerative Diseases (NDDs) in Ayurveda

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ABSTRACT

Amongst all the neurodegenerative diseases (NDDs) including Alzheimer's disease (AD), Parkinson's disease (PD), and many more have tremendously shown harmful effects on human health. Ayurveda may possibly offer new treatment choices for patients with neurological disorders, which is a less expensive and socially reasonable option in comparison to traditional treatments using synthetic drugs. Indian medicinal plants have been in need of treating infections since antiquated occasions in India. Commonly used plants are *Withania somnifera*, *Mucuna pruriens*, *Bacopa monnieri*, and *Centella asiatica* on NDD patients. Numerous medicinal plants and their products like secondary metabolites are accounted for with the capacity to mitigate the harmful effects of NDDs. The significant ability distinguished, through which phytochemicals apply their neuroprotective impacts of neurological wellbeing in maturing, anticancer, antiapoptotic, acetylcholinesterase, and inhibition of monoamine oxidase and neurotrophic functions. There is rising worldwide interest toward homegrown plants because of their regular beginning and lesser aftereffects than ordinary synthetic drugs that have been depicted with undesirable however unavoidable secondary effects. Plants have shown additional neuroprotective ability in response to proinflammatory cytokines involving IL-6, IL-1b, TNF, and seen that there is an increased level of antioxidant activities, while decreased levels of oxidants and acetylcholinesterase action were repressed in the sensory system by these plants. Subsequently, the impacts of the medicinal plants and their dynamic components in showing recuperative potential against NDDs, neuroinflammation and synapse dysfunction.

Keywords: Neurological Disorders, *Withania somnifera*, *Bacopa monnieri*, *Centella asiatica*, and *Mucuna pruriens*.

SESSION IV
Environmental
and
Industrial Biotechnology

ICABB_E401_Dhe

Metabolic Engineering of *Saccharomyces Cerevisiae* for Heterologous Production of (-) Geosmin

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ABSTRACT

Petrichor is the distinct fragrance of earth that smells after first rain. Soil-dwelling organisms release chemical called Geosmin, which is responsible for this earthy aroma. (-)-Geosmin has been used widely in the fragrance industry to recreate this earthy aroma. The traditional production strategies of geosmin mainly focused on extraction from native sources and chemical synthesis. Over the last few decades, diverse group of microorganisms like Bacteria, fungi and algae have been shown to produce Geosmin. Recent advances in synthetic biology have opened several routes for the heterologous production of complex biological flavours and fragrances compound. In this study, we have shown that *Saccharomyces cerevisiae*, a prominent fungal host for synthetic biology, can be used to produce geosmin. We first evaluated the performance of the well characterized germacradienol/geosmin synthase from *Streptomyces coelicolor*. The recombinant *S. cerevisiae* showed geosmin production, although at low levels. For better conversion of germacradienol to geosmin, through bioinformatic analysis, we identified another germacradienol/geosmin synthase gene from *Amycolatopsis* sp. When heterologously expressed in *S. cerevisiae*, it led to a 5-fold increase in geosmin production. This study offers an alternative, sustainable and environment friendly approach to produce geosmin that belongs to a diverse class of terpenoids.

Keywords: Petrichor, Geosmin, Heterologous Expression, *Saccharomyces cerevisiae*.

ICABB_E402_Vang

Study of Rotifers of Hasanparthy Lake in Relation to Physico-Chemical Properties of Warangal District, Telangana

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ABSTRACT

Rotifers are one of the most important components in zooplankton community. They play a crucial role in interlinking food chain in the aquatic ecosystem. The purpose of this work was to collect and identify the rotifers up to species level; to find physic-chemical parameters of water and their effects on rotifer population. In the present study were conducted from June 2016 to 2017 May in Hasanparthy Lake to investigate rotifer population and their relationship with physic-chemical parameters such as Water temperature (25-00°C-30.02°C), P^H (8.05-8.75), DO (5.00-9.51mg/l), TDS (270.0-380.2mg/l), TH (90.5-200.5mg/l), TA (102.5-190.6mg/l), CL (40.55-86.50mg/l), Ca (19.50-29.60mg/l), Mg (20.65-43.50mg/l), BOD (1.5-4.8mg/l), NO₃ (0.06-9.55mg/l), PO₄ (0.15-0.45mg/l), and NH₃ (0.01-0.05ppm). In total 38 species were identified. Brachionidae 10 species, Euchlanidae 4 species, Lecanidae 8 species, Lepadellidae 5 species, Testudinellidae 3 species, Trichotridae 2 species, Aspalanchidae 2 species, Notommatidae 2 species and Fillinidae 2 species were identified. Percentage of rotifer families are Brachionidae (27%), Lecanidae (21%), Lepadellidae (13%), Euchlanidae (11%), Testudinellidae (8%), Trichotridae (5%), Aspalanchidae (5%), Notommatidae (5%) and Fillinidae (5%). It is concluded that most of the physic-chemical and biological parameters in the Hasanparthy freshwater lake showed a monthly pattern from the observations; it is observed that the rotifers showed a greater abundance. The rich variety of rotifers indicates the trophic status of the water body as well as its nature for the survival of fishes.

Keywords: Rotifera, physic-chemical parameters, Hasanparthy Lake.

ICABB_E404_Aja

Cost-Effective Production of Bacterial Cellulose Using Agro Waste

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ABSTRACT

Bacterial cellulose (BC) is a natural biopolymer that is produced by bacteria. BC is a highly purified form of cellulose with versatile properties and various applications that makes it attractive for several industries. Isolation of three BC producing strains from different fruit juice/beverages such as pineapple juice, mosambi juice and kombucha tea was performed. On the basis of gel consistency and intactness, strain derived from kombucha tea was selected. Low-cost production of BC using 6 different types of agro-materials (sugarcane molasses, coconut water, yellow date, pineapple leaves, pineapple peels and beetroot) was carried out. Among all of them the highest production was observed in pineapple peel waste with 14.5g BC production in 50 ml media after 7 days. Production was higher compared to synthetic media like Hestrin- Schramm (HS) and Yamanaka. Further, to increase BC production different nitrogen sources i.e., ammonium sulphate, beef extract, yeast extract, peptone, tryptone, sodium nitrate and thiourea were utilized. Ammonium sulphate showed maximum production of BC at 16.48 gm in 50 ml media after 7 days. BC production will be optimised using statistical approaches to increase yield.

Keyword: Bacterial Cellulose; Biopolymer; Agro-Waste Utilization; Pineapple Peel, Cost Effective Production.

ICABB_E405_Anu

Microbial Xylitol Production using a Newly Isolated *Candida Tropicalis* K2 from Lignocellulosic Wastes

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ABSTRACT

The generation of valuable chemicals and fuels from lignocellulosic biomass or agricultural waste is the primary objective of a biorefinery in the present context of climate change and pollution. By reinforcing C5 and C6 sugars produced from agro-industrial waste, microbial cell factories may be used to produce commercially viable biochemicals on a long-term basis. Most of the microbial systems lack pentose utilizing machinery because pentoses are the less preferable source of carbon for their growth and development. The efficient use of pentose and hexose sugars is critical for integrated biorefinery. Exploration of organic waste from various habitats (sugar mill/ industrial waste/ vegetable waste/ sewage and forest) led to screening and isolation of xylitol producing yeast which was phylogenetically identified as *Candida tropicalis* K2. The newly isolated strain was explored, and fermentation parameters were optimized for xylitol production. D-xylose and lignocellulosic biomass (corn cob and albizia pod) were used for xylitol production with isolate K2. Isolate K2 produced 90 g/L xylitol with a yield of 0.90 g/g and volumetric productivity of 1.5 g/L/h, when 100 g/L of xylose was used along with 20 g/L of glycerol as a co-substrate in batch fermentation. Moreover, with non-detoxified corn cob and Albizia pod hydrolysate isolate K2 showed the yield and volumetric productivity of 0.67 g/g & 1.07 g/L/h and 0.70 g/g and 0.80 g/L/h, respectively. Therefore, the isolate *Candida tropicalis* K2 would be a good candidate for the xylitol production using high xylan containing lignocellulosic biomass.

Keywords: *Candida tropicalis*, Xylitol, Lignocellulosic.

ICABB_E406_Sam

Effect of Paracetamol Toxicity on Non-Target Organism –*Nostoc Muscorum*

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ABSTRACT

Global occurrences of pharmaceuticals and their metabolites in the aquatic system have become a major threat. Their continuous use and excretory secretions, reach to aquatic environment through sewage and causes harmful effect on non-target fauna and flora. Paracetamol is one of the most used drugs also in during covid-19 period and safest for humans. It is available in the market easily due to no prescription needed. In hospital's wastewater treatment plant (WWTP) and sewage treatment plants it is found in higher amounts than other drugs. It pollutes the water and affects adversely in micro-organisms by producing reactive oxygen species. The main of my study was to now the effect of toxicity of paracetamol in cyanobacteria. Paracetamol decreased the growth of organism by inhibiting photosynthesis. Protein content of *Nostoc muscorum* was reduced by the toxicity of the drug. Paracetamol exerted its effect by enhancing the oxidative stress of organism. To combat the effect of ROS, enzymatic and non-enzymatic antioxidants activated.

Keywords: Paracetamol, Oxidative Stress, Proline, Antioxidant.

ICABB_E407_Raj

Simultaneous Saccharification and Fermentation of Lignocelluloses

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ABSTRACT

Bioethanol derived from petroleum as an alternative source to transportation fuels that are concentrating worldwide to address energy security, energy costs, and global warming shortcomings associated with liquid fossil fuels. Fossil fuels have already caused a lot of damage to the environment and contributed to increasing global warming. To some extent, partial replacement of gasoline for biofuels has improved the situation. But technically, compression-based engines are considered suitable for biodiesel and DME, while spark-ignition engines are suitable for bioethanol. In addition to political (energy security), climate (global warming) and economic (SFT) production of bioethanol may be important for many developing countries for many reasons. Biomass can be produced in developing countries for bioethanol on wastelands, creating employment opportunities, as well as reclaiming wastelands and the environment can also benefit. The ability to produce rural income from the production of high-value products (such as liquid fuels) is attractive. In this, the possibility of export earnings through the sale of industrial bioethanol to the countries is strong.

Keywords: DME (Dimethyl Ether), SFT (Saving Foreign Treasury).

ICABB_E408_Tha

Evaluation of Teratogenic Activity of Formulated Agar from Brown Seaweed by Using Zebrafish Model

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ABSTRACT

For cosmeceuticals-based research, marine-based components or active molecules are still undiscovered. *Turbinaria conoides*, brown seaweed, has a number of biological properties that are important for nutraceutical and medicinal applications. The goal of this study was to check if *T. conoides* has any antioxidant and toxicity characteristics. *T. conoides* agar was isolated and transformed into a topical application formulation. UV and FTIR spectroscopy were used to confirm the structural characterisation of the formulated agar. The antioxidant capabilities and biochemical content of prepared agar were determined. At room temperature, the prepared agar was confirmed to be stable and sterile. At a concentration of 1 mg/ml, the prepared agar was determined to be toxic. By increasing the concentration of agar from *T. conoides*, the formulated agar demonstrated greater antioxidant activity. The developmental toxicity of zebrafish embryos aged 24, 48, 72, and 96 hours was investigated. The study found that the formulated agar showed dose dependent toxicity and higher antioxidant activity. The prepared agar showed dose-dependent toxicity and increased antioxidant activity, according to the study. This research contributes to the usage of prepared agar as an anti-aging lotion in the marine environment.

Keywords: Agar, Formulation, Anti-oxidant, FT-IR, Zebrafish.

ICABB_E409_Pri

Impact of Leachates from Plastics - A study at the Level of Organisms & Environment

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ABSTRACT

Plastics and their incessant impact on environment are a global concern. Plastic production its utilization and various additives in plastic are resulting in increased pollution. Plastics and leachates from plastics were reported to have deleterious impact on aquatic life and were also found to affect microbial life. Abiotic environmental stresses such as: UV radiation, temperature, pH and pressure do trigger the release of leachates from plastics. Furthermore, plastics leachates represent a broad class of organic contaminants and also heavy metals namely Zn, Cu, Cd, Pb etc. When plastics are subjected to environmental stresses some of the additives in the plastic readily leach out. These additives are thought to have potential to enter food web (terrestrial, marine, aerial) and impart adverse effects both at the level of individual organisms and at the level of ecosystem. Present lifestyle utilizes huge amounts of disposable and “single-time use” plastics. This greatly increased the risks of exposure to plastic leachates. Repeated intake of leachates from plastics can intensify the impact on both the environment and biotic life leading to long term and irreversible complications. There is growing interest in the possible health threat posed by plastic leachates that interfere with the endocrine system, reproductive system and also found to have neurotoxic, cancerous effects. This manuscript is a critical review of impact of plastics and leachates from plastics at organisms’ level i.e., prokaryotes, eukaryotes, their metabolism, physiology and reproduction.

Keywords: Plastic Leachates, Additives, Organic Contaminants, Heavy metals, Abiotic Environmental Factors.

ICABB_E410_Aru

Remediation Potential of *Brassica juncea* for Ciprofloxacin

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ABSTRACT

Antibiotics' ability to fight against any bacterial infection had led to its exploitation by humans. Widespread use of antibiotics has caused various after-effects on humans, plants, animals, and microbes. Due to the illegal dumping of pharmaceutical waste from hospitals and pharma industries the soil gets contaminated by antibiotics. This further leads to the contamination of drinking or groundwater and also enters into the food chain through plants and crops. Antibiotic contamination also causes the emergence of antibiotic-resistant bacteria and genes in the environment and among humans. One of the best ways to remove antibiotics from the environment is Phytoremediation. It is a cost-effective, sustainable and green remediation technique. In this study, the remediation of ciprofloxacin by *Brassica juncea* was assessed. The study was carried out by setting a pot experiment for a period of 21 days. After 21 days the toxicity analysis and remediation assessment of pot soil and plants were performed. The antibiotic analysis in soil and plant samples was performed through HPTLC. The root & shoot length, chlorophyll content, carotenoid content, biomass content, were also estimated. The results revealed that *Brassica juncea* is a promising plant species for the phytoremediation of ciprofloxacin antibiotics.

Keywords: Antibiotics, Ciprofloxacin, Contamination, Pharmaceutical, Phytoremediation, Sustainable.

ICABB_E411_Rit

Impact of E-waste on Plants and Animals: Review

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ABSTRACT

Advancement in technology has enormously increased the manufacturing of E-products which ultimately lead to the rapid generation of E-waste. E-waste is the major component of solid waste stream as management of E-waste is still mostly unregulated. Management and regulation of E-waste is necessary as it is composed of various toxic components such as PCBs (Polychlorinated biphenyls), TBBPA (tetrabromobisphenol A), and PBB (polybrominated biphenyl) along with various heavy metals which can have a very negative impact on living organisms. Only 12-13% of E-waste is handled with care or under supervision of authorized sectors. In order to isolate commercially valuable metals from E-waste unauthorized sectors handle this waste in an inappropriate manner which causes them to leach into the soil and are transported to ground water level as well as, nearby plantation. It can also get mixed in the air. Heavy metal toxicity causes disturbance in various physiological processes of plants and animals. Manual power engaged in the E-waste dismantling process can cause various lung, skin, heart and nervous system related diseases. This review deals with the impact of different components of E-waste on the plants and animals. Thus, concluding that, there is a direct need to handle this waste in a relevant and eco-friendly manner to avoid its harmful impact.

Keywords: E-waste, Heavy metals, Toxicity, Impact, Plants.

ICABB_E413_Har

Impact of Solar Panels on the Environment

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ABSTRACT

Sunlight is a non-depleting, renewable, and environmentally benign source of energy. Enough sunshine energy hits the globe every hour to meet the world's annual energy requirement. Solar energy is created for a variety of purposes, including industrial, commercial, and domestic. It is easily able to extract energy from direct sunlight. As a result, it is incredibly efficient and does not pollute the environment. The authors worked at solar energy derived from sunlight and explored its future trends and characteristics. The work also attempted to assess the efficacy of solar power plants at several locations across the country, including AIIMS Jodhpur, Patanjali, and IOCL Ghaziabad. Amount of sunlight received in these different places was also calculated, by which we were able to rectify the level of pollution(smog) at these places. Functioning of solar panels and various sensors used, is also analysed.

Keywords: Renewable Energy, Solar Panel, Photovoltaic Cell, Environmental and Health Impact.

ICABB_E414_Nav

A Review on Impact of Agrochemicals on Soil Enzymes

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ABSTRACT

Soil is a living, dynamic system, and one of the most significant natural resources on the earth. Soil is the basis for life and every living organism is completely reliant on it directly or indirectly. Soil is important for a variety of reasons, including providing habitat for animals and microorganisms, providing food for humans, providing nutrients for plants, contributing to biodiversity and having the potential to contribute in the combat and mitigation of climate change. The continued use of agrochemicals in agriculture for high crop productivity has a negative impact on soil. These agrochemicals contaminate the soil, causing the soil to lose its fertility. The presence of enzymes in the soil is linked to soil fertility. Soil enzymatic activity is an essential parameter of soil quality because it responds to changes in the soil environment or management practice changes more quickly and easily than other variables. Soil enzymes convert organic substances into inorganic nutrients that are easily taken by plants, as well as assist in the breakdown of exogenous toxic compounds to encourage plant growth. Soil enzymes such as dehydrogenases is important in energy production, urease in urea degradation, phosphatase inorganic phosphate degradation, protease in protein degradation, invertase and amylase in polysaccharides degradation, and other enzymes are important. Soil enzymes are primarily produced by soil microorganisms and their activity is directly linked to the soil microorganisms. In recent years, several studies have shown that soil enzyme activities are negatively affected due to the chemical application in agriculture. Use of agrochemicals in agriculture reduces soil microorganism's population and decreases their activity by interrupting their important cellular biochemical process. In this study, we focused on the impact of agrochemicals on soil enzymatic activity.

Keywords: Agriculture, Agrochemicals, Soil Enzymes, Microorganisms and Degradation.

ICABB_E415_Urv

Acclimatization of Anaerobic Microbial Inoculum (AMI) and Its Evaluation for Biodegradation of Synthetic Night Soil

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ABSTRACT

To improve sanitation, hygienic separation of human excreta is of paramount importance for public health and welfare. DRDE, Gwalior has developed biodigester technology for disposing human-waste in diverse geo-climatic conditions including the specially designed fermenter (Biodigester) and cold active anaerobic microbial inoculums (AMI) as seed material. Anaerobic microbial inoculum is based on cattle dung as a feeding substrate which is not efficiently degrading the real human fecal matter. Therefore, there is a need to improve the seed inoculum. In the present study, we acclimatized inoculum for the enhancement of the overall biodegradation of human waste, by using the synthetic night soil (SNS) with similar composition as human-waste to acclimatize AMI for obtaining a high-performance inoculum. To understand the effect of acclimatization on inoculum, the experiment was conducted in batch mode for 120 days using different ratios of AMI vs. SNS for anaerobic digestion of synthetic night soil. During the acclimatization the parameters (pH, total solids (TS), total suspended solids (TSS), volatile suspended solids (VSS), chemical oxygen demand (COD), percentage of methane production, biogas, and MPN count for methanogens, were measured. The AMI: SNS ratio (1:1) has shown the maximum methane, biogas production and 4.4 log/100 ml MPN count for methanogens. The adaptability of acclimatized inoculums was further tested at lab-scale bioreactor to compare with AMI. Maximum production of biogas and reduction in COD, TS, VS, TSS and VSS was observed with acclimatized inoculum during the degradation process.

Keywords: Biodigester technology, AMI, SNS, Acclimatization, MPN count for methanogens, Methane, Biogas.

ICABB_E416_Teh

Exploring the Cellulase Production Potential of Five Thermophilic and Thermotolerant Fungi Isolated from Compost by Solid State Fermentation of Rice Straw

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ABSTRACT

Cellulases are group of hydrolytic enzymes mainly of three types includes endoglucanase (EC 3.2.1.4), exoglucanase (EC 3.2.1.91) and β -glucosidase (EC 3.2.1.21). It is the third largest industrial enzyme having wide range of industrial applications: in pulp and paper industry, laundry and detergent, bio fuel production, food and feed, textile industry, medical application as well as in agricultural industry. *Rhizomucor pusillus* FWC-B, *Aspergillus fumigatus* FWC-G, *Rhizopus microspores* NADEP-W, *Aspergillus fumigatus* PC-LG and *Aspergillus quadrilineatus* PC-W are different thermophilic/thermotolerant fungi isolated previously from samples of compost and identified through sequencing of ITS region and further bioinformatics analysis. Considering importance of cellulases in various sectors present study aims at determining the cellulase production potential of these thermophilic & thermotolerant fungi using rice straw as substrate under SSF. The fermentation was carried out for eight days for all fungi, and filter paper activity as total cellulase activity, endoglucanase activity and total protein was estimated from crude extract on each day. Among all fungi *Aspergillus fumigatus* PC-LG gives the highest endoglucanase activity of 16.19 IU/g ds and FP activity of 1.23 IU/ g ds on sixth day of fermentation followed by *Rhizomucor pusillus* FWC-B which gives endoglucanase activity of 10.44 IU/g ds and FP activity of 0.58 IU/g ds on fifth day of incubation. All the isolated fungi show significant potential of cellulase production and as they are thermophilic/thermotolerant in nature their enzyme can be further characterized to be used for industrial processes occurring at higher temperature. All the assays were run in triplicates and the enzyme activity data of all isolates have been subjected to statistical analysis through ANOVA and Tukeys multiple comparison test in GraphPad prism 9.

Keywords: Cellulase, Fungi, Thermophilic, Thermotolerant, Fermentation.

ICABB_E417_Adi

An Assessment of the Impact of the National Lockdown During Covid 19 Pandemic on Air Pollution in India

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ABSTRACT

The COVID-19 virus was declared a “global pandemic” during 2019 and then a “lockdown” was implemented in the affected areas, to control the spread of this virus. The nation wise Lockdown was imposed from the 24th March 2020 onwards and has resulted in significant improvement in air quality in the country. Air quality has become a primary concern in India as more than 70% of Indian cities violating the prescribed standards of PM₁₀ and PM_{2.5}. As we all know, major sectors contributing to air pollution are mainly transported, industries, power plants, construction activities and biomass burning. Due to restricted activities during lockdown period, these sources are expected to lower the concentrations of particulate matter and other contributor to air pollution. Average reductions of 43% and 61% were observed in PM_{2.5} and NO_x concentrations in Delhi during the period of lockdown in 2020 in comparison to 2019. Present article aimed to analyse the effect of lockdown during COVID-19 pandemic in air quality in terms of concentration of ozone, particulate matter, nitrogen dioxide, sulphur dioxide and carbon monoxide, derived by air quality stations and reported by CPCB for the pre-lockdown and lockdown phases-I and II, and for corresponding periods in 2019.

Keywords: Air pollution, CPCB, Ozone, COVID-19, PM_{2.5}, PM₁₀.

ICABB_E418_Van

Utilization and Recycle of Agro Waste to a Natural Organic Products

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ABSTRACT

Agriculture waste (Agrowaste) is the food waste produced as by product of human activities and in a very huge amount. Measuring the amount of waste generated written in terms of “Ton”. It’s surprisingly unbelievable that million tons of waste generated each year. Recycling of waste is the one of major necessity of developing as well as developed countries. Food loss or wastage occur at each and every step till human consumption. According to the estimation of the Food and Agriculture Organization (FAO) each year 1.3 billion tons of food waste due to accident (natural disturbances) or intentionally by some competitors. In the current scenario, most of the countries making committees, doing partnerships to completely eradicate the world’s one of the major problems how to recycle waste to reuse the materials and how to feed 1.6 billion population in 2050. By collaboration countries now consider this issue as one the biggest issue and awaking people to avoid excess use of fossil fuels and start doing research on this sensitive topic. Current time is correct time to start work upon it applying skills and protocols to achieve some good valuable products and save the beauty of environment for future generation. The concept of Utilization of Agrowaste is booming topic of this era. Scientists are performing their research some of them are getting successful in their research to conserve natural resources (fossil fuels). Most famous product Biodiesel. Feel o Peel is also a new upcoming unique and innovative idea to contribute in save fossil fuels and Feel o peel is the natural organic skincare that is purely organic and made via a transforming solid Agrowaste (peel of fruits and vegetables) to organic skincare.

Keywords: Agrowaste, Peel, Organic, Solid Waste, Skincare, Food and Agriculture Organization, Transform.

ICABB_E419_Sam

An Insight into Bacterial Cellulose as an Alternative Substratum for Animal Cell Culture

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ABSTRACT

Recently, biomaterials and tissue engineering have received a lot of attention with the focus on developing appropriate biopolymer or biomaterial with modified properties to generate functional tissue for specific applications. The development of novel bio materials based on bacterial cellulose (BC), as an alternative to conventional culture dishes has received great attention over the past few years. Various advantages conferred by biomaterials as a substratum for cell culture includes lesser requirements for growth supplements, superior cytocompatibility, impart moist environment, provides a highly porous, biocompatible and biodegradable arrangement. There are several reports on structural modifications of bacterial cellulose to improve its physicochemical properties to widen the applicability. The versatile nature of BC eases the chemical, surface modifications with adjustable mechanical characteristics. In addition, the sustainable nature of bacterial cellulose-based materials makes BC an economically viable and valuable feedstock. The aim of this review is to discuss the advances in bacterial cellulose-based material through physical, biochemical and chemical modifications and also investigate the use of BC composites for animal cell culture technique and utilization of modified bacterial cellulose to reduce dependency on the animal and human derived growth supplements for animal cell culture.

Keywords: Bacterial Cellulose, Tissue Engineering, Regenerative Medicine, Cell Culture, Composite.

ICABB_E420_Gar

Strategies For Large Scale Production of Bacterial Cellulose

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ABSTRACT

Bacterial cellulose (BC) is a natural biomaterial produced by bacteria as a supportive cell covering. It has received substantial interest over the past few years because of its high purity, crystallinity, biocompatibility, improved mechanical strength, good water holding, non-genotoxicity and biodegradability. Owing to these properties, BC has been used in a variety of applications including drug delivery, food, pharmaceutical, biomedical etc. One of the major limitations associated with the use of BC is high cost of production and low yield. To overcome these limitations, researches have proposed a number of strategies for improving BC production, including the design of upgraded bioreactors, culture media optimization and use of agro-industrial residues. Utilization of agro-industrial residues mainly from food, agriculture and breweries industries offers advantages of making BC production cost-effective and zero solid waste generation. Several research efforts are also focused on the development of new and improved BC-producing microbial strains gives the BC-production process a significant boost. The designing of genetically modified microbial strains has exhibited improved BC production. Here, we summarize various aspect of BC production focused on various bacterial strain, carbon and nitrogen sources used, role of culture media components, use of agro-industrial residues and various culture strategies used. In order to improve the physicochemical properties of BC to widen its applicability in regenerative medicine and several other areas, in situ and ex situ methods used in BC modification has also been discussed.

Keywords: Bacterial Cellulose, Zero Waste, Agro-Industrial Residues, Modification.

ICABB_E421_Tan

Bioremediation: Microbes for Environmental Clean-up

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ABSTRACT

The use of conventional methods for the treatment of various hazardous chemicals is widely known. Generally, the waste is treated by various industries before its release into the environment. After the treatment of waste, the treated effluents and solids are separated and disposed off into the environment. Despite current treatment technology, the various harmful pollutants persist in soil and water, which adversely affects the environment. Bioremediation is now being used to reduce and manage the environmental waste. The process usually takes place in soil/water systems where the pollutants/contaminants are degraded into eco-sustainable compounds with the help of bio-remediators such as: bacteria, archaea, and fungi that either cleans the environment naturally or can be genetically engineered in order to eliminate various pollutants. In the present study, various efficient bioremediation techniques have been discussed which are very reliable in eliminating the hazardous environment pollutants thereby cleaning up the environment.

Keywords: Environmental Waste, Microorganism, Bacteria, Fungi, Genetic Engineering.

ICABB_E422_Arc

***Pseudomonas-Trichoderma* based inoculants for Remediation of Most Commonly Used Insecticide Profenofos**

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ABSTRACT

Use of pesticides is vital for the protection of different crop plants. However, the excessive uses of these lead to their accumulation in the environment, particularly agricultural soils. These pesticide residues deteriorate the soil quality and make it unfit for plant growth, ultimately decreasing crop productivity. Profenofos (PFF) is a highly applied broad-spectrum insecticide, and it is expected to be used more frequently in the coming times. The presence of halogen in its structure further complicates the toxicity issue and its environmental fate. Profenofos is a highly toxic compound that is widely used and readily available in many areas, and the microbial degradation of its toxic residues is of particular interest and should be investigated. In the current study, isolates of *Trichoderma* and *Pseudomonas* both in isolation and as consortia were assessed for their ability to tolerate Profenofos and to promote plant growth. *Trichoderma* showed very high tolerance to Profenofos (above 1000 ppm). Infact inoculation of *Trichoderma* resulted in marginal increase in root, shoot as compared to the control. At 0 ppm (absolute control) *Trichoderma* treatment increased root length by 32 %, shoot length by 14 %. At 100 ppm PFF stress, its treatment increased root length by 55 %, shoot length by 26 % compared to negative control (PFF 100ppm). Comparative analysis of host plant biomass at 0 ppm and 100 ppm+ *Trichoderma* showed 35 % increase in biomass, which indicates the isolates ability to reverse the impact of PFF pesticide. The consortia of fungus and bacteria showed improved tolerance to Profenofos stress while improving overall plant growth. The present study suggests the advantages of consortium-based treatment for remediation of PFF residues.

Keywords: Profenofos (PFF), *Trichoderma*, *Pseudomonas*, Consortium, Plant Growth Promotion.

ICABB_E424_Him

Impact of E-Waste Recycling on Soil and Water

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ABSTRACT

During the last few decades electronic and electrical industry has accomplished immense growth. E-waste is considered precarious as some components of electronic equipment contains hazardous heavy metals. In India, there is less consciousness about recycling of electronic waste. E-waste generally composed of Discarded keyboards, monitors, printers, fax machines, mobile phones, audio equipment and batteries if they are improperly disposed can leach Lead and other heavy metals into soil and ground water. E-waste recycling sites in Mandoli, Delhi is actively involved in dismantling, acid extraction of metals and disposing of e-waste. High concentration of heavy metals adversely affects soil fertility. E-waste is composed of Polychlorinated biphenyls, Polybrominated biphenyls, brominated flame retardants. Informal activities with E- waste results in release of hazardous substances in environment which can be devastating effects on health of an individual and environment.

Keywords: E-Waste, Heavy Metals, Soil, Dismantling, Disposing, Hazardous.

ICABB_E425_Harp

Rice Husk - An Agrowaste, as an Adsorbent for Methylene Blue Dye Removal

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ABSTRACT

Rice husk is generated in massive amount as byproduct of rice milling industry. One waste causing pollution could be used to treat another type of pollution in order to protect environment. Air pollution caused due to burning of rice husk is a hot topic of present scenario. Our batch study aimed to utilize agrowaste i.e., rice husk as an adsorbent for removal of methylene blue dye present in effluents. Influences of five parameters like pH (3-9), temperature (20°C-40°C), agitation rate (100-225 rpm), time (15-120 min) and adsorbent concentration (0.1-5 g) on the sorption efficiency was studied during the process. Maximum methylene blue dye removal efficiency i.e., 92.1% was obtained when 0.5g of rice husk was used for treatment at 30°C with pH-7 and 175 rpm for 90 minutes. Our results revealed that rice husk can be applied as an effective low-cost adsorbent material for the biosorption of methylene blue from aqueous solutions.

Keywords: Rice Husk, Methylene Blue, Pollution, Biosorption, Removal Efficiency.

ICABB_E426_Adit

Biomedical Waste Production and its Safe Management During COVID-19 Pandemic in India and Worldwide: Challenges and Management Strategies

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ABSTRACT

Arrival of COVID-19 pandemic in the world creates a great drop down in human health, country's economy and environmental pollution, in almost every nation. The sudden rise in COVID-19 in India and all over the world generated massive pollution of biomedical waste and plastic pollution which have created challenges and is a matter of concern in waste management, especially in developing countries. Safe disposal of biomedical waste and plastic waste is very important otherwise, this will lead to a waste pandemic. During the first and second wave of COVID-19, hospitals discharged single use items such as: PPE kit, gloves, antibiotics, unused medicine etc. which has created massive environmental pollution. In this scenario, more awareness is needed towards environmental protection and it becomes more necessary to manage the biomedical and plastic waste to protect our environment. This review article will discuss country-wise waste production before and during the COVID-19 pandemic, its occurrence and describes where all it is successfully managed, all over the world. This article also summarizes the regulatory framework for biomedical waste management, policy interventions for COVID-19-based biomedical waste, possible management strategies, and perspectives in the Indian context.

Keywords: Biomedical Waste, COVID -19, Pandemic, Plastic Waste, Waste Management.

ICABB_E434_Sri

Remediation of Heavy Metals Using Microbial Consortium – A Review

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ABSTRACT

The outcomes of anthropogenic era have led to the pollution through heavy metal in various ecological niches. This in turn has resulted in the decline of biodiversity and has caused diseases & disorders in various biological systems such as prokaryotes and eukaryotes which includes plants, animals, humans and microbes. This review highlights on the impact of heavy metal pollution on various bio-systems. There are several remediation strategies which are discussed. Though there are physical and chemical strategies adopted, biological approach has been a major technology that can effectively remove heavy metals. The review also suggests various applications of microbial consortium and co-cultivated cultures in the field of enhanced bio-remediation. The novelty of this review is to hypothesize that an effective microbial consortium which includes bacteria, fungi, algae for the effective removal of heavy metals.

Keywords Bioremediation, Microorganisms, Microbial Consortium, Chromium, Lead, Cadmium.

ICABB_E435_Ang

Green Synthesized Nanoparticles as a Biofilter Media

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ABSTRACT

Green synthesis of nanoparticles is an emerging trend in green nanotechnology as it is less toxic, ecofriendly and cost effective. Green synthesized nanoparticles are derived by using various biological agents obtained from different natural sources such as: plants, bacteria, algae and fungi, and nowadays the natural products obtained from plants are majorly being used to mediate synthesis and gaining more attention among the researchers from around the world. A variety of these nano-materials are used in the treatment of industrial wastewater containing toxic heavy metals as these are biocompatible and have higher efficiency. Green nanoparticles remove heavy metals from wastewater without loss of their stability and thus purify the water for reuse and recycling and could solve many issues related to water quality around the globe. One of the recent approaches in industrial wastewater treatment is using biofilter which is cost effective; however, the shelf life of the filter media is the challenge to researchers and scientists as the technology transfer from laboratory scale to industrial scale is difficult. The present work is about synthesizing plant product mediated nanoparticles as a biofilter media for the removal of toxic heavy metals such as chromium, arsenic and lead. The materials used for the synthesis include tulsi leaves, banana peel extract etc and the synthesized nanoparticles were characterized by UV visible spectroscopy and SEM analysis. The size ranges of the synthesized nanoparticles were observed in between 20–42 nm for Fe₃O₄, 18-25 nm in size for silver nanoparticles. The efficiency of removal of heavy metals by these nanoparticles is evaluated.

Keywords: Green Nanotechnology, Wastewater Treatment, Plant – Mediated Synthesis, Biofilter, SEM Analysis.

ICABB_E436_Anki

Formulation and Evaluation of Starch Based Bio Plastics

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ABSTRACT

Petro- based synthetic plastics are introduced many years prior, now it become as a necessary part of the life. It has wide applications in several industries such as; pharmaceuticals, packaging, carry bags, automobiles, cosmetics, etc. Conventional plastics are one of major source of environmental pollutions. These non-degradable plastics, thus accumulates and release toxic chemicals and gases. These toxins are easily entering in to food chain and cause effecting the people health. Due to their various negative impact on environments, researches are going on to synthesis the biodegradable or bio plastic which can substitute these petro- based plastics, bio plastics can be synthesise by renewal resources, for example, cassava, potato, wheat, corn, rice and so. This work aims to optimizing the formulation of starch-based bio plastic through few additives like; glycerol, citric acid and gelatine. These fillers have unique properties; Glycerol is used as a good plasticizer; citric acid can improve the stability and also act as plasticizer and Gelatine helps to make it brittle and elastic. This work also addresses the biodegradability of these prepared bio plastics. The biodegradability rate was assessed under different conditions; soil, water and in microbial activity by ASTM G21 method at different temperatures.

Keywords: Bioplastic, Glycerol, Biodegradable.

ICABB_E437_Van

Bioremediation of Mercury Using Mercury Resistant Bacteria and Fungi

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ABSTRACT

Mercury is one of the most hazardous heavy metals. It is liquid at room temperature and is extremely volatile due to its low vapor pressure, which is one of its distinguishing characteristics. Mercury contamination is a global issue that poses a threat to the environment and living organisms. Bioremediation means removal of pollutants from the environment by converting toxic heavy metals into less toxic form with the help of microbes or its enzymes. Microbes have developed a mercury detoxification system based on the mercuric reductase enzyme's, intracellular reduction of mercuric Hg²⁺ to non-toxic Hg⁰ and its subsequent diffusional loss from the cell [mercury resistance operon (mer)] takes place. Research was done by scientists in which mercury resistant bacterial strains were isolated from metal contaminated areas. *Pseudomonas aeruginosa* and *Bacillus licheniformis*, two highly potent isolates capable of mercury remediation, were screened among them. Isolates' potential to reduce mercury levels suggested that they could be utilized to develop bioremediation methods to purify mercury-contaminated waste and environment. In another investigation, filamentous fungi were found to be useful in the bioremediation of mercury toxicities. Filamentous fungi, *Aspergillus flavus* strain KRP1 isolated from forest soil, was used to detect its remediation activity against mercury contamination. The strain was found resistant to mercury (II) pollution, making it ideal for future exploration in mercury decontamination. The strain appears to have potential for bioremediation of aqueous substrates containing mercury (II) via a biosorption mechanism. This review analyses the microbes reported to have remediation potential.

Keywords: *Aspergillus flavus*, *Bacillus licheniformis*, Bioremediation, Biosorption, Mercury, Mer Operon, *Pseudomonas aeruginosa*.

ICABB_E438_Stu

Bioremediation of Nickel

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ABSTRACT

Heavy metals are introduced into the environment through anthropogenic processes. These heavy metals have become a global problem because they adversely impact human health. Bioremediation is used to remediate the toxic heavy metals from the environment by microorganisms or its enzymes. Bioremediation is preferred over physicochemical methods because most heavy metal salts are water-soluble and cannot be separated by physical separation methods. Also, physicochemical methods are ineffective and expensive when the concentration of heavy metals is very low. Bioremediation includes sustainable remediation technologies to rectify and re-establish the natural condition of soil and helps in getting rid of heavy metal pollution. Therefore, Bioremediation is preferred as it is highly efficient, cost effective and eco-friendly. Nickel is carcinogenic to humans, which causes systemic manifestations including lung cancer. This review aims to investigate the Ni resistant bacteria and its efficacy in bioremediation. Bacteria reduce metals as a detoxification mechanism. They use mechanisms like ATP binding Cassette transporters efflux system, biomass formation etc. Bacteria can significantly remove 70-85% nickel content from the soils after bioremediation process. Bacteria can physically remove considerable amounts of positively charged cationic metals through bioaccumulation or biosorption. At low concentrations, bacteria take up the available metal more quickly. However, metal ions diffuse to the biomass surface by intraparticle diffusion at high concentrations. Additionally, Ni is demonstrated as chemoattractant to bacterial cells under stressful conditions. For future research, more bacterial species can be explored for enhancing the current methods for bioremediation of heavy metals.

Keywords: Bioremediation, Carcinogenic, Chemoattractant, Detoxification, Nickel.

ICABB_E439_Rad

Heavy Metals in Food and Associated Health Risks: A Review

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ABSTRACT

Environmental pollution due to increasing anthropogenic perturbations is of major concern. Mass accumulation of heavy metals such as; chromium, lead, cadmium, cobalt, nickel, arsenic, mercury etc. due to industrialization and non-biodegradability, is causing subsequent accumulation in food crops. They are noxious to overall human health and affect nutrient status of plants. Some plants are hyperaccumulators that readily uptake and accumulate heavy metals from the polluted soil. WHO/FAO has set maximum allowable concentrations (MAC) for HM intake, above which its consumption is threatful. This review emphasises on health hazards caused due to heavy metal accumulation in food.

Keywords: Heavy Metals, Food Crops, Health Risks, MAC, Toxicity.

ICABB_E440_Pra

Bio-Mining: A Sustainable Method for Metal Extraction

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ABSTRACT

Mining sector is said to be one of the most major form of environmental pollution because of the type of processes and the position of the ore. Mining industry is likely to disturb and destruct the ecosystem and wildlife in many possible ways. So major challenge for the mining industries is to supply metal and minerals without further degradation of ecosystem. With this growing concern we opted for an eco-friendly way of mining using micro-organisms. Use of organisms for the extraction of metal has been seen since 18th century, this method of metal extraction is now being termed as “bio-mining”. The review article is about the methodology involved and the use of bio-mining for the benefit of environment. The process of bio-mining can be achieved by two different procedures. One is bio-leaching in which we directly extract metal from its constituent ore and second is bio-oxidation in which we make the metal in the ore more accessible so that we can extract it easily by the use of conventional mining techniques. A wide diversity of micro-organisms like *T. ferrooxidans* and *L. ferrooxidans* are used in the above-mentioned processes. The commonly extracted metals are copper, gold, nickel etc. The use of bio-mining can further be extended to reclaim the land already degraded by the conventional mining methods. It can also be employed for handling e-waste which is further elaborated in the article. Bio-mining being both eco-friendly and economic has led to its worldwide acceptance.

Keywords: Bio-Mining, Bio-Leaching, Micro-Organisms, Bio-Remediation.

ICABB_E441_Razi

Physicochemical Characterization of Fungal Chitosan Extracted from *Trichoderma longibrachiatum* in Submerged Cultivation

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ABSTRACT

Considering the versatile nature of biopolymers, World has seen recent surge in the use of biopolymers for various applications. Chitin and chitosan are the second most abundant biopolymers found on the earth. Chitin is a natural polysaccharide and is a major component of exoskeleton of crustaceans, insect cuticles and fungal cell wall. Chitosan is obtained from chitin via demineralization and deacetylation process using several chemicals. This leads to environmental pollution. including is chitin. There is a need for sustainable production strategy of chitosan. Fungal source can be an excellent raw material for extraction of chitosan. Due to high potential of chitosan as a functional biomaterial, it is gaining attention in various fields. In this study, an attempt has been made to culture *Trichoderma longibrachiatum* ITCC 7839 in three different culture media (Potato dextrose broth, Yeast Potato Dextrose broth and Sabouraud dextrose broth) for biomass production in submerged cultivation. Potato Dextrose Broth (PDB) yielded highest biomass. Biomass was then processed to obtain chitosan and was air dried. Physicochemical characterization (FTIR and XRD) was carried out to determine its chemical structure and crystallinity. Commercial chitosan was used as a standard. FTIR analysis showed the presence of signature peaks in fungal chitosan and commercial chitosan.

Keywords: Chitin, Fungal Chitosan, *Trichoderma longibrachiatum*, FT-IR, XRD.

ICABB_E442_Prati

Study of Cellulase Enzyme Production and Activity by Microbial Fermentation

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ABSTRACT

This study aimed to analyze the most appropriate methods for quantitative rate of growth of cellulase enzymes in lignocellulosic biomass (LCB) for the application of biofuel production. Cellulose can be hydrolyzed to glucose monomers using chemicals such as strong acid or biological catalysts cellulase. Cellulase enzymes can be produced from various microorganisms such as fungi, bacteria yeast, and some animals also. For our study, we consider *Aspergillus niger* as the most potent and easily producible strain by using soil on malt extract agar and potato dextrose agar medium which confront the growth of enzyme in large quantity. By using a potent strain rate of growth of cellulase enzyme can be improved in lignocellulosic biomass. Quantitative and qualitative estimation of enzyme can be done by using several approaches such as Thread cutting method, Filter paper collapsing method, Spectrophotometric method, Flat band method, Branch and swain method, CMC method and so on. Among all of them spectrophotometric method is the most applicable approach for the quantification of cellulase enzyme. The growth can be monitored by studied their growth kinetic parameters such as cellulase activity, amount of substrate, and protein activity through a graphical representation of pre-treated biomass concentration in different phases. The kinetic study, catalytic activity, and optimization through different parameters may increase the production of the enzyme during hydrolysis by using fugal strain species. Thus, this abstract intends to describe potent microorganism that are more appropriate, fast-growing cells, time-saving, economically effective and their growth estimation approaches. Basis of future scenario the bioethanol production is eco-friendly and cost-effective by using this approach.

Keywords: Cellulase Enzyme, Microorganism Cultivation, Growth Estimation, Spectrometric Approach, Growth Kinetics.

ICABB_E443_Somy

Xylanase Enzyme Production by Using Microbes for the Biofuel

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ABSTRACT

As we know biotechnology is one of the focused scientific fields where all the highest development processed during the last few decades. It is the grouping of biological, physical and engineering, technical sciences in order to complete the hi-tech application using a biological system. So for Processing the above, we use the xylanase enzyme (Endo-1, 4-β-), which is a class of biological enzymes used to degrade the linear polysaccharide i.e. xylan into xylose, thus it will help in breaking down one of the major components of plant cell walls i.e. hemicelluloses which is a major component of lignocellulosic biomass and thus also help in breaking of cell-wall that play a major role in bioethanol production. Xylanase have the property to process the pre-bleaching and the bioconversion of the lignocellulosic biomass into the usable feedstock as well as a usable nutrient. As we know nowadays the industries are looking for the alternate and best eco-friendly approach so using the xylanase for biofuel production is one of the major steps towards the biogreenery approach. This paper reviewed many of the research papers then get to know that Xylanases are produced by fungi, bacteria, yeast, marine algae, protozoans, crustaceans, seeds. By following the last few recent research obtain some of the best microbial sources for the xylanase production were listed are *Micrococcus* sp., *Bacillus* sp., *Aspergillus Flavus* & *A. niger*, *Fusarium* sp. In yield of Xylanase, the fungal strain considers i.e., *Fusarium sporotrichoides* by the SDA medium confront the growth. In the yield of Xylanase a few parameters were determined i.e., the fermentation method, carbon & nitrogen source, pH, temperature, ionic effects, incubation time, aerations, and species. The kinetic study, catalytic activity, and optimization through different parameters may increases or help in the production of enzyme during hydrolysis by using fugal strain species. The production of xylanase on large number of scales is expensive because it requires a huge amount of enzyme. It Concluded that using of microbes are more appropriate and best approach for biofuel production, fast growing cells, time saving and economically effective. So, on the basis of future scenario the bioethanol production is ecofriendly and cost-effective by using the enzymatic approach.

Keywords: Lignocellulosic, *Fusarium* Species, Optimization, Kinetic Growth, Xylanase Enzyme, Biofuel.

SESSION V
Nanotechnology
and
Drug Delivery

ICABB_N501_Ans

Natural Agent Loaded Microsponge Gel for the Treatment of Arthritis

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ABSTRACT

Rheumatoid arthritis is an autoimmune disease that is chronic and progressive, characterized by systemic inflammation, the bone, cartilage, tendons, and ligaments of joints are destroyed. All of these joint damage results in deformities and bone erosion which are extremely painful for patients. Many synthetic medications are prescribed as conventional treatment for rheumatoid arthritis, but they have side effects that can adversely affect the therapeutic outcome. In Ayurvedic literature, *Calotropis procera* is mentioned for the treatment of inflammation and arthritic disorder. The bark and leaves of *Calotropis procera* are known to show analgesic effect and anti-inflammatory properties. The leaves contain mainly the chemical constituents α amyrin, α amyrin acetate, β sitosterol, urosolic acid which are responsible for the anti-inflammatory effects, anti-arthritis activity and analgesic effect. A microsponge drug delivery system is a porous, strongly cross linked, polymeric microsphere, a polymeric system composed of porous microspheres that can entrap huge amount of drug and release drug into the skin in sustained manner over long period of time, which could be loaded into a formulated product such as gel, cream, liquid and powder. The present work is focused on the development of microsponges of *Calotropis procera* by quasi emulsion solvent diffusion method and loaded them in gel to deliver the drug in form of a novel drug delivery system (NDDS) as a topical formulation for the treatment of arthritis. The current investigation showed that the *Calotropis procera* markedly reduced the paw inflammation, as a result, *Calotropis procera* has a great potential in the treatment of Rheumatoid arthritis (RA).

Keywords: Rheumatoid Arthritis (RA), Natural Agent, Microsponges, Novel Drug Delivery System (NDDS).

ICABB_N503_Nee

Formulation Development of Oral Drug Delivery System Loaded with Herbal Drug for Urolithiasis

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ABSTRACT

Kidney stones are a frequent occurrence in India and other developing nations. Kidney stones impacted 10-12 % in developed countries. Kidney stones are the most prevalent type of stone found in both men and women. Kidney stones are small, pebble-like substances made from chemicals in your urine. They are formed in the kidneys when high levels of certain substances, such as minerals or salts, get into the urine. Bryophyllum pinnatum leaves showed preventive effects against renal calculi formation and validate its ethnomedicinal use in urinary disorders. It further supports its therapeutic potential for the treatment of urinary calculi. Microsponges are porous, polymeric microspheres that are used mostly for topical use and have recently been used for oral administration. Microsponges are designed to deliver a pharmaceutically active ingredient efficiently at the minimum dose and also to enhance stability, reduce side effects, and modify drug release. To overcome all these problems, we move to prepare an extended-release formulation with a combination of the hydrophilic and hydrophobic polymer matrix to maximize the drug loading and prevent drug loss. Polymeric matrix sustained the release with therapeutically effective concentration achieved in the systemic circulation over an extended period of time, thus achieving better compliance of patients.

Keywords: Microsponge, Control Release, Oral Drug Delivery System, Topical; Drug Delivery System, Kidney Stone.

ICABB_N504_Adi

Poly (Methylacrylate) As a Novel Polymer Material for Designing Oral Drug Delivery Systems with Controlled Release Properties

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ABSTRACT

The oral route of drug administration in the gastrointestinal tract is by far the most common, and it can be used for both systemic drug delivery and treating local gastrointestinal diseases. Drug delivery to specific regions of the upper or lower gastrointestinal tract can also be improved with the right formulation. Polymers make up a large portion of the materials used in controlled release formulations and drug-targeting systems due to their diverse topology and chemistry. By providing controlled release of therapeutic agents in constant doses over long periods of time, cyclic dosage, and tunable release of both hydrophilic and hydrophobic drugs, they have contributed significantly to the advancement of drug delivery technology. Eudragit is a brand of polymethacrylate-based copolymers with a wide range of applications. Anionic, cationic, and neutral copolymers based on methacrylic acid, methacrylic/acrylic esters, or their derivatives are included. Eudragits are amorphous polymers with glass transition temperatures ranging from 9 to 150 degrees Celsius. Eudragits are inert, non-biodegradable, and non-toxic. Eudragit L, which is anionic and soluble at pH > 6, is used for enteric coating, whereas Eudragit S, which is soluble at pH > 7, is used for colon targeting. The physicochemical properties and applications of various grades of Eudragit in colon-specific/enteric-coated/sustained release drug delivery and taste masking are discussed in this review.

Keywords: Microbeads, Poly (Methylacrylate), Controlled Release, Copolymer.

ICABB_N505_Bha

Effective Inhibition of Common Human Pathogen Using an Eco-Friendly Leaf Extract of *Murraya koenigii* Assisted Herbal Silver Nanoparticles

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ABSTRACT

The techniques used for the green synthesis of nanoparticles accompanied by clinical applications have been extensively used in nanotechnology due to their capability to provide safe, eco-friendly, inexpensive and firmness. This study focused to assess the antimicrobial activity of silver nanoparticles (AgNPs) synthesized using the aqueous leaf extract of *Murraya koenigii*. Considering that, we have evaluated the ability of phytochemical present in *Murraya koenigii* leaves extract to reduce AgNO₃ and analaptic potentials of Silver nanoparticles (AgNPs) containing this plant extract towards the clinical strains of microbes. The optimization of different conditions like concentration, pH, temperature and reaction period were carried out to synthesise AgNPs. The nanoarchitecture elements were interpreted using visual observation, UV-Vis spectrophotometry and Scanning Electron Microscopic (SEM) analysis. The antimicrobial effects of AgNPs towards the clinically significant 5 different strains *Klabseilla mobilis*, *Staphylococcus aureus*, *Proteus vulgaris*, *Pseudomonas aeruginosa* and *Candida albicans* were studied using standard disc diffusion method. This green synthesis method is quick, facile and does not involve the use of any detrimental and expensive chemicals. The results showed that Curry leaf plays a crucial role in the reduction and stabilization of silver to silver nanoparticles. The results of the standard disk diffusion method revealed that AgNPs displayed antimicrobial activity.

Keywords: Silver Nanoparticles; *Murraya Koenigii*; UV-Vis Spectrophotometer; SEM; Antimicrobial Activity.

ICABB_N506_Neh

Formulation and Evaluation of Polyherbal Matrix Tablet for Anti Hepatitis Activity

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ABSTRACT

The present research explores the hepatoprotective activity of various extracts against experimental hepatotoxicity. Hepatotoxicity is the injury or liver damage caused by exposure to drugs; it is an adverse drug reaction that may be uncommon but serious. It has been observed that when several herbs are combined in a specific ratio, the medicinal effect is increased while toxicity is reduced. The present research explores the hepatoprotective activity of various extracts against experimental hepatotoxicity. Polymers are the building blocks of a pharmaceutical drug delivery system because they control drug release from the device. Polymers are used to protect drugs from the physiological environment and to extend their release time in order to improve their stability. In the present study polyherbal matrix tablets were prepared by the wet granulation method using aqueous extracts of punarnava, and chirata and excipients Talc, sodium benzoate Magnesium stearate and sodium alginate polymer. This research focuses on matrix tablets, which are one of the most practical methods for developing sustained-release dosage forms, as well as the approaches used in their formulation and evaluation. The therapeutic efficacy of a sustained release matrix tablet with improved efficacy can be increased. It also emphasizes the significance of polyherbalism and matrix Tablet. Herbal products may contain a single herb or a combination of several herbs that are thought to have complementary and/or synergistic effects. Polyherbal delivers safe and effective results while increasing patient compliance. Based on the foregoing, we can conclude that a sustained release matrix tablet can overcome the problems associated with traditional oral drug delivery, and increase the dosage form's efficiency. The matrix forming polymer can be used to successfully prepare matrix tablets that release the drug in a controlled manner. A simple and cost-effective method for the formulation of matrix tablets. Sustain release matrix system is a novel drug delivery system that will be beneficial in the future.

Keywords: Hepatoprotective, Polyherbal, Matrix Tablet, and Hydrophobic Polymer.

ICABB_N507_Aas

Immunotherapy: A Treatment for Breast Cancer

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ABSTRACT

Breast Cancer is a major global concern due to a lack of early diagnostic and therapeutic options, affecting both men and women. In this era of technological innovations, researchers are working on numerous aspects of breast cancer research, which could lead to the development of appropriate point-of-care, non-invasive, and diagnostic aids for early breast cancer detection and management. With rapid development in the field of technology, cancer immunotherapy has a huge potential to reform cancer treatment. TDLNs (tumour-draining lymph nodes) are the major locations for initiating immune responses and are found to be the site for most breast cancer metastasis. Reversing the immunosuppressive environment in TDLNs is crucial for improving the malignancy's fate, but it remains a difficult technical issue. Exosome-based research is an upcoming topic aimed at determining and comprehending the role of exosomes in breast cancer diagnosis, immune response, and clinical outcomes. The exosome surface can be genetically engineered to overexpress genes that can promote effector T cell expansion. Due to their immunogenicity and molecular transfer function, exosomes have significant promise in cancer immunotherapy. Injection of smart exosomes can activate effector T cells and enhance the antitumor immune response and slow tumour growth. Exosomes' role in immunotherapy can increase efficacy, reduce toxicity and chances for recurrence of breast cancer.

Keywords: Breast cancer; Exosome; Immunogenicity; Immunotherapy; Lymphocyte; Treg.

ICABB_N508_Ree

A Review on the Application of Nano-Herbal Formulation in the Diagnosis and Treatment of Kidney Disease and Their Limitations

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ABSTRACT

Recently nanomaterials have been explored for controlling and detection of various pathological conditions including kidney diseases. Kidney disease has become a public health and economic burden all over the world. There are different types of nano-structures that increase the stability and effectiveness of drug compounds and thus increase their pharmacokinetics. Due to the ineffectiveness of current therapy, there has been growing interest in treatments including natural products as complementary or alternative choices. Owing to their low or no side effects nano-herbal formulation of natural or herbal compounds may help to increase their bioavailability and so their efficacy. In the present review, existing experimental study, the current challenges, clinical strategies of NPs and forthcoming prospects and limitations in the diagnosis and management of kidney disease have been addressed.

Keywords: Kidney Disease; Nanoparticles; Treatment; Diagnosis; Limitation.

ICABB_N509_Ais

Solid Self Nano Emulsifying Drug Delivery System of Preparation Poorly Soluble and Less Bioavailable Drug

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ABSTRACT

Several drugs are less soluble and have a low bioavailability. Self-Nanoemulsifying Drug Delivery Systems (SNEDDS) were developed for such drugs in order to overcome the difficulties. The ability of various surfactants and co-surfactants to emulsify selected oily phases was tested. Ternary phase diagrams were created to identify nano-emulsification areas in the selected systems. Diclofenac, a nonsteroidal anti-inflammatory drug (NSAID), is a BCS Class II drug with poor aqueous solubility and dissolution. Peptic lesions caused by diclofenac sodium develop without pain in 50% to 60% of cases, delaying early diagnosis and potentially leading to complications. Diclofenac Sodium is a nonsteroidal anti-inflammatory, analgesic, and antipyretic medication with a high solubility above pH 5 and a very short half-life. When taken orally, it causes a variety of side effects, including gastric-duodenal ulcers. The use of dry, solid powders of solid SNEDDS would help to overcome the limitations of liquid SNEDDS by improving patient compliance and stability. Our findings suggest that the SEDDS formulation could be used as an alternative to traditional oral Diclofenac formulations to improve dissolution rate and thus bioavailability.

Keywords: Oral Bioavailability, Self-Nano-Emulsifying Drug-Delivery Systems (SNEDDS), Liquid SNEDDS, Solid SNEDDS, Pseudo Ternary Phase Diagram.

ICABB_N510_Nan

Advances in Cell Separation Using Micro and Nanotechnology

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ABSTRACT

Cell separation using micro- and nanoscale technologies offer several advantages over conventional, macroscale separation systems in terms of sample quantities, economical, portability, and prospective for integration with other analytical scientific techniques. One of the most difficult challenges include isolating a phenotypically pure cell culture from a heterogeneous sample. With the development of applications from preparatory to clinical, there is a need to develop systems with high separation purity and efficiency. Noteworthy contribution of cell separation is deviated towards biomedical research and medicine and comprehensive latest cell separation methods. We are going to discuss three cell separation techniques all of which are microfluidic. Affinity based methods are (1) Magnetic sorting, wherein magnet-based cell sorting, and magnetic particle-based cell separation systems have been discussed which comprise of nanoscale elements and (2) Fluorescence. Fluorescence-Activated Cell Sorting (FACS) is a technique that allows plant growth and maturation based on phenotypes. In this, the current state of the art for FACS methods in plants is observed by means of case studies of research. (3) Microfluidic cell lysis is a technique that lyse the undesired cell populations in a mixed suspension while leaving behind the desired cells. Suitable examples have been discussed from each category with prominence on micro- and nanotechnology. For all of the techniques, the construction of the devices is such that they can be operated in an extensively parallel fashion to elevate scale-up and throughput without altering the purity and potency.

Keywords: Cell Separation, Nanotechnology, Cell Sorting, Fluorescence, Microfluidic, Magnetic Sorting.

ICABB_N511_Har

Studying The Action of Inhaled Essential Oils and Edible Oils Aerosol Nanoemulsions on Respiratory Distress

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ABSTRACT

The liquid in liquid dispersion reduced to a size ranging between a few hundred nanometers are called nanoemulsions. These formulations have been utilized in the food, cosmetics, and pharmaceutical industries, for a variety of benefits that they offer. Nanoemulsions are currently being studied and analyzed for their target-specific drug delivery mechanism. They have been used for the treatment of disorders varying from cancer to metabolic disorder and also serve as therapeutic agents. Due to their small size and high specificity, they're considered to be a breakthrough in the drug development sector. Several categories of natural products like essential oils, root extracts, leaf extracts, etc. have been explored for the preparation of nanoemulsions targeting a wide range of disorders. Essential oils from sources like lavender, tea tree and eucalyptus etc. and edible oils like: mustard oil, soybean oil and olive oil, are known to be rich in several bioactive compounds exhibiting a broad spectrum of actions, including their antimicrobial, anti-cancer, anti-inflammatory, and antioxidant activities. Several compounds from these products have been shown to have potential inhibitory or regulatory factors against Acute Respiratory Distress Syndrome (ARDS), which is a highly fatal condition with soaring mortality rates. Preparation of inhalable or nebulisable nanoemulsions from essential and edible oils might be helpful in curbing this syndrome and its comorbidities. In this work, the authors aim to discuss the target specific mechanism of action, of nanoemulsions prepared from essential and edible oils; and their specific aerosol performance in order to enhance the current treatment procedure for treatment of ARDS.

Keywords: ARDS, Nanoemulsions, Essential Oils, Edible Oils, Nanoformulations.

ICABB_N512_Med

Recent Advancements in Drug Delivery of Schizophrenia

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ABSTRACT

Schizophrenia is mental disorder which can cause various psychological disturbances like hallucinations, paranoia, delusions, thought disorders, mood disorders and many more. The nature of this disease appears to originate from various environmental or genetic disruption of brain development. Genesis of psychotic symptoms have been found to be a result of disturbed dopaminergic neurotransmission. Synaptic function plays a very important role here and it has been found that its dysfunction often leads to abnormalities of neuronal connectivity possibly involving interneurons. Unfortunately, the precise nature, location and timing of those events is still unknown. Various psychological therapies combined with antipsychotic drugs have been the current line of treatment for this disease but still there is an urgent need for better and simpler ways of treating it with more efficiency. Advances in Epidemiology, neuroscience and genomics have led us to a great understanding of this disorder in these recent years and therefore the opportunities for further scientific advances are many, but so are the challenges. Since, the data available pertaining to Schizophrenia in public domain is scarce and scattered, hence, this review aims to provide a comprehensive view of the epidemiology, clinical manifestations, and etiology, diagnosis and treatment strategies of Schizophrenia. This review also provides insight into the commercialized drugs presently available for this disease in the US pharmaceutical market. It elucidates the patent and exclusivity scenario of different broad-spectrum anti-epileptic drugs as well as recently approved orphan drugs using FDA Orange book. Further, it predicts the launch dates for generic drugs based on expiration of patent and exclusivity of the branded (new) drugs.

Keywords: Dopaminergic, Neurotransmission, Synaptic, Antipsychotic, Patent, Exclusivity.

ICABB_N513_Shr

Acute Respiratory Distress Syndrome and RNAi Based Therapeutic Strategies

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ABSTRACT

Acute respiratory distress syndrome (ARDS) is a disease with a high mortality rate, it develops due to physiological changes in the lung that can arise from a variety of direct or indirect injuries. RNA interference (RNAi) is a mechanism that can help in creating therapeutic effects by inducing gene silencing and hence increasing the chances of survival for people with severe diseases. It can be achieved by employing either of the four major RNAi interventions; short-interfering RNA (siRNA), short hairpin RNA (shRNA), micro RNA (miRNA), and piwi-interacting RNA (piRNA). The delivery of these therapeutics can be viral vector or non-viral vector based. It is a pathbreaking intervention currently being pursued to treat not only the diseases like hemophilia, hypercholesterolemia, HIV, viral hepatitis, cancer, metabolic disease, and neurodegenerative disorders but also, the pulmonary diseases. RNAi can be employed in targeting the release and expression of several pro-inflammatory cytokines, gene silencing for differential NO expression and selectively modulating the pathways of growth factors and their receptors responsible for disruption of alveolar which is the primary cause of ALI (Acute Lung Injury) that further manifests into the fatal condition of ARDS. *In-vitro* experiments with the likes of A549 cells and HUVEC (Human umbilical vein endothelial cells); and animal gene-knockout models have given major insights on delivery mechanisms of these therapeutics. In this review, we will be looking at the different RNAi techniques that have been investigated to improve the curative mechanism in order to modify and improve the current treatment strategies for ARDS.

Keywords: ARDS, RNAi, Therapeutics, siRNA, Gene Silencing, Vector-Based Delivery and Pulmonary Drug Delivery.

ICABB_N514_Raj

Development and Administration of Resveratrol Loaded Liposomes Alleviate Bleomycin-Induced Lung Injury and Improve Lung Physiology in Idiopathic Pulmonary Fibrosis: An *in Vitro* and *in Vivo* Study

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ABSTRACT

Idiopathic Pulmonary Fibrosis is a chronic condition characterized by the uneven thickening of alveolar epithelium impairing the lung's ability to exchange gas. Resveratrol, an anti-inflammatory agent, has the potential to stall EMT, but it has low oral bioavailability with high metabolism. This study explores the liposomal encapsulation techniques to improve the delivery of resveratrol, and to evaluate increased therapeutic effects of resveratrol-loaded liposomes. The resveratrol-loaded P90G and Soya Lecithin liposomes were prepared with an encapsulation efficiency of 94% and 92%. The average size and zeta-potential of the liposomes were estimated to be 150 nm and -20 mV, respectively. The drug release of liposomes was found to be sustained and 16.61% in 6 hours in simulated gastro-intestinal fluid. The Liposomes exhibited significantly higher uptake in comparison to free resveratrol on Caco-2 cells. Administration of 10 µg/mL bleomycin induced EMT in A549 cells, and confocal microscopy of resveratrol-loaded liposomes treated cells show a reduction of collagen levels in comparison to the untreated cells. The induced pulmonary fibrotic rats (Bleomycin 2.5 mg/kg) treated with oral administration of 10 mg/kg Resveratrol-loaded liposomes to the showed decrease in TNF-α, IL-1β, and IL-6 and, improved lung physiology in comparison to free resveratrol. Moreover, the collagen levels were decreased when the rats were treated with resveratrol liposomes and the overall fibrotic score was decreased. These results show that resveratrol-loaded liposomes can alleviate EMT and restore epithelial population of the lungs. Thus Resveratrol-loaded liposomes can be commercially utilized to treat idiopathic pulmonary fibrosis.

Keywords: Tras-Resveratrol, Resveratrol, Epithelial-Mesenchymal Transition, Nutraceuticals, Liposomes, Pulmonary Surfactants, Lipids, Fibrosis, Airway Patency, Chronic Lung Injury, COPD, TGF, Idiopathic Pulmonary Fibrosis, Interstitial Lung Diseases.

ICABB_N515_Sha

Nanodrug Formulations as Potential Interventions for Persistent Lymphoid HIV Eradication and Prevention

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ABSTRACT

With the advent of combinational antiretroviral therapies for HIV, lives of people living with this condition have become much easier, yet we do not have a complete cure for the same. Treatment procedures for such diseases still center around making the positive subjects reach undetectable levels, which means that the viral load cannot be detected in their plasma. However, the residual viral load in lymph nodes of affected individuals still persist even after years on Antiretroviral drugs. Current nano-drug delivery interventions are able to target the viral load in plasma but the drug accessibility and delivery in the lymph nodes is still a challenge. Here we present the usage of nanomaterials as therapeutic agents, increasing the scope of drug transportation and solubility in order to target the viral load in lymph nodes. Moreover, oral administration of preventive drug formulations PREP (Pre-Exposure Prophylaxis) for partners of positive individuals leading to enhanced or better performance is also dealt with. Finally, future prospects relating to nanobots, microscopic vesicle liposomes, nanoemulsions and other drug delivery systems along with their advantages and disadvantages will also be discussed.

Keywords: Nanoformulations, HIV, Drug-Delivery, PREP, Lymph Nodes, Plasma.

ICABB_N516_Vin

Nasal Nano Formulation for Adult and Paediatric Corticosteroids Use: Way Ahead

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ABSTRACT

Background: Intranasal corticosteroids are cortisone-like medicines from family of steroids. They are used to relieve the, rhinorrhoea, irritation, discomfort of hay fever, allergies, nasal polyps, and other nasal problems and are accepted as safe and effective first-line therapy for allergic rhinitis. As the nasal mucosa passage is highly vascularised, immunogenic, and more patient compliant after oral route so nasal delivery of therapeutics are more viable alternative to parenteral route. Several intranasal corticosteroids are available (beclomethasone, dipropionate, budesonide etc.) and though are efficacious in treating seasonal allergic rhinitis and as prophylaxis for perennial allergic rhinitis but their adherence to the nasal cavity is not effective equally. There medicative use has shown promising results in relieving most of the nasal congestion and allergic responses in early as well as late-phase symptoms but due to their low adherence capacity to the nasal cavity due to mucociliary clearance (MCC) is a concern. The study explores and puts forward the latest advancements in nasal nanotechnology for improving the therapeutic delivery besides providing the controlled release of corticosteroids across the sinonasal cavity. Also, we tried to understand the biochemical interactions among the steroidal drugs, opted nanomaterials and the nasal biological ecosystem altogether along with its effects on surface receptor binding, drug release as well as stability of drugs. There are many nano-based approaches employed for developing an efficient intra nasal drug delivery system, ranging from chitosan and PLGA nanoparticles, Carbon nanotubes (CNTs), mucoadhesive nano-emulsions/gels etc. Elaborate discussions on varying agents are limited to potency, patient preference, dosing regimens, and delivery device and vehicle are imperative.

Keywords: Corticosteroids, Nasal Nano Formulation, Rhinorrhoea, Intra Nasal Drug, Beclomethasone, Mucociliary Clearance.

ICABB_N517_Shi

Electrochemical Biosensors for Cancer Detection: A Review

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ABSTRACT

Global statistics reports cancer to be a second fatal disease that has affected a large portion of the human society. Mortality rates for cancer have a direct correlation with the stage of diagnosis. It can be reduced if cancer is diagnosed at an early stage. Conventionally, physical examination in conjunction with tissue biopsy, image analysis, and laboratory tests for tumor markers, endoscopic examinations are used for diagnosis of cancer that are generally invasive in nature and are stressful for patients. With the advent of liquid biopsy, tumor biomarkers (proteins, DNA, miRNA) can be detected in different body fluids, reducing the distress to patients, dramatically. Circulating tumor markers like DNA or miRNA, if can be detected at lower concentrations, can be the much-needed solution for early diagnosis of cancer, improving survival rates. Furthermore, fast, sensitive, simple, and cost-effective diagnostic devices can be developed using these biomarkers. This paper presents a comprehensive overview on recent developments of electrochemical biosensors for detection and quantification of various biomarkers for cancer diagnosis. This review focuses on the approaches of direct electrochemical detection with different designs of probe, intercalating agents, redox- labelled probe, different nanomaterials and immobilization methods.

Keywords: microRNA; Electrochemical Biosensor; Cancer Biomarker; Redox-Indicator, Liquid Biopsy.

ICABB_N518_Ras

Synthesis and Characterization of Sulfur and Sulfur-Selenium Nanoparticles Loaded on Reduced Graphene Oxide and Their Antibacterial Activity Against Gram-positive Pathogens

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ABSTRACT

Bacterial infections have a huge impact on human health and continuous use of antibiotics for treatment has led to emergence of multidrug-resistant bacteria. This antibiotic resistance further adds to its detrimental effects. One such formidable bacteria is Methicillin-resistant *Staphylococcus aureus* (MRSA), responsible for endocarditis, bacteraemia, osteomyelitis and skin and soft tissue infections in humans along with serious clinical infections. Similarly, vancomycin-resistant enterococci (VRE) are associated with nosocomial infections leading to high mortality rate in Europe and USA. Development of nanomaterials for use in healthcare industries has emerged as a boon for clinical communities. The objective of this study is to evaluate antimicrobial property of synthesized rGO nanocomposites namely rGO-S and rGO-S/Se on Gram positive pathogens, *S. aureus* and *E. faecalis* and to elucidate its mechanism of action. In our study, rGO-S/Se exhibited 90% antibacterial activity as compared to rGO and rGO-S against the bacteria as shown by suspension and CFU assay. Concentration and time dependent growth curve analysis was performed on *S. aureus* with nanomaterial rGO-S/Se which demonstrated bacteriostatic activity of the NPs synthesized. Fluorescence microscopy with FITC labelled nanoparticles revealed physical contact between nanomaterial and bacterial cells as a requirement for its antimicrobial efficacy and atomic force microscopy of rGO-S/Se treated cells displayed morphological aberrations in *S. aureus*. Further experiments revealed involvement of simultaneous multiple actions such as ROS generation and loss of a thiol containing redox regulator GSH which contributes towards increased oxidative stress in bacteria. Our results suggest a possible three-pronged approach of bacterial cytotoxicity by these graphene-based materials.

Keywords: MRSA, VRE, GSH Loss, Nanoparticles, Oxidative Stress, Antimicrobial Resistance, Antimicrobial Activity.

ICABB_N519_Ali

Quantum Dots Based Aptasensor for the Ultra-sensitive Detection of Heavy Metals

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ABSTRACT

For decades, heavy metal ion contamination of the environment has been a major global concern due to industrial development and resource exploitation. Traditional methods for detecting heavy metal ions, on the other hand, adhere more strictly to the requirements of detection equipment, sample pretreatment, experimental environment, and so on. Over the years, aptasensors have been developed for the detection of metal ions. Aptamers have the advantages of high specificity and sensitivity, easier synthesis and chemical modifications, better thermal stability, lower immunogenicity and low cost, making them ideal recognition elements in the development of biosensors, providing a new direction platform for heavy metal ion detection. In this work, water soluble quantum dots were synthesized and further conjugated with peptide and aptamer to be used as an efficient sensing platform for detection of contaminants such as metal ions. Characterization techniques like UV-VIS, fluorescence spectroscopy, were done.

Keywords: Quantum Dots, Aptasensors, Peptide, Aptamers, Heavy Metal.

ICABB_N521_Salo

Large Scale Production of Human Monoclonal Antibodies Using a Wave Bioreactor

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ABSTRACT

The biologics had attracted the interest of global scientific fraternity and bio-pharmaceutical manufacturing units due to relatively high market demand and competitiveness to produce them at low cost. The invent of single use products and their application in discovery, pre-clinical and manufacturing of bio-pharmaceuticals, had taken the world with stride and had brought revolutionary changes indicated by the replacement of the most acceptable stainless-steel reactors with disposable polymeric bioreactors. Single-use technologies provides a cost effective and time saving solution by being compliant to current good manufacturing practices (cGMP), sterilization validation (CIP / SIP) and assisting high density culture of organisms. The disposable bioreactors come in various designs and size for production strategies optimization and biologics manufacturing. Among the single use bioreactors, Wave Bioreactors were the first reactors that were introduced in 1996 and used for the pilot scale culturing of mammalian cell for the production of one of the most common biologics, monoclonal antibodies. Wave bioreactor, shifted the paradigm of culturing cells in a stirred or pneumatically driven system to the rocking of bag (disposable) that was used as reactor, on a rocking platform for mixing and aeration. The rocking movement of the bag leads to production of wave like undulations in the media, and thus the name. The recent studies on comparison of conventional stainless-steel reactors, hollow fiber reactors and single use disposable bioreactors had shown comparable yield of monoclonal antibodies. This further obtrudes disposable reactors as a suitable, cost effect replacement to conventional reactor and with similar yield of metabolite. Some studies have explored the role of aeration and sparger type on monoclonal antibodies production. The existing studies have also indicated the role of rocking behavior on aeration, cell growth rate and monoclonal antibodies production using animal cells. The studies underway are exploring the strategies to overcome major limitation of the scalability associated with disposable bioreactors.

Keywords: Monoclonal Antibody, Disposable, Biologics.

ICABB_N522_Vai

Different Types of Nano Formulations for Treating Breast Cancer

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ABSTRACT

Breast cancer is one of the common cancers in women in all over the world. One of the promising alternative treatments for breast cancer is nanomedicines or nano formulations. Designing of nanomedicines helps to immune cells engage and subsequently helps to eliminate the cancer cells. Doxil and Abraxane are two of the preexisting formulations products used for breast cancer adjuvant therapy with approving clinical outcomes. However, they were initially designed for generic anticancer purpose, not specifically for the treatment for breast cancer. There are almost about 1.5 million new cases which are reported each year. Doxil and Abraxane are the two most successful nano formulations widely used for treating the breast cancer. Doxil is the first FDA - approved nano-drug which is PEGylated liposomal formation of doxorubicin. It's designed to lower the systemic toxicity without compromising the anticancer effect of doxorubicin. Moreover, Abraxane is found to be albumin bound paclitaxel. Paclitaxel is a nanoparticle processed from human beings which is non-covalently bonded into 130nm. There is no doubt that the breast cancer is one of the most deadly and toughest to get treated. As nanomedicine or nano formulation is one of the promising new therapeutic options to treat breast cancer. In our review work we have taken deeper account of the nanoformulations available as a chemotherapy regime of breast cancer.

Keywords: Cancer, Nanomedicine, Drug Action.

ICABB_N523_Vais

Heavy Metal Toxicity and Its Effects on Neurogenerative Disorders

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ABSTRACT

Central Nervous System CNS plays a very essential role in the functioning of the brains and any anatomical or physiological alteration results in irrevocable neuronal damages such as- cognitive impairments, proteinopathies etc. These damages occur specifically when the brain needs a continuous supply of oxygen for its normal functioning and the same is interrupted then the working of brain also gets disturbed immediately and the irreversible damage can quickly follows such as degeneration changes further causing initiation of neurodegenerative diseases (NDD's). In NDDs there is constant loss of clustered neuronal cells and are connected with aggregates of proteins, which further results in disease like Alzheimer's disease, Parkinson's disease, ALS, Etc. Apart from many sources which are responsible for causing oxidative stress and neurodegenerative pathology, the interaction of human system and intoxication with heavy metal is one of the leading causes which generally came from industrial processes, ground water, contaminated food, etc. It is also shown in epidemiological studies, that these heavy metals cause degeneration of neurons in various ways via DNA Damage, disturbing brain enzyme activities, etc. Heavy metals target proteins and processes which are mainly involved in early onset of any disease such as LPO, DNA and Genotoxic Damage, etc. This heavy metal toxicity also causes dysfunctions of mitochondria and infers with normal functioning of cells. In our study we listed many such researches and evidences that shows the adverse effect of metal toxicity on our CNS and causing NDDs.

Keywords: Cognitive Impairments, Proteinopathies, Genotoxic Damage, Alzheimer's Disease, Parkinson's Disease.

ICABB_N524_Nav

Optical Sensor Comprising a Novel Green Synthesized Carbon Quantum Dots for Determination of Ciprofloxacin

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ABSTRACT

The green approach has gained a lot of attention due to its remarkable optical properties for preparing the carbon quantum dots (CQDs) from natural precursors. In this work, a fluorescent and innovative green synthesized CQDs based optical sensor was fabricated for ciprofloxacin (CPX) detection. For the first time, fluorescent CQDs was synthesized from *Cinnamomum tamala* (commonly known as tejpat) leaves extract employing a facile one-step hydrothermal process. This method did not require oxidizing agent, surface passivation, or any other inorganic salt. Current study was done to achieve a 31% quantum yield which is very high at 340 nm excitation wavelength for determination of CPX. In addition, the research displayed that the developed fluorescence-based sensor comprising green synthesized CQDs had a wide linearity range from 1 to 100 µM with a limit of detection of 6.06 M.

Keywords: Quantum Yield, Green Synthesis, Fluorescent, Ciprofloxacin, Carbon Quantum Dots.

ICABB_N525_Shu

Point of Care Diagnostic Paper Microfluidic Device for Early Detection of Neonatal Sepsis

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ABSTRACT

Neonatal infection, and in its severest form, sepsis, are leading causes of morbidity and mortality in the neonatal population, representing 24% of newborn deaths worldwide. In spite of advances in neonatal care, timely identification of an infected newborn remains a significant diagnostic challenge. The preterm infant can suffer rates of sepsis up to 1000-fold higher than the full-term infant and bears the brunt of the associated mortality and lifelong sepsis-survivor morbidity. We intend to deliver an accurate novel microfluidic platform to diagnose sepsis based on critical illness stratification markers and uncover the potential for translational interventions that may improve neonatal infection-related outcomes. This is empowered by microfluidic advancements that are robust and easy to use with little training. Furthermore, this technology provides comprehensive measures of the functionality of blood biomarkers such as Serum Amyloid A(SAA), C-Reactive Protein (CRP) and Procalcitonin (PCT) in one paper device. Collectively, this technique requires a total of ~50 microliters (μl) of blood, which makes them particularly useful for preterm infants where sample volume is limited, and facilitated the early as well as accurate detection of neonatal sepsis infection. This approach will generate new tools for diagnosing sepsis in the newborn and predicting clinical outcomes potentially improving long-term outcomes while reducing hospital costs.

Keywords: Neonatal Sepsis, Serum Amyloid A, C-Reactive Protein, Procalcitonin, Paper Microfluidics, Point of Care Diagnostics.

ICABB_N526_Nam

Pancreatic Cancer Diagnosis: A Brief Overview

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ABSTRACT

We present a brief overview of pancreatic cancer and advancements in diagnostic methods to improve survival rates. Though pancreatic cancer stands last among other cancers, however ranks seventh leading cause of the death worldwide. Major reason being delayed diagnosis and hence high mortality rates due to non-specific symptoms, or lack of symptoms and poor sensitivity and specificity of the diagnostic methods at early stage. Conventionally used methods for pancreatic cancer like magnetic resonance imaging (MRI), computed tomography (CT scan), endoscopic ultrasound (EU), positron emission tomography (PET) and tissue acquisition with needle aspiration are discussed. Finally, up-to-date knowledge of newer biomarkers (for solid as well as liquid biopsy in terms proteins, circulating tumor DNAs, micro RNAs etc) as well as current research trend in terms of diagnostic device development is presented. The focus of the review is to highlight the challenges encountered in early-stage diagnosis of cancer.

Keywords: Pancreatic Cancer, Early Diagnosis, Biomarkers.

ICABB_N527_Shri

A Method of Preparation for Superparamagnetic Iron Oxide Nanoparticles Containing Mixed Crystal Manganese Ferrite Core (Mn-SPION) for the Development of Biomolecule Probes for Detection and Management of Diseases

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ABSTRACT

We describe a method of preparation of superparamagnetic iron oxide nanoparticles containing mixed crystal manganese ferrite [Mn_{0.1}Fe_{0.9}Fe₂O₄] core (Mn-SPION). These particles can be used as basic building blocks in the architecture of nanoparticle based biomedical probes. All the four basic components of nanoparticle based biomedical probes: the core, the coating, the targeting biomolecule and a label were prepared and evaluated. Mn-SPION were prepared by co-precipitating technique by simultaneous mixing of ferrous, ferric and manganous salts followed by precipitation with ammonium hydroxide solution under carefully controlled experimental conditions. Mn-SPION was further stabilized by biocompatible coating with oleic acid in an aqueous medium. Mn-SPION was characterized by X-ray diffraction (XRD), dynamic light scattering (DLS), scanning electron microscope (SEM), fourier-transform infrared spectroscopy (FTIR) and vibrating sample magnetometer (VSM). Average size of Mn-SPION as determined by DLS was found to be less than 60nm. Using Mn-SPION and by combining magnetic properties with radioisotopes, Mn-SPION based biomolecule probes were developed for the potential use in nuclear medicine. Suitability for *in-vivo* nuclear medicine applications were demonstrated by preparing ^{99m}Tc - 2, 3-dimercaptosuccinic acid (DMSA) (III) - Mn-SPION probe for potential multimodal nuclear medicine imaging based on SPECT-MRI. ¹²⁵I labelled monoclonal antibody – Mn-SPION was prepared to demonstrate the amenability of nanoparticles for functionalization with radioiodine labelled monoclonal antibodies. Magnetizable cellulose containing manganese ferrite core was also prepared by entrapping Mn-SPION nanoparticles in cellulose matrix for use in *in-vitro* nuclear medicine applications such as RIA, IRMA, cell separation, affinity chromatography etc.

Keywords: Nanoparticles, Nuclear Medicine, Radioisotopes, Mn-SPION, Magnetizable Cellulose.

ICABB_N528_Roh

Antimicrobial Actions of Self-assembled Nano-Architectures of Fmoc Phenylalanine Hydrogels

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ABSTRACT

The rapid emergence of the antibiotic resistance in pathogenic microorganisms is causing serious threat to the human health. In the pursuit of new and more efficient antimicrobial agents, hydrogels are attaining lime light due to their numerous advantages such as high hydrating capacity, biocompatibility, stability, local application at infectious. They also have diverse medical applications including antimicrobial, drug delivery, tissue engineering, wound fillers and implant coatings. Hydrogels of Fmoc-protected peptides and amino acids have attained momentum due to their ease of synthesis and cost effectiveness. For these gels, gelation is triggered by adjusting the pH of the solution using various pH inducers. Herein, we report the formation of Fmoc-phenylalanine (Fmoc-F) based hydrogels using glucono- δ -lactone (GdL), sodium acetate (NaOAc), oxalic acid, tri sodium citrate (TSC) as pH inducers and their antimicrobial activity against both gram-positive and gram-negative bacteria which contradict the previous reports, claiming the antimicrobial activity against only gram-positive bacteria. The characterizations of the gels were carried out using multimode plate reader, rheometer, FE-SEM, ThT binding assay, circular dichroism (CD) and Zeta potential. This study has helped us to understand the impact of pH inducers in the hydrogelation, mechanism behind enhanced antimicrobial efficacy as well as, fluorescence properties attained by hydrogel. In addition to this, this study has also helped us to understand stability as well as, impact of pH on amyloidic properties of hydrogel.

Keywords: Fmoc F Hydrogel, Self-Assembly, Antimicrobial Activity, Amyloidic, pH Modulators, Fluorescence Hydrogel.

ICABB-N529_Ponti

Role of Nanotechnology in Bioremediation: The Cosmos of Nanoremediation

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ABSTRACT

Bioremediation is one of the fields in biotechnology that holds the utilization of microbes to break down the hydrocarbon contaminants present in the soil and water bodies to bring off a green collar environment. Generally, modified microorganisms are utilized to eradicate or remove the pollutants present in the bodies to an admissible limit. Though the procedure of bioremediation is moderate, the complexity and the state of existence of the contaminants pose a major drawback to microbial bioremediation. Nanotechnology, an interdisciplinary field of science, plays a productive role in biofabrication operations. It stands out to be an efficient solution to this anthropogenic disaster. Nanoscale particles are more efficient and have an enormous surface area in comparison to micro and macro particles. This feature enhances both catalysis and the reduction of chemicals to diminish the pollutants of interest. Nanoparticles hold a wide diversity of materials like dendrimers, bimetallic particles, nanoscale zeolites, metal oxides, enzymes, and carbon nanotubes which are used in the remediation process. Hence, this technology offers a new production of nanomaterials for the recovery of the environment. This process provides economical solutions to the testing problems for habitat remediation.

Keywords: Bioremediation; Nanoscale; Nanoremediation; Nanoparticles; Dendrimers; Nanotubes.

ICABB_N530_Rash

Recent Developments in Female Reproductive Tract Drug Delivery Nanotechnology for HIV and HSV

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ABSTRACT

As per WHO, over a million sexually transmitted infections are acquired on a daily basis. Out of all STIs, the viral incurable ones, human immunodeficiency virus (HIV) and herpes simplex virus (HSV or herpes) dominate the world map. Combination antiretroviral medication has significantly improved treatment, but it must be used for the rest of one's life, has significant side effects and people get immune to treatment who developed resistance. Nanotechnology is a new interdisciplinary topic that is transforming medicine in the twenty-first century. Polylactic(L) acid (PLLA), poly lactic-co-glycolic acid (PLGA), polyethylene-oxide (PEO) and (poly)caprolactone encapsulation delivers antiherpetic acyclovir (ACV) and antiretroviral tenofovir (TFV) into EpiVaginal tissue via pH-responsive electrospun fibers. FDA approved tablet called Truvada® comprises emtricitabine and TFV. Tenofovir is capable of inhibiting both HIV-1 and HSV-2, however a higher dosage of tenofovir is required in case of HSV-2. Electrospun fibres are a potential multipurpose infection prevention platform. Nanoparticles (PEO, PVA, PVP) when studied in application to electrospun fibres to deliver lectin Griffithsin (STI prevention biological, denoted as GRFT) on mice for upto 90 days and it showed complete inhibition to HIV and HSV-2. GRFT showed striking results in-vivo safety profiles for test animals used. However, there are just a few delivery systems that can efficiently transport biologics to the female reproductive tract at this time (FRT). Dye-loaded PLGA nanoparticles can be utilised to minimise leaking in the vaginal mucosa. This study aims to provide a comprehensive overview of drugs and treatments for HIV and HSV, problems faced in reproductive tracts while delivering drugs and finding suitable substitutes.

Keywords: HIV, HSV, Nanoparticles, Electrospun Fibres.

ICABB_N531_Nan

Nanoformulations for Acute Respiratory Distress Syndrome

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ABSTRACT

Acute Respiratory Distress Syndrome (ARDS) is a deadly pulmonary illness wherein fluid fills up inside the lumen of lung alveoli which leads to upsurge in inflammatory cytokines that induce hypoxemic respiratory failure. It affects millions of people globally and has a high mortality rate as per the severity of lung injury. The traditional techniques for treating ARDS are simply restrained to handling the symptoms of the syndrome by using drugs like: corticosteroids, statin or by protective lung care like extracorporeal membrane oxygenation (ECMO) also called extracorporeal life support (ECLS) and lung ventilators, which have been observed to be inefficient and unsuccessful. Regardless of pulmonary nanomedicine being a domain that remains largely under-explored, there are several nano-modified carriers like Polymeric NPs, Liposomes, Dendrimers and Gold NPs, that have been found to permeate the lung epithelium and largely offer targeted drug delivery for the treatment. These ideal nanoparticles have great drug bioavailability which could be further enhanced by altering the surface properties and hence, help evade detection by the immune system of the body. Cell hitchhiking-based drug delivery system is one of the finest novel drug delivery systems suggested to even out the disadvantages associated with free nanocarrier. Circulatory cells like erythrocytes (RBCs) are majorly preferred vehicle for hitchhiking as they improve circulation time of nanocarrier in body. Long-term potential toxicity of nanocarriers needs to be carefully monitored in the successful product development for ARDS. This article aims to focus on different kinds of nanoformulations currently available for Acute Respiratory Distress Syndrome (ARDS) and the cell hitchhiking-based targeted drug delivery system.

Keywords: Acute Respiratory Distress Syndrome, Pathophysiology, Nanoformulations, Drug-Delivery System, Cell Hitchhiking.

EDITORS' PROFILE



Prof. Pammi Gauba is Head, Department of Biotechnology & Dean (International Affairs & Sponsored Projects) at JIIT, Noida. She has experience of 30 years in teaching and research, at different institutes in India and abroad. Prior to joining JIIT, she worked as an Adjunct Professor in Marymount College, Arlington, and NOVA College, Alexandria, USA. Apart from teaching in various colleges, she also worked in NCERT as a Research Associate and Lecturer. She did her Masters (Organic Chemistry) and PhD from Rohilkhand University, where her research was focused to investigate the "Incidence of Lactose Intolerance in case of Infantile Diarrhoea". Her current research is about bioremediation of Organic and Inorganic pollutants and investigations of heavy metal toxicity in raw herbs. She is a Life Member of Indian Science Congress Association, Society of Biological Chemist of India, The Association of Microbiologists of India (AMI) and Bioinformatics organisation. She is the Editor of 3 Books and has 14 Book chapters to her credit. She has filed 3 patents and has more than 45 National and International publications in peer-reviewed journals. She has been granted Research Projects from the Ministry of Science and Technology, Govt. of India, ICMR, AYUSH and Ministry of Forest and Environment.



Dr. Rachana is a Professor in the Department of Biotechnology, Jaypee Institute of Information Technology, Noida. She was working at SPTM, NMIMS University, Mumbai, before joining JIIT Noida. She post-graduated in Biotechnology from IIT Roorkee in 1998 and achieved her doctorate from IIT Bombay in 2006. She has qualified NET-LS and GATE in Life Sciences. She has been the recipient of DBT fellowship during her masters and JRF and research fellowship, from MHRD during her Ph.D. She has 2 Indian patents, 2 monographs, 19 chapters, 2 textbooks, and has more than 43 International and National articles to her credit. She has received many awards from various National and International bodies. She has been working with Natural products to cure diseases like diabetes, asthma, respiratory infections, skin cancer, neurological disorders, and COVID-19. She has got grants from AYUSH, NMPB, Govt of India. She is a lifetime member of Indian Pharmaceutical Association, Biotechnology Society of India, Medicinal and Aromatic Plant Association of India, and Mumbai Haematology Group. She remained a member of American College of Clinical Pharmacology (ACCP) for ~4 years. She was an Advisor on the South Asian Chapter of ACCP's Student Outreach Committee (SOC) and IPA-SF Edufest. She has been actively writing in scientific magazines such as CII, Ingredients of South Asia (International), Pharmabiz, and Biospectrum.



Dr. Shazia Haider is working as Assistant Professor at the Department of Biotechnology, Jaypee Institute of Information Technology, Noida. Prior to joining JIIT, she was working as a Senior Research Officer in All India Institute of Medical Sciences, New Delhi, and as a Postdoctoral Fellow at School of Computational and Integrative Sciences, Jawaharlal Nehru University, New Delhi. She has also worked as an Assistant Professor in the Department of Biotechnology, Sharda University, Greater Noida. She did her Ph.D. in Biotechnology with Bioinformatics as a specialization, from Jamia Millia Islamia, New Delhi. She has more than 12 publications in reputed International Journals like; Briefing in Bioinformatics, Oxford, Scientific Report, mSystems, PlosOne, Frontier in Microbiology etc., an E-letter in Science Journal. She has actively participated in International and National Courses at the University of California, USA, European Bioinformatics Institute, UK. She had been awarded project fellowships from different government funding agencies like DBT, DST, ICMR, and SERB; received an award from the Department of Medicine, University of California, and San Diego, USA, and got best oral presentation award as a "Young Scientist Colloquium" from INSCR. Recently, she also received the 7th Venus International Women Awards (VIWA-2022) as "Young Woman Researcher in Bioinformatics" in the discipline of Engineering. The Research interest of her group is in Systems Biology of Bioinformatics, Functional Genomics and Molecular Biology with Protein and Genome Informatics in Human diseases.

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