Proceedings

International Conference on Advances in Biosciences and Biotechnology

Theme

Recent trends in Biosciences and Biotechnology

ICABB - 2021
(28th - 30th January 2021)

Organized by

Department of Biotechnology
Jaypee Institute of Information Technology
A-10, Sector - 62, Noida, Uttar Pradesh, India

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Asian Journal of Pharmaceutics & Clinical Research

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PROCEEDINGS OF

INTERNATIONAL CONFERENCE ON ADVANCES IN BIOSCIENCES AND BIOTECHNOLOGY- 2021

(January 28th – 30th, 2021)

JOURNAL PARTNERS:

- **The Pharmaceutical and Chemical Journal [ISSN 2349-7092]**
- **Current Trends in Biotechnology and Pharmacy [ISSN 0973-8916 (Print), 2230-7303 (Online)]**
- **Asian Journal of Pharmaceutical and Clinical Research [ISSN 0974-2441(Print), 2455-3891(Online)]**

ABOUT THE INSTITUTE

Jaypee Institute of Information Technology, Noida was established in the year 2001 and has been declared as a "Deemed to be University" under Section 3 of UGC Act 1956 in the year 2004. JIIT, NOIDA, a leading Engineering Institute in Delhi NCR, is constantly ranked amongst top 50 in the leading surveys. JIIT's state-of-the-art, environmentally conditioned campus comprises smart buildings with Wi-Fi connectivity covering the Academic Block, Business School cum Research Block, Faculty Residences, Student Hostels and Annapurna. Well-equipped modern laboratories and an intellectually stocked Learning Resource Centre with books and E-Resources provide a pleasant and stimulating ambience. The institute offers varied courses ranging from bachelors to PhD in the field of engineering and technology. It aims to make its students the best in the world in terms of innovation, entrepreneurship, creativity and management.

ABOUT THE DEPARTMENT

The Department of Biotechnology at JIIT, NOIDA, established in 2002, remains committed to provide research-informed teaching and learning, and a vibrant R&D environment. Faculty with rich research exposure in academia and industry, both in India and abroad, contributes to the department academic core. The curriculum of different programs provides engineering interface and integrates core subject area knowledge with professional development; focusing on entrepreneurship, analytical and research skills. The research emphasis is reflected in the active doctoral program, publications in international/national journals, and sponsored research projects totalling approximately INR-9.44 Crores from premier national funding agencies.

ABOUT THE CONFERENCE

The International Conference on Advances in Biosciences and Biotechnology (ICABB-2021) aims to unite multi- disciplinary fields of biology, biosciences, and medical biotechnology on a single platform. It will provide a platform to bring academicians, researchers, scholars, technocrats from academia and industry to share their ideas, knowledge, and experience. This is the 6th International conference being organized by the Department of Biotechnology.

This year, the theme of the proposed conference is 'Recent trends in Biosciences and Biomedical Research'. This conference aims to provide an opportunity to participants, delegates and researchers along with other stakeholders to share scientific advancements in various disciplines of biosciences and biomedical research and to get acquainted with novel or alternative strategies to seek an answer to various global challenges.

Scientific Programme

International Conference on Advances in Biosciences and Biotechnology
ICABB-2021
(28th-30th January, 2021)

Theme: Recent trends in Biosciences and Biomedical Research

Day 1- Thursday, 28th January, 2021

9:00 AM -10:00 AM	**Inauguration and Welcome Note**
Technical Session I: Medical and Nanobiotechnology	
10:00 AM -10:45 AM	**Keynote Speaker**- Neuronal differentiation of human progenitor cells: a window from genetics - **Prof. Subrata Sinha** (HOD, Department of Biochemistry, All India Institute of Medical Sciences, Ex-Director NBRC)
10:45 AM -11:30 AM	**Keynote Speaker-** Improved immunogenicity of carbohydrate based vaccines using polymeric nanoparticles- **Dr. Amulya K. Panda (National Institute of Immunology)**
11:30 AM -1:30 PM	**Oral presentations**
11:30AM -1:30 PM	**E-Short Presentations**
1:30 PM -2:30 PM	**Lunch Break**

Technical Session II:Food and Microbial Biotechnology	
2:30 PM -3:15 PM	**Keynote Speaker-**Prebiotics Based on Enzymatic Catalysis- **Prof. Subhash Chand** (Formerly, Professor & Head, Department of Biochemical Engineering and Biotechnology, IIT Delhi)
3:15 PM -4:00 PM	**Keynote Speaker-** Defeating cancer stem cells through targeted protein nanoparticles- **Dr. Esther Vázquez (Universitat Autònoma de Barcelona)**
4:00 PM -5:00 PM	**Oral presentations**
4:00 PM -6:00 PM	**E-Short Presentations**

Scientific Programme

International Conference on
Advances in Biosciences and Biotechnology
ICABB-2021

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Theme: Recent trends in Biosciences and Biomedical Research

Day 2- Friday, 29th January, 2021

Technical Session III: Omics and Computational Biology	
9:15 AM-10:15 AM	**Keynote Speaker-** To function or not to function- **Prof. Sridhar Hannenhalli** (Center for Cancer Research, National Cancer Institute)
10:15AM -11:00 AM	**Keynote Speaker-** Structural Insight on Biodegradation of Emerging Pollutants- **Prof. Pravindra Kumar** (Professor, Department of Biotechnology, Indian Institute of Technology Roorkee)
11:00AM -1:00 PM	**Oral presentations for Sessions III and IV**
11:00AM -1:00 PM	**E-Short presentation for Sessions III and IV**
1:00 PM -2:00 PM	**Lunch Break**

Technical Session IV: Natural products and human health	
2:00 PM -2:45 PM	**Keynote Speaker-** Natural Products and Human Health - **Prof. T. Pullaiah-** (Department of Botany, Sri Krishnadevaraya University, Anantapur)
2:45 PM -3:30 PM	**Keynote Speaker-** Exploring xeno-tumor heterogeneity: A potential source of anticancer agents by using A novel and specifically designed VTGE method- **Prof. Nilesh Kumar Sharma** (Dr. D. Y. Patil Biotechnology and Bioinformatics Institute, Pune)
3:30 PM -5:00 PM	**Oral presentations for Sessions V**
3:30 PM -5:30 PM	**E-Short presentations for Sessions V**

Scientific Programme

International Conference on
Advances in Biosciences and Biotechnology
ICABB-2021

(28th-30th January, 2021)

Theme: Recent trends in Biosciences and Biomedical Research

Day 3- Saturday, 30th January, 2021

Technical Session V:Agriculture, Environment, and Industry	
9:15 AM-10:15 AM	**Keynote Speaker-** Quantitative and Reproducible Cell-Based Bioassays to Advance Immunotherapy Programs- **Dr. Gopal B. Krishnan** (Promega Corporation, – Wisconsin, USA)
10:15 AM -11:00 AM	**Keynote Speaker-** Carbon Sequestration by Microalgae: An Omics Perspective- **Dr. Pavan Jutur**(Group leader, Omics of Algae, Industrial Biotechnology,International Centre for Genetic Engineering and Biotechnology)
11:00 AM -11:45 PM	**Keynote Speaker-** Circular Economy and Waste Management- **Mr. Mahesh Babu** (IL&FS Environmental Infrastructure & Services Ltd.)
11:45 PM -1:00 PM	**Valedictory, Vote of Thanks & Closing Ceremony**

MESSAGE FROM EXECUTIVE CHAIRMAN

MANOJ GAUR
Executive Chairman

JAIPRAKASH
ASSOCIATES LIMITED

January 13, 2021

Message

It is indeed a matter of great pleasure that the **Department of Biotechnology, Jaypee Institute of Information Technology, Noida** is organizing the **"International E-Conference on Advances in Biosciences and Biotechnology"** from 28th January to 30th January 2021, with its theme as **"Recent trends in Biosciences and Biomedical Research"**.

The world is currently facing a global pandemic without precedence in our lifetime. The leading organizations and scientists across all disciplines are exploring new or novel products, of global importance, to develop a sustainable society. The role of researchers and scientists from across the globe is paramount to address the leading problems.

The conference will provide an opportunity to participants, delegates and researchers along with other stakeholders to share scientific advancements in various disciplines of biosciences and biomedical research. It will enable them to get acquainted with novel or alternative strategies to seek an answer to various global challenges.

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

With best wishes,

Manoj Gaur

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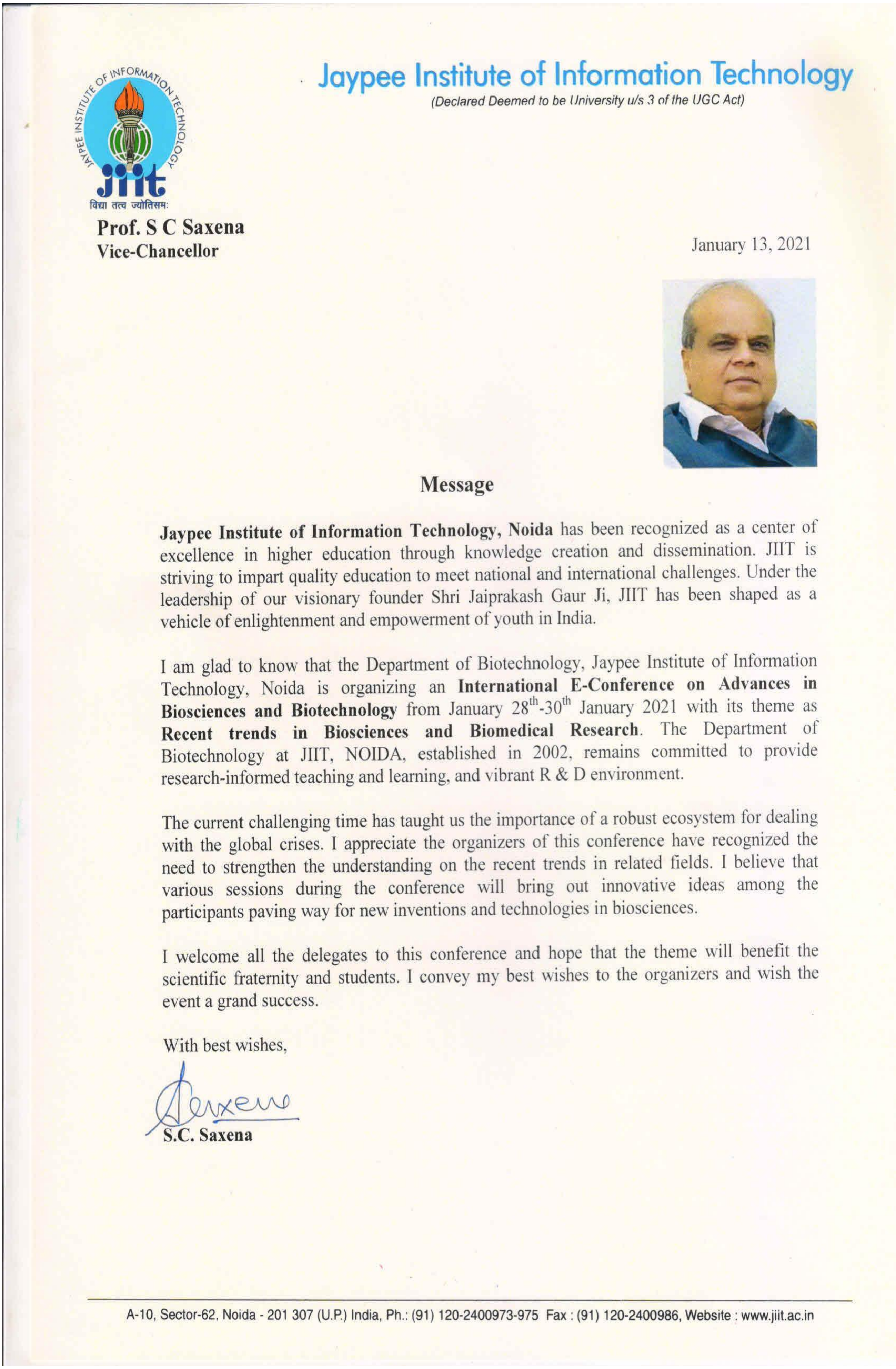

Jaypee Institute of Information Technology
(Declared Deemed to be University u/s 3 of the UGC Act)

Prof. S C Saxena
Vice-Chancellor

January 13, 2021

Message

Jaypee Institute of Information Technology, Noida has been recognized as a center of excellence in higher education through knowledge creation and dissemination. JIIT is striving to impart quality education to meet national and international challenges. Under the leadership of our visionary founder Shri Jaiprakash Gaur Ji, JIIT has been shaped as a vehicle of enlightenment and empowerment of youth in India.

I am glad to know that the Department of Biotechnology, Jaypee Institute of Information Technology, Noida is organizing an **International E-Conference on Advances in Biosciences and Biotechnology** from January 28th-30th January 2021 with its theme as **Recent trends in Biosciences and Biomedical Research**. The Department of Biotechnology at JIIT, NOIDA, established in 2002, remains committed to provide research-informed teaching and learning, and vibrant R & D environment.

The current challenging time has taught us the importance of a robust ecosystem for dealing with the global crises. I appreciate the organizers of this conference have recognized the need to strengthen the understanding on the recent trends in related fields. I believe that various sessions during the conference will bring out innovative ideas among the participants paving way for new inventions and technologies in biosciences.

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 wish the event a grand success.

With best wishes,

S.C. Saxena

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Jaypee Institute of Information Technology
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MESSAGE FROM ORGANIZERS

It gives us a great pleasure to extend a warm welcome to all the delegates to International E-Conference on Advances in Biosciences and Biotechnology (ICABB 2021) on "Recent trends in Biosciences and Biomedical Research", being organized by Department of Biotechnology, Jaypee Institute of Information Technology, Noida from 28th Jan to 30th Jan, 2021. This conference aims to amalgamate multi- disciplinary fields of biology, biosciences, and medical biotechnology on a single platform. It will provide a platform to bring academicians, researchers, scholars, technocrats from academia and industry to share their ideas, knowledge, and experience. This is the 6th International conference being organized by the Department of Biotechnology.

Biosciences and Biomedical Research is one of the most important aspects of Life Sciences Research, especially in such a time when the world is reeling under health crisis due to global pandemic COVID-19. The conference will provide a vibrant platform to share the advancements and research findings and would provide an enriching experience to all the participants. The three-day scientific program would cover major breakthroughs in the area of Biosciences and Biomedical Research including Medical and Nanobiotechnology; Food and Microbial Biotechnology; Omics and Computational Biology; Natural products and human health, and Agriculture, Environment and Industry.

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

We are extremely grateful to all the national and international speakers for accepting our invitation. We are also thankful to our Advisory Committee Members for their continuous support and guidance. The event has been made possible with sincere efforts of all the faculty members of Department of Biotechnology, staff from administrative and finance departments. The constant efforts of the student volunteers who have worked round the clock are appreciated immensely. The support from our publishing partners and sponsors is highly acknowledged.

Finally, on behalf of the organizing committee we hope that the interaction with eminent speakers would enhance the knowledge and provide an enriching experience. Thank you all once again, and we look forward to a productive event.

	Reema Gabrani	
Prof. Pammi Gauba	Prof. Reema Gabrani	Dr. Garima Mathur
Chairperson	Convener	Convener

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PROF. SUBRATA SINHA

Neuronal differentiation of human progenitor cells: a window from genetics

Subrata Sinha
Department of Biochemistry, AIIMS, New Delhi 110029

Dyslexia is a common disability and manifests as reading difficulty. It does not include difficulties resulting from global deficiencies, either in intelligence or in social opportunity, but is a specific deficit. It could be predisposed by different genes, and also by gene-environment interactions. There may be different biological components acting in different individuals, giving rise to what are called different 'endophenotypes' - a common endpoint on the assessment scale resulting from diverse biological causes. It has a strong familial pattern. There is a strong genetic component, to dyslexia. Methods of classical genetics as well as next generation sequencing have been utilized. There have been a number of candidate genes demonstrated with varying degrees of replicability. We are studying large extended multi-generational families from different endogamous groups in order to understand the genetics biology of dyslexia predisposition. It is expected that the relative genetic homogeneity within the families would assist in the identification of susceptible genes. This was done by carefully assessing the family members to attribute the disability, or lack of it within the family members. Selected members were assessed by exome sequencing, and the significant results verified in the entire family. The alteration giving the strongest association was studied. This was identified to be a 2 nucleotide alteration in the shared stretch of the promoter of the coding BASP1 gene and its divergent lnc RNA that was transcribed in the opposite direction. The same results were also obtained by a bioinformatics related process, whereby publically available data was analysed for lncRNAs associated with the neuronal commitment of progenitors. This coding gene/divergent lncRNA combination has been studied in human fetus derived neuronal progenitors and has been shown to code for a novel pathway critical to the neuronal differentiation of progenitor cells. This pathway intersects with another genetic locus associated with inherited dyslexia, DYX1C1, which codes for the transcription factor TCF12, which also binds the BASP1 promoter at the same site as the lncRNA.

Our studies show how the study of the genetics of disease can help in getting insights into differentiation pathways.

DR. AMULYA K. PANDA

Improved immunogenicity of carbohydrate based vaccines using polymeric nanoparticles

Amulya K Panda
National Institute of Immunology, New Delhi-110067

Apart from improving the immunogenicity of antigen, polymeric nanoparticle particle based formulation has high potential to deliver carbohydrate based vaccines. Most of the carbohydrate based vaccines elicit poor immune response and don't elicit memory antibody response. Anti-polysaccharide antibody responses are generally weak and characterized by lack of memory, isotype restriction and delayed ontogeny. Traditionally carbohydrates are conjugated to protein carriers to improve its immunogenicity. It was observed that many carbohydrates based antigen when entrapped PLGA/PLA nanoparticles elicited memory antibody response from single point immunization. The antibody titers were not only high but also protective indicating the suitability of nanoparticle based delivery system for improving the immunogenicity of carbohydrate based vaccines. The proof of principle of nanoparticle in improving the immunogenicity of carbohydrate antigen was demonstrated using Vi polysaccharides and Pneumococcal polysaccharide antigens. Detail analysis of immune response from polymeric formulation being carried out to understand how carbohydrate antigens induce immunological memory without being conjugated to carrier protein. Major emphasis of the laboratory is now to develop nanoparticle based Pneumococcal vaccine. The activities have been in three different areas such as (i) use of carbohydrates from different serotypes of *S. pneumonia* and its immunological evaluation, (ii) purification and characterization different immunodominant protein from *S. pneumonia* and its evaluation and (iii) conjugation of pneumococcal protein with polysaccharides and its immunological evaluation. The use of nanoformulation has further improved the immunogenicity of conjugate vaccines. The detailed molecular mechanism of improved antibody response through involvement of germinal centre reaction and along with that of Tfh cells while using nanoparticle based immunization opens up new possibilities. Nanoparticles thus not only promote improved delivery of antigen but help in immunomodulation.

PROF. NILESH KUMAR SHARMA

Exploring xeno-tumor heterogeneity: A potential source of anticancer agents by using A novel and specifically designed VTGE method

Ajay Kumar [1], Jainish Kothari, Seethamma T N, Swati Swami, Nilesh Kumar Sharma [1*]

Cancer and Translational Research Lab, Dr. D.Y. Patil Biotechnology & Bioinformatics Institute, Dr. D.Y. Patil Vidyapeeth, Pune, Maharashtra, India, 411033

[1]Corresponding author*

Background:

Metabolic reprogramming within cancer cells is suggested as a potential barrier to chemotherapy. Additionally, metabolic tumor heterogeneity is one of the factors behind discernible hallmarks such as drug resistance, relapse of tumor and formation of secondary tumors. A role of metabolic tumor heterogeneity is seen to display xeno-tumor heterogeneity between ruminants and humans.

Methods:

A novel and specifically designed metabolite (100 to 1000 Da) fractionation system as vertical tube gel electrophoresis (VTGE) was employed for the profiling of metabolites in urine of various ruminants and human samples. DNA metabolizing and cell based assays were conducted to assess the distinctive activity of urine metabolites of ruminants and humans. Furthermore, a specific methodology was developed to identify intracellular metabolites identified in cancer cells treated with goat urine metabolites. Next, in silico a tool was employed to reveal molecular targets of novel goat urine anticancer tripeptide metabolites.

Results: Data revealed that goat urine specific metabolites possess distinctive DNA metabolizing activity and anti-proliferative properties. VTGE helped to identify a novel tripeptide Glu-Glu-Arg in the intracellular compartment of HCT-116 colorectal cancer cells. This novel tripeptide Glu-Glu-Arg from goat urine showed anticancer potential and that was able to inhibit the AP-1 transcriptional complex.

Conclusion:

Our data highlights the novel understanding on xeno-tumor heterogeneity and VTGE methodology helped to explore goat urine derived tripeptide as an anti-proliferative agent.

PROF. THAMMINENI PULLAIAH

Natural Products and Human Health

T.Pullaiah*

Department of Botany, Sri Krishnadevaraya University,

Anantapur 515003, A.P.

Plants have been the richest source of several products which are of immense use to man. Many higher plants are major source of natural products used as pharmaceuticals, agrochemicals, flavour and fragrance ingredients, food additives and pesticides. Noteworthy among them and next to those of food value are the substances of medicinal importance. The search for new plant derived chemicals should be a priority in current and future effort towards sustainable conservation. The metabolic pathways that are essential for sustaining life and organization of plant body such as synthesis of starches, proteins, nucleic acids and fats are regarded as primary metabolism. The other series of reactions that enable the plant to interact successfully with the biotic and abiotic environments are considered to constitute secondary metabolism. Often these two-primary and secondary metabolic pathways are closely interconnected in a plant system. About 20,000 compounds (including alkaloids, steroids, peptides etc) are known to occur as the products of secondary metabolism and a majority of these have medicinal or pharmaceutical importance.

Important natural products of medicinal importance include: Paclitaxel from *Taxus brevifolia* and other species of *Taxus*, Camptothecin from *Camptotheca acuminata* and *Nothapodytesnimmoniana* is used for the treatment of different types of cancers. Vincristin and vinblastin from *Catharatnhus roseus* is used for the treatment of hodgkin’s disease and leukaemia in children. Digoxin from *Digitalis lanata* is being used for the treatment of coronary diseases. Quinine from *Cinchona calisaya* and *C. succirubra* and artemisinin from *Artemisia annua* and other species of *Artemisia* is used for the treatment of malaria. Silymarin from *Siybum marianum* is used for curing liver diseases. Shikonin from *Lithospermum erythrorhizon* is used for the treatment of burns and sunburns. It is also used as herbal lipstick. L-dopa from *Mucuna pruriens* is used for curing parkinson disease. Diosgenin from *Dioscorea* species is used for as birth control pill. 80 million women use it per day. Morphine and codeine from *Papaver somniferum* are used as analgesic. Atropine from *Atropa belladonna* is used as a muscle relaxant. Other important plant products used for treating various human diseases include forskolin from *Coleus forskohlii*, andrographolide from *Andrographis paniculata*, berberine from *Coptis japonica* and *Thallictrum rugosum*, hypericin from *Hypericumesculentum*, saikosaponin from *Bupleurum falcatum*, reserpine and serpentine from *Rauvolfia serpentina,* withanolides from *Withania somnifera*, stevioside from *Stevia rebaudiana*.

Many of these plants are being harvested from wild source depleting their resource. There is every necessity to cultivate them and obtain the produces by other biotechnological methods for their sustainable utilization.

PROF. SRIDHAR HANNENHALLI

To function or not to function

Sridhar Hannenhalli*
Center for Cancer Research, National Cancer Institute Building, MD

The functions of only a minority of genes in any species is known. And even in those cases the functional annotation is highly incomplete and largely devoid of context. At an even more fundamental level, how can we know whether a gene serves any relevant biological function in a given context. In this informal presentation we will discuss a few vignettes related to the broad questions of context-specific functions of genes, in a variety of contexts from bacterial response to drugs, normal tissues, and cancer.

DR. GOPAL B. KRISHAN

Quantitative and Reproducible Cell-Based Bioassays to Advance Immunotherapy Programs

Gopal B. Krishnan*
Promega Corporation, USA

Monoclonal antibody mediated immunotherapy has the capacity to boost ongoing anti-cancer immune responses to overcome diseases such as cancer. Immunotherapy enables the immune system to better fight cancer and has proven to be a promising therapeutic strategy. The human immune system is regulated by a complex network of inhibitory and stimulatory receptors that regulate T Cell function that is promising new immunotherapy targets for the treatment of a variety of cancers and autoimmune disorders. These therapies combine different strategies to release the brakes on the immune system with the aim of eliminating tumor cells even more efficiently. A major challenge in the development of antibody-based biologics is access to quantitative and reproducible functional bioassays. Existing methods rely on primary cells and measurement of complex functional endpoints. These assays are cumbersome, highly variable and fail to yield data required for drug development in a quality-controlled environment. To address this need, a suite of cell-based functional bioassays have been developed to determine the potencies of candidate antibody drugs and ligand proteins targeting Fc receptors (ADCC, ADCP), interrogate modulation of immune checkpoint receptors individually (e.g., PD-1, LAG-3, TIM-3, GITR, 4-1BB etc.) and in combination (e.g. PD-1+CTLA-4, PD-1+LAG-3), as well as Cytokines (IL-2,IL-12, IL-15 etc.) and Growth Factors (TGF-b, RANKL, VEGF etc.). These bioassays consist of stable cell lines that express luciferase reporters driven by response elements under the precise control of mechanistically relevant intracellular signals. The bioassays are prequalified according to ICH guidelines and show the precision, accuracy and linearity required for routine use in potency and stability studies. Thus, the bioassays reflect mechanisms of action for the drug candidates designed for each immune checkpoint receptor and demonstrate high specificity, sensitivity, and reproducibility. The assay signals are robust, linear, specific, and have good repeatability. Therefore, these assays can serve as valuable tools for antibody screening, characterization, and stability studies in immunotherapy drug development, and have been implemented in high-throughput settings for potency and stability studies.

Dr. PANNAGA P. JUTUR

Carbon Sequestration by Microalgae: An Omics Perspective

Mukul S. Kareya, Iqra Mariam, Asha A. Nesamma and Pannaga P. Jutur*
Omics of Algae Group, Industrial Biotechnology, International Centre for Genetic Engineering and Biotechnology, New Delhi 110067, India
**Corresponding author*

Photosynthetic organisms fix inorganic carbon through carbon capture machinery (CCM) that regulates the assimilation and accumulation of carbon by ribulose-1,5-bisphosphate carboxylase/oxygenase (Rubisco). However, few constraints that govern the central carbon metabolism are regulated by the carbon capture and partitioning machinery. In order to divert the cellular metabolism toward lipids and/or biorenewables it is important to investigate and understand the molecular mechanisms of the CO 2 -driven carbon partitioning. In this context, strategies for enhancement of CO 2 fixation which will increase the overall biomass and lipid yields, can provide clues on understanding the carbon assimilation pathway, and may lead to new targets for genetic engineering in microalgae. In the present study, we have focused on the physiological and metabolomic response occurring within marine oleaginous microalgae *Microchloropsis gaditana* NIES 2587, under the influence of very-low CO2 (VLC; 300 ppm, or 0.03%) and high CO2 (HC; 30,000 ppm, or 3% v/v). Our results demonstrate that HC supplementation in *M. gaditana* channelizes the carbon flux toward the production of long chain polyunsaturated fatty acids (LC-PUFAs) and also increases the overall biomass productivities (up to 2.0 fold). Also, the qualitative metabolomics/proteomics have identified metabolites and/or proteins with the significant fold change in VLC as compared to HC. In conclusion, our focus is to understand the entire carbon partitioning and metabolic regulation within these photosynthetic cell factories, which will be further evaluated through a multiomics approach for enhanced productivities of biomass, biofuels, and bioproducts (B 3).

Keywords: *Microchloropsis*, carbon dioxide, oleaginous microalga, biomass, photosynthetic cell factories

DR. ESTHER VÁZQUEZ

Defeating cancer stem cells through targeted protein nanoparticles

Esther Vazquez*
Universitat Autonoma De Barcelona

The urgent need of more efficient therapeutic platforms in cancer push towards the development of nanoscale drugs targeting metastatic stem cells. We have approached this issue by the design of modular, fully functional proteins with the ability to self-assemble into nanoparticles of controlled size and to target and internalize cancer stem cells through solvent-exposed specific receptors. These nanoparticles have been tailored as vehicles for conventional anti-tumor drugs, to increase their selectivity and decrease their toxicity through an improved biodistribution. However, the same protein-based platform can be re-designed into tumor-targeted, intrinsically therapeutic protein-only nanoparticles. In absence of any external vehicle, these materials perform as both drug and carrier simply by incorporating a therapeutic domain with anti-tumor activity.

PROF. PRAVINDRA KUMAR

Structural Insight on Biodegradation of Emerging Pollutants

Pravindra Kumar
Department of Biotechnology, IIT Roorkee,
Roorkee, Uttrakhand-247667, India.

Elimination or mitigation of the toxic effects of chemical waste released to the environment by industrial and urban activities relies largely on the catalytic activities of microorganisms-specifically bacteria. Given their capacity to evolve rapidly, they have the biochemical power to tackle a large number of molecules mobilized from their geological repositories through human action (e.g., hydrocarbons, heavy metals) or generated through chemical synthesis (e.g., xenobiotic compounds). Whereas naturally occurring microbes already have considerable ability to remove many environmental pollutants with no external intervention, Biphenyl dioxygenase of *Burkholderia xenovorans* LB400 BphAE (LB400)) is a multicomponent Rieske-type oxygenase that catalyzes the dihydroxylation of biphenyl and many polychlorinated biphenyls (PCBs). The structural bases for the substrate specificity of the enzyme's oxygenase component (BphAE(LB400)) are largely unknown. BphAE (p4), RR4 and II9, variants obtained through directed evolution, transform several chloro biphenyls, including more efficiently than BphAE(LB400). Here, we compare the structures of BphAE(LB400) and its variants and examine the biochemical properties of these enzymes. This study provides important insight into how Rieske-type oxygenases can expand substrate range through mutations that increase the plasticity and/or mobility of protein segments lining the catalytic cavity. Additionally, the Phthalate dioxygenase system (PDOS) initiates the aerobic breakdown of phthalate by forming cis-dihydrodiol phthalate with consumption of NADH and O2. Here we present the structural insights into phthalate dioxygenase (PDO) for the biodegradation of plasticizers.

PROF. SUBHASH CHAND

Prebiotics Based on Enzymatic Catalysis

Subhash Chand
Formerly, Professor & Head, Department of Biochemical Engineering & Biotechnology, Indian Institute of Technology Delhi, Hauz Khas, New Delhi – 110 016, India

Prebiotics are physiologically active molecules / preparations, (also known as nutraceuticals) that have the ability to provide specific medical or health benefits. These ingredients, when included in the food, promote the growth of healthy microbial flora (probiotics) in the human gut, thus providing health benefits. Enzymatic catalysis being natural process has become important for deriving bioactive food supplements.

Peptide based prebiotics

Bioactive peptides are fractions of protein that combine the nutritional benefits of protein with additional health benefits, such as, immune enhancement, improved gut function and weight management. Food proteins contain encrypted within their structures specific fragments or peptides that have the ability to alter physiological functions. Enzymatic hydrolysis of bovine beta-lactoglobulin, alpha-lactalbumin derived from milk and whey protein concentrate can inhibit angiotensin–1–converting enzyme (ACE) and can potentially replace/supplement conventional anti-hypertensive drugs, which act by inhibiting ACE. These peptides being naturally derived have the advantage of not displaying the debilitating side effects associated with the intake of chemical ACE inhibitors. A number of protein hydrolyzing enzymes (e.g. pepsin, trypsin, chymotrypsin etc.) with specific sites of action on the protein molecules are commercially available that can be used singly or as a mixture to achieve partial hydrolysis of naturally available bulk proteins. ACE inhibitory peptides can then be enriched by methods such as ultrafilteration.

Caseinophosphopeptides (CPP) represent a group of milk protein derived peptides having potential property of preventing tooth decay and improved calcium absorption. By keeping calcium in soluble form, CPPs enhance passive calcium absorption. Peptide D4 is another oligopeptide mixture derived from edible proteins that lower the serum Triglyceride levels and regulates dietary fat absorption. Another group of food protein derived physiologically active components are represented by peptides enriched in glutamine. Glutamine peptides (GPs) have two main activities. First, they are source of glutamine that becomes essential during exhaustion and illness. Second, GPs protect the stressed cells against the loss of the energy carrier – ATP. Glutamine peptides can be produced from cereal proteins using commercially available food grade proteases.

Oligosaccharides as prebiotics

Oligosaccharides of various types are found as natural components in many health foods – fruits, vegetables, milk and honey. In addition to providing useful modification to food flavours and physicochemical characteristics, many of these sugars possess properties beneficial to consumers – non-cariogenicity, low calorific value and most important the ability to stimulate the growth of bifidobacteria in the colon. With the exception of soybean oligosaccharides and lactulose, oligosaccharides are manufactured using enzymatic processes from simple sugars – sucrose and lactose by transglycolation reaction or formed by controlled hydrolysis of polysaccharides – starch, inulin or xylan.

In recent years, chitosan (derived from chitin} oligosaccharides have emerged as wide-spectrum nutraceuticals in view of their diverse biological activities – antimicrobial, antioxidant, anticancer and immune-stimulant effects.

Lipid based nutraceuticals

Oils and fats (primarily consisting of triacylglycerols) play an important role in human nutrition. Besides providing a source of energy in the diet, they influence many physiological and metabolic processes. Designer lipids are tailor- made fats and oils with improved nutritional or physiological properties resulting from modification in the composition and positional distribution of fatty acids. MLM type lipids, in which the medium chain fatty acids (having 6-12 carbon atoms) are attached to sn- 1,3 position and long chain fatty acid or polyunsaturated fatty acids (having more than 12 carbon atoms and double bonds) at sn-2 position, have been useful for clinical purposes as rapid energy source for patients suffering from malabsorption of lipids, lowering cholesterol levels, hypertension, inflammatory & immune disorders & in the prevention and treatment of arthritis. The presentation would cover an over-view on the above subject along with suitable examples of the enzymes / processes involved.

MR. MAHESH BABU

Circular economy and Waste Management
Mr. Mahesh Babu
IL&FS Environmental Infrastructure & Services Ltd.

IL&FS Environmental Infrastructure and Services Limited is leading integrated waste management company in India since the year 2007. The company believes in creating scalable circular economies through its waste processing and recycling facilities. With its extensive sectoral experience, the company aims to minimize rejects by following the Integrated Waste Management approach. Some of the success stories include the composting facility in Okhla and India’s First Euro norm Compliant Waste to Energy facility in Ghazipur, East Delhi that has generated over 125 million units of green electricity by processing over 1.3 million ton solid waste.IL&FS Environment has also established replicable solutions for Burari Plant for C&D waste Management and at Gulmeher which is a CSR initiative bringing life back to flower waste by skilling waste pickers into artisans. We at IL&FS Environment are totally committed to continuous innovations in Waste Management to inculcate 5R principles of Circular Economy.

Abstracts for
Oral and E-Short
Presentations

SESSION I: MEDICAL AND NANOBIOTECHNOLOGY

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ICABB_M101	CRISPR/Cas9: A Modern Tool for Disease Diagnostics
ICABB_M102	Lipid-Nanoparticles Assisted mRNA-Based Cancer Immunotherapy
ICABB_M104	Assessment of improvement by nutraceuticals on rotenone-induced neurodegeneration in *D. melanogaster* strains
ICABB_M105	Computational validation of Apocynin as NADPH Oxidase (NOX) Mediated ROS Modulator
ICABB_M106	Application of Nanotechnology in Curbing the Pathological Causes of Alzheimer’s
ICABB_M107	The androgen receptor pathway as a therapeutic target for prostate cancer
ICABB_M108	Potential Point-of-Care Biosensors for the detection of COVID-19
ICABB_M109	Tumor Hypoxia: an avenue to target and treat tumors using siRNA mediated nanoparticles
ICABB_M110	Ethics related to CRISPR applications
ICABB_M111	Clinical application of circulating tumour DNA in early diagnosis of cancer
ICABB_M112	Transgenic rodent model of the Alzheimer disease mirroring: Amyloid-beta pathology and its role in drug development
ICABB_M113	Gene Therapy Strategies for Tackling Hutchinson-Gilford Progeria
ICABB_M114	Mechanism of action in Acute respiratory distress syndrome
ICABB_M115	Recent interventions caused by monoclonal antibodies for the treatment and diagnosis of covid-19
ICABB_M116	The Role of epigenetics in age-related neurodegenerative diseases
ICABB_M117	Dermal fillers for redefining facial structure: types, procedure and effects.
ICABB_M118	Genetic Approaches To Treat Alzheimer’s Disease
ICABB_M120	AI in neurosciences: route to precision medicine
ICABB_M121	Crispr/cas9: A powerful genome editing technique for treatment of breast cancer
ICABB_M122	Metabolomic insights for identifying candidate biomarkers for diagnosing and managing NAFLD
ICABB_M123	CRISPR-Cas9 Gene editing tool: Advances and Challenges
ICABB_M124	Random Insertion Transposon Mutagenesis of *Mycobacterium fortuitum* Identified role of Anthranilate Phosphoribosyltransferase (trpD) in Biofilm Formation and Hypoxic Stress Survival
ICABB_M125	Chimeric Dengue E protein enhances secretion of Dengue viral like particles (VLP)
ICABB_M126	Ammonium Sulphate, Lithium Chloride, and Mannitol enhance solubilisation of the

	chimeric human Interferon Regulatory Factor-1 (IRF-1) in *Escherichia coli*: A tumour suppressor protein
ICABB_M127	Unfolding the Chikungunya virus-human proteins interactions
ICABB_M128	Transfer of phobias and mental illness through genes
ICABB_M129	Crispr cas9: the latest trend in designer babies
ICABB_M130	Regenerative medicine
ICABB_M131	Freedom to Operate Search: Intellectual Property Assessment of Pharmaceutical Products
ICABB_M133	Artificial womb – the future of humankind
ICABB_M134	Identification of Drug candidates for Breast cancer-Drug Repositioning
ICABB_M135	Healing of Nature During the Lockdown COVID-19
ICABB_M136	Nanomedicine in brain cancer treatment
ICABB_M137	Mucormycosis: Fungal Infection re-explored
ICABB_M138	Nanomedicine for the treatment of brain disorders
ICABB_M140	Nanoparticles for the treatment of alzheimer's disease
ICABB_M142	Development and validation of a sensitive and rugged method for Bioanalysis of Ramipril and its metabolite in Plasma samples
ICABB_M143	Hydroxychloroquine Induced Cardiotoxicity
ICABB_M144	Pharmacological induction of autophagy as a potential therapeutic target for Japanese encephalitis
ICABB_M145	Adipose-derived mesenchymal stromal cells in regenerative medicines: new perspective and challenges
ICABB_M146	Pancreatic Cancer: Biomarkers for Early Diagnosis
ICABB_M147	Multiphase CFD Analysis of Separation of Blood Constituents in a Centrifuge
ICABB_M148	Proteomic analysis of cardiac myoblasts under hyperglycaemic conditions
ICABB_M149	Identification of miRNAs under hyperglycaemic conditions in cardiac myoblasts
ICABB_M150	Anticancerous Drug Induced Cardiotoxicity: A Major Concern
ICABB_M151	ACE-2& CCR4 Receptors: Critical Targets to Combat Cardiotoxicity
ICABB_M152	Application of optimization methods in mental health
ICABB_M153	COVID- 19 transmission from Mother to the Child during pregnancy: A Review
ICABB_M154	Exploring of Anticancer potential of Mosambi (*Citrus limetta*) peel extracts

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ICABB_F203	Systematic analysis of the indica rice PHD-Finger gene family and their response in salinity stress
ICABB_F204	Addressing the Non-Specific Amplification in RCA: A Comparison of Three Different Ligation Techniques for Preparing Circular DNA
ICABB_F205	Need for Probiotic products
ICABB_F206	Clove (*Syzygium aromaticum)* and Black pepper (*Piper nigrum*) as promising antimicrobial agents against common food borne pathogens
ICABB_F207	Quorum Sensing and its role in Virulence
ICABB_F209	Goat Milk-A nectar behind the poison
ICABB_F210	Ageing, Dairy Product Consumption and Prostate Cancer Risk
ICABB_F211	Effect of UV-B irradiation on Bioactives of Edible Mushroom Powder
ICABB_F212	Extremophiles: Medical Potentials Explode
ICABB_F213	Study the detection of aflatoxin B1, B2, G1, G2 in commercialized infant formula
ICABB_F214	Insights into bacterial cellulose biosynthesis
ICABB_F217	Functional Properties of Bioactive Peptides derived from Milk
ICABB_F218	Millets: An emerging new trend in functional food
ICABB_F219	Urban Inland Water Bodies and Microbial Shift
ICABB_F221	Evaluation of the lichen Parmelia sp. for molecules of high medicinal value
ICABB_F222	Metabolic Interventions of Gut Microbiota in Diabetic Cardiomyopathy
ICABB_F223	Genetically Engineered microorganisms for the degradation for environmental

	pollutants
ICABB_F224	Microbiome
ICABB_F225	Mining for Nonribosomal Peptide Synthetase and Polyketide Synthase of Burkholderia species genes with extensive potential for biotechnological use.
ICABB_F227	Current trends in fungal chitosan production and applications
ICABB_F228	Bacterial cellulose composites: an advanced biomaterial

SESSION III: OMICS AND COMPUTATIONAL BIOLOGY

ICABB ID	TITLE OF THE ABSTRACTS
ICABB_O301	*In-silico* drug screening studies of potent inhibitors against Main protease (Mpro) for COVID-19
ICABB_O302	An integrative bioinformatics analysis for identifying hub genes in human immunodeficiency virus
ICABB_O303	Genomic analysis of ciprofloxacin induced *Salmonella typhimurium* mutants
ICABB_O304	*In silico* characterization of potential biomarkers in prostate cancer adenocarcinoma
ICABB_O305	Big Data Analysis of Alzheimer's Disease for Early Prediction
ICABB_O306	Binding energy comparison of antibody-antigen interaction in SARS-CoV-2 with respect to Antibody Dependent Enhancement
ICABB_O307	Music Preference as a Predictor of Mental Health: Developing Spotify Mood Analyser to Predict Mental Health
ICABB_O308	Virtual screening of compounds from Aureobasidium strain TD-062 obtained from the Thar Desert of India
ICABB_O309	Effect of Natural Compounds on Glioblastoma Multiforme Pathways
ICABB_O311	Evolutionary genomics of olfactory gene family in *Drosophila*
ICABB_O312	Substrate specificity of Paraben towards liver esterase: A bioinformatics approach
ICABB_O313	Mutational Analysis in Bacteria using Computational Tool – MutaNET
ICABB_O314	Transfer learning-based Attention gated Siamese network for Human and SARS-CoV-2 protein interactions
ICABB_O315	Genome-wide identification and characterization of metal binding gene families in legumes: Method and strategies.
ICABB_O316	Production of therapeutic antibodies for disease treatment

ICABB_O317	Approaches to Enhance Aptamer Substrate Binding
ICABB_O318	Computational approach for Identification of potential genes against colorectal cancer
ICABB_O319	*In silico* Approaches to Investigate Cardioprotective Phytoconstituents as TMAO Inhibitor
ICABB_O320	Effect of phyto-compounds on SARS-CoV2
ICABB_O321	Nutritional profiling of Desi and Kabuli chickpea genotypes and assessment of protein quality based on Essential amino acid score and *in-vitro* protein digestibility
ICABB_O322	Structural characterization of Klebsiella pneumoniae Cysteine Synthase Complex using integrative structural biology approach

SESSION IV: NATURAL PRODUCTS AND HUMAN HEALTH

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ICABB_N401	Evaluating multiple phytocompounds of *Carica Papaya* Leaves extract for bacterial skin infections by computational and experimental validation
ICABB_N402	Therapeutic and Nutritional importance of *Cordyceps sinensis*
ICABB_N403	The correlation of gut microbiome with persistent depressive disorder and MDD in population
ICABB_N404	Study of the genetic variations in different variants of *Tribulus terrestris* L. (gokshura) through DNA RAPD analysis.
ICABB_N405	Molecular Docking of resveratrol & piperine natural compound with serotonin transporter (SERT)
ICABB_N406	Molecular pathways in vulvar squamous cell carcinoma: implications for target therapeutic strategies
ICABB_N407	Genetic Transformation and Ectopic Over Expression of Cytochrome P450 monooxygenase (P450) gene (CYP88D6) in *Glycyrrhiza glabra.*
ICABB_N408	*Azadirachta indica* and its potential uses against SARS-CoV-2
ICABB_N409	The phytocompounds from *Vateria indica* and their therapeutic potential
ICABB_N410	Plant Secondary Metabolites: Effect of Stress and Defense responses in their Production
ICABB_N411	A study on the antioxidant, antidiabetic and cytotoxic properties of a polyherbal formulation
ICABB_N412	Anti-proliferative effect of phyto-compounds in human glioblastomas multiforme cell lines
ICABB_N413	Ginsenosides: A transpiring Nutraceutical
ICABB_N414	Pharmacological importance of Secondary Metabolites from Plants
ICABB_N415	Role of flavonoids against COVID – 19
ICABB_N416	In vivo evaluation of withcoagulin in experimentally induced hypertension and myocardial infarction in Albino rats
ICABB_N419	Suppression of pathways of brain inflammation by fisetin in PTZ-induced kindling in mice.
ICABB_N420	Raw and Aged Garlic Extract: A Comparitive Analysis
ICABB_N421	Hydrogen Sulfide in Cardioprotection

SESSION V: AGRICULTURE, ENVIRONMENT, AND INDUSTRY

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ICABB_AG502	Bioethanol production from rice straw residues
ICABB_AG503	Residual effect of herbicides on soil microflora of bajra (*Pennisetum glaucum* l.)
ICABB_AG505	Purification of Cellulase Enzyme from Peel of *Colocasia esculenta*
ICABB_AG506	Heavy metal induced neuronal toxicity serving as a precursor to NDDs
ICABB_AG507	Negative impact of covid-19 on the environment
ICABB_AG509	Exploring phytoremediation potential of *Vigna radiata&V. aconitifolia* under Cr(VI) induced stress in hydroponics
ICABB_AG513	Microbial degradation of plastic waste
ICABB_AG514	Environmental impacts of Coronavirus
ICABB_AG515	Polymer Biosynthesis Pathways in Microorganisms
ICABB_AG516	Antibiotics in soil and water and its impact on living organisms
ICABB_AG517	Impact of informal E-waste recycling activity on Soil
ICABB_AG518	*Vetiver Grass*: Potential tool for Phytoremediation of Heavy metals
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ICABB_AG520	Laundry Detergents : A Brief Overview
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ICABB_AG524	Fungal mediated conversion of food waste to compost
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ICABB_AG529	A Review of multiple application of Tannase and developing zero waste technology
ICABB_AG530	Impact of pesticides and biopesticides in the presence of Salt stress on *Cicer arietinum*

	and *Phaseolus vulgaris* plants
ICABB_AG531	Environmental impact, monitoring, toxicity and biodegradation of organophosphate weedicide Anilfos: A critical review
ICABB_AG532	Mitochondria as an important target in heavy metal toxicity
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ICABB_AG535	Removal techniques of nitrate removal- Review
ICABB_AG536	Role of travel cost method as a Non-Market Valuation Method in determining Economic cost of the recreational sites in India: A bioeconomic perspective
ICABB_AG537	Presence and Remediation of Amoxicillin and Tetracyclin by *Ocimum basilicum*: A sustainable approach

Session I

MEDICAL AND NANOBIOTECHNOLOGY

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ICABB_M101

CRISPR/Cas9: A MODERN TOOL FOR DISEASE DIAGNOSTICS

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Abstract

Clustered Regularly Interspaced Short Palindromic Repeats, or CRISPR is the adaptive immune system of prokaryotes that retains protospacer of phages and plasmids from past infections, as spacers flanked between palindromic repeats in a CRISPR array. The crRNA binds with tracrRNA and Cas9 protein to form gRNA which binds with the complementary protospacer of the viral DNA. Cas9 protein, an endonuclease, then chops off the viral DNA 3 base pairs before PAM leading to disintegration of the viral genome, thereby preventing infections. This technology has gained widespread attention amongst scientists and researchers due to its versatility, accuracy, and simplicity of utilization compared to its opponents ZFN and TALEN. A gRNA complementary to the gene sequence that is to be silenced, removed, or replaced is synthesized in the lab and introduced in the host cell. Cas9 opens the host's DNA helix for its hybridization with gRNA and thereafter slices the target sequence leading to the identification of functions of a particular gene and substitution of mutated/non-functional genes with functional sequences via vectors. The technology has been employed in devising treatments for not only genetic disorders like Sickle-Cell Anemia and Muscular Dystrophy but also, novel coronavirus infection, Cancer, and several other bacterial and viral diseases. It has also been administered in the creation of testing kits for COVID-19 pneumonia infection leading to early diagnosis and reduced dispersal. As the tool can be employed at somatic as well as germline levels, it opens doors to speculation from researchers and ethicists regarding its applications.

Keywords: Protospacer, CRISPR Array, crRNA, tracrRNA, PAM, vectors, COVID-19

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LIPID-NANOPARTICLES ASSISTED mRNA-BASED CANCER IMMUNOTHERAPY

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Abstract

Recently, mRNA emerged as a promising alternative to traditional vaccine strategies due to its high immunogenicity, suitability for large-scale, low-cost, faster production, superior safety profile, and its potential to encode for almost any protein. mRNA vaccines with their intracellular antigen synthesis, have been shown to be potent activators of a cytotoxic immune response. Efficient delivery of mRNA vaccines will be the key for their success. Among potential nonviral vectors, lipid nanoparticles are particularly promising as they can be synthesized with relative ease in a scalable manner, have minimum carrier cytotoxicity, protect the mRNA against degradation, facilitate endosomal escape, and can be targeted to the desired cell type by surface decoration with ligands. Messenger-RNA encoding antigen when encapsulated by lipidnanoparticles, effectively excites the growth of dendritic cells andencourages the initiation and production of antigen-specific T cells. Once mRNA is adopted by the host cells, its transcripts get directly translated into cytoplasmand the developing antigens go to the antigen presenting cells to stimulate animmune response. In this review, we summarize recent advances in the development of lipid nanoparticles for mRNA-based immunotherapies and their applications in cancer treatment. In conclusion,the lipid nanoparticle formulation presented here is a promising vector for mRNA vaccine delivery. Further optimization, including the incorporation of different adjuvants, will likely enhance the potency of the vaccine.

Keywords: mRNA vaccines, lipid nanoparticles, cancer treatment, cytotoxic T-cells, dendritic cells, antigen presenting cells.

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ASSESSMENT OF IMPROVEMENT BY NUTRACEUTICALS ON ROTENONE-INDUCED NEURODEGENERATION IN *D. melanogaster* STRAINS

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Abstract

Nutraceuticals play an important role in the reduction of free radical generation in the cells. This property is used in the present organismal study to see the effects of the aqueous extracts on Parkinson's model *Drosophila melanogaster*. Aqueous extracts of the different parts of the *Punica granatum* (peel and pulp); *Carica papaya* (peel) *Foeniculumvulgare* (seeds), *Trigonellafoenum-graecum* (seeds)and *Urtica dioica* (dried leaves) were used to evaluate the ameliorative potential of these plants on *in vivo* model. In this study, wild type *Drosophila melanogaster* (Oregon R^+) and overexpressed transgenic (*hsp26* and *hsp70*) and RNA*i* lines (*hsp70*) were used to evaluate the organismal effects in rotenone (test chemical) treated flies and rotenone along with extracts of different plants. All strains of Drosophila flies were reared on rotenone (0.05ppm) mixed standard corn-sugar medium alone, rotenone along with aqueous plant extract, 5.0mM copper sulphate (Positive control) and normal food without rotenone (Control). Climbing ability and memory power were examined in wild-type, transgenic and mutant strains of Drosophila, and all exhibited statistically significant ($P<0.5$) improvement in the plant extract treated groups. Among all the phyto-extracts used in the study, the *Urtica dioica*,peel and pulp of *Punica granatum* elicited maximum ameliorative potential although not at the same intensity in all Drosophila strain. Different extracts exhibited a different degree of improvement in different assays. Altogether, overexpression of *hsp70* and *hsp26* showed better outcomes in said parameters as compared to wild-type or RNA*i* flies.

Keywords: Fennel, fenugreek, nettle leaves, pomegranate, papaya peel.

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COMPUTATIONAL VALIDATION OF APOCYNIN AS NADPH OXIDASE (NOX) MEDIATED ROS MODULATOR

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Abstract

Several neoteric research studies have explored to identify and characterize the role of Apocynin (APO) in eliminating the neuropathic pain along with its potential as an effective drug for peripheral nervous systems. Apocynin, an aromatic ketone, tends to elicit non–specific inhibitory NADPH oxidase responses which encompasses several cytosolic constituents (p67phox, p40phox, p47phox and GTPase Rac1) and membrane associated complexes (p22phox and gp91phox). Inhibition of NADPH oxidase is facilitated by APO binding to membrane protein; thereby not only primarily halts the ROS production but also possesses the ROS scavenging attributes due to which it is considered as a potential therapeutic agent in neurodegenerative disorders (NDD). The current research study is aimed to evaluate several facets of APO's interaction with specific proteins p67phox, ph40phox, p47phox along with their composite of p47phox & p67phox (PDB ID – 1K4U) by critically assessing the pharmacokinetic parameters to ensure efficient APO expression over NADPH oxidase activity and its docking studies to ensure the efficient binding of APO to the targets hence inhibits its translocation or binding with membrane associated component. An elaborative *in-silico* research study was conducted to further reinforce the interaction and specific binding.A successful *in-silico* study was compiled initiating with elaborate pharmacokinetic profiling of ligand via ADME toxicity analysis. Homology Modeling was conducted by MODELLER 9.25 to retrieve the accurate 3-D model of the proteins which was further employed to carry out Active Binding Site Prediction along with the Molecular Docking Studies and stability analysis. Results from ADME offer several biochemical parameters such as cellular toxicity, lipophilicity, solubility, adsorption, and metabolism of the drug. *In-silico* analysis illustrates the active site prediction which was validated by molecular docking that was permitted to view the 3D conformation of target protein–ligand interaction showing the specific binding affinities evaluated at the lowest energy levels.

Keywords: Neurodegenerative disorders (NDDs),Antioxidant ability, Molecular docking, Free radical scavenging, NADPH oxidase.

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APPLICATION OF NANOTECHNOLOGY IN CURBING THE PATHOLOGICAL CAUSES OF ALZHEIMER'S

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Abstract

Alzheimer's disease is a disorder that results in cognitive impairment. These problems might be brought about by hereditary and natural factors, pathologies in cycles including protein accumulation which lead to neurodegeneration or dysregulation of the resistant cycle, or irregularities concerning the turn of events and capacity of the cortex of the brain. The diagnosis and prognosis of Alzheimer's disease (AD) and circulating miRNAs are among the most promising candidates. Some of them have been reliably recognized as AD-specific miRNAs and their targets often tend to be involved in underlying AD pathophysiological processes. Just a few candidates-such as acetylcholinesterase inhibitors-are currently being used as an effective treatment despite screening various drugs against different molecular targets of AD. However, the targeted delivery of these drugs to the central nervous system (CNS) has many drawbacks, including poor solubility, low bioavailability, and decreased efficacy due to blood-brain barrier impediments. Latest developments in nanotechnology present opportunities in the delivery of active drug candidates to address certain limitations. In recent couple of years, battles have been accounted to build up the nanovesicles for drug conveyance utilizing the blood-brain barrier (BBB). In targeting many therapeutic moieties, Nano drug delivery systems are promising by easing the penetration of drug molecules through the CNS and enhancing their bioavailability. Recently, a broad variety of nano-carriers have been adapted to produce effective therapeutics with sustained release and enhanced efficacy, such as polymers, emulsions, lipo-carriers, solid lipid carriers, carbon nanotubes, metal-based carriers, etc. In animal models, gene transfer strategies to the brain have helped to test several fascinating tracks, some of which could in the future merit clinical applications in AD patients. Here the evolving role of miRNA in AD is reviewed, their implications for AD pathophysiology, and their potential role as future biomarkers.

Keywords: Alzheimer's disease, therapeutics, miRNA, brain delivery, blood-brain barrier (BBB), CNS, drug delivery.

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THE ANDROGEN RECEPTOR PATHWAY AS A THERAPEUTIC TARGET FOR PROSTATE CANCER

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Abstract

Prostate cancer is a leading form of cancer among men of all ages worldwide. The androgen receptor pathway plays an important role in the development and functioning of this type of cancer. The pathway basically revolves around the functioning of androgens like testosterone or dihydrotestosterone (DHT) along with androgen receptors (ARs) to activate the special DNA binding sites or the androgen receptor elements (AREs) present in the nucleus leading to the activation of several target genes. These target genes are responsible for prostate carcinogenesis and progression, and can be an indicator of the same.

The blocking of AR sites by inhibitors such as enzalutamide or by flutamide does not let the androgens bind and is one of the most effective methods to control prostate cancer. Whereas some of these AR inhibitors show certain side effects, therefore, the usage of common dietary compounds like resveratrol are being proposed as effective therapeutic alternatives. Another component, heat shock protein (HSP), renders the AR inactive and maintains the AR in the correct spatial conformation to bind androgens. The use of certain HSP inhibitors such as VER155008 and onalespib disrupt its functioning leading to an inhibitory effect on the AR expression. Hence the AR pathway and its components are excellent therapeutic targets to control prostate cancer.

Keywords: Androgen receptors, Dihydrotestosterone (DHT), Heat shock protein (HSP), Inhibitors.

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POTENTIAL POINT-OF-CARE BIOSENSORS FOR THE DETECTION OF COVID-19

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Abstract

Rapid and precise diagnosis of COVID-19 suspected cases plays an important role in appropriate medical treatments and quarantine measures. Early screening of COVID-19 is important to reduce the risk of spread before antigen/real-time polymerase chain reaction (RT-PCR) tests are conducted. In this view, Point-of-care Biosensors provide fast, inexpensive, and easily accessible results by responding to COVID-19 specific biological specimens. The review paper summarizes various biomarkers/indicators for the diagnosis of coronavirus disease along with existing biosensors that differ based on their transduction mechanism. Electrochemical, Optical, Surface plasmon resonance (SPR), Surface-enhanced Raman scattering (SERS), Field-effect transistor (FET), Piezoelectric, Polydimethylsiloxane (PDMS) based, and other flexible materials such nanosheets, paper, and film-based biosensors are discussed. The review sums up the existing status of current diagnostic methods, their limits, and the advantages of biosensor-based diagnostics over the conventional methods for screening suspected patients. Lastly, the current challenges and future perspectives have been discussed. It is hoped that this analysis will support clinicians and scientists to develop new biosensing platforms for point-of-care (POC) diagnostics to manage coronavirus disease.

Keywords: COVID-19, Biosensors, POC devices, Biomarkers, Diagnostics.

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TUMOR HYPOXIA: AN AVENUE TO TARGET AND TREAT TUMORS USING siRNA MEDIATED NANOPARTICLES

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Abstract

Hypoxia is a state wherein the adequate availability of oxygen is low in the body or portion of the body. It is the major identification mark for solid tumors; as a tumor develops, it grows beyond its blood supply, leaving a section of the tumor with an environment where the oxygen concentration is significantly inferior to in healthy tissues.

Hypoxia responsive nanoparticles (HRNPs) are the current state-of-the-art technology being evaluated in several preclinical studies, globally. HRNPs are a nano-sized theranostic i.e. an amalgamation of a hypoxic region identifying diagnostic and a therapeutic module. The major advantage conferred by this theranostics is the specificity of action (targeting the hypoxic regions of the tumor), higher therapeutic efficacy, and avoiding any off-target delivery of an anti-tumor therapeutic intervention.

The HRNPs can be diverse and be generated by several combinations of hypoxia imaging molecules and therapeutic interventions. 2-nitroimidazole, azobenzene derivatives, radiosensitizers, and bioreductive prodrugs are commonly used hypoxia-sensitive moieties. The present compilation elaborates on the widely popular documented hypoxia imaging and therapeutic modules of the HRNPs. Further, we also discuss an interesting cutting edge HRNP developed by Li., et al, wherein the theranostic comprises of a combination of mPEG-b-(PLG-g-NI) Dye with a siRNA against CDC20, an oncogenic hallmark of aggressive tumors.CDC20 gene is an essential regulator of the cell division cycle. It acts as a regulatory protein interacting with other proteins at multiple points within the cell cycle.

In summary, we highlight the science/design, advantages, disadvantages, and opportunities of siRNA\HRNPs.

Keywords: Hypoxia, tumor, genome instability, apoptosis, HRNPs, siRN*A.*

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ETHICS RELATED TO CRISPR APPLICATIONS

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Abstract

CRISPR (Clustered Regularly Interspaced Short Palindromic Repeat) is a ground breaking technology that allows scientists to edit genomes with unprecedented precision and efficiency. It is cost effective and can be used on any cell, whether it be microorganism, plant, animals or humans. It can help understand diseases such as HIV or cancer, and promises a cure for thousands of genetic diseases such as color blindness and hemophilia. One of the major applications is 'Designer Babies' (gene editing human embryo), which also raises some ethical concerns. The embryo's inability to express an autonomous decision is one of the major ethical challenges of germ line engineering. CRISPR can be used to eliminate various genetic diseases, but it could also offer choices on offspring's physical attributes or intelligence quotient. If this technology becomes a realistic medical practice, then it can create divisions between those who can afford it and those who cannot, which will in turn create genetic divisions, separating enhanced individuals from unenhanced ones. As a result, several scientific organizations, and the National Institutes of Health all over the world have called for a moratorium on such experimentation. We must consider the ramifications in advance and engage in a global conversation about how to best harness this technology, so that we can ensure that this technology does not fall into wrong hands. Ultimately, designer babies represent great potential in the field of medicine and scientific research, but there remain many ethical questions that need to be addressed beforehand.

Keywords: Cas9, Designer Babies, Gene editing, Ethical questions.

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CLINICAL APPLICATION OF CIRCULATING TUMOR DNA IN EARLY DIAGNOSIS OF CANCER

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Abstract

The current sampling methods of cancer that are invasive and sometimes pose biological complications have led to the invention of a new, less expensive and non-invasive diagnostic tool, called liquid biopsy of circulating tumor DNA (ctDNA). Cell free DNA of cancer patients mainly includes germline DNA from normal cells and minority ratio of ctDNA. Out of which, ctDNA originates and possesses genetic defects from cancer cells. Fragments of ctDNA are released into the bloodstream and tissue fluid mainly after apoptosis and necrosis of the tumor cells. Apart from plasma, ctDNA is also found in body fluids such as urine, cerebrospinal fluid and saliva. The current detection methods for these ctDNA mainly includes Polymerase Chain Reaction (allele specific PCR), Next-Generation Sequencing (NGS) and droplet digital PCR. The potential use of ctDNA as a biomarker in early cancer diagnosis has been demonstrated by various studies. However, low concentration of ctDNA in tumor samples and undetected mutations, raise certain challenges in diagnosis of the disease. This has created an urgent need for quality assurance of isolation and detection procedures of ctDNA. The current study reviews the challenges in this field and advancements that have occurred in the recent past.

Keywords: Circulating tumor DNA, Liquid biopsy, Tumor, Early cancer detection.

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TRANSGENIC RODENT MODEL OF THE ALZHEIMER DISEASE MIRRORING: AMYLOID-BETA PATHOLOGY AND ITS ROLE IN DRUG DEVELOPMENT

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Abstract

Alzheimer's disease (AD) is a type of neurodegenerative disorder characterized by gradual degeneration of neurons and this leads to manifestations of the disease and is responsible for behavioral and cognitive impairments. The number of people affected by Alzheimer's disease is enormous; approximately 50 million people worldwide are the victims of this disease. In spite of enormous efforts put in by the scientists throughout the world, this disease remains incurable. Amyloid plaques and the neurofibrillary tangles are the two main hallmark features related to Alzheimer pathology. So far, no such *in-vivo* experimental models available for this disease which could represent the real human AD pathology. Therefore, the need for developing animal models characterizing all the aspects of Alzheimer's disease has increased. This review highlights various experimental models for AD, including, transgenic rodent model available to study amyloid-beta pathology in AD. This review further discusses the pathological characteristics and shortcomings of these transgenic rodent models and also suggests that this model can be further enhanced as a proper tool in testing novel therapeutics for AD.

Keywords: Alzheimer disease, transgenic rodent model, Amyloid beta pathology, drug development.

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GENE THERAPY STRATEGIES FOR TACKLING HUTCHINSON-GILFORD PROGERIA

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Abstract

Hutchinson-Gilford Progeria Syndrome (HGPS) is a rare autosomal dominant, genetic disorder leading to accelerated ageing at a very early age. According to The Progeria Research Foundation, about 350 to 400 children are living with progeria in the world today. Individuals born with this disease survive only up to their mid-teens to early twenties. HGPS is caused due to mutation in the LMNA gene, coding for Lamin-A protein, which is the structural scaffolding that holds the nucleus of a cell together. The single nucleotide substitution mutation (C1824T) prevents proper translation of prelamin-A to Lamin-A, and generates a toxic protein called 'Progerin'. The accumulation of Progerin is the reason for the appearance of various phenotypes of this disease, which are similar to the effects of old age. Gene therapy is a promising tool to reduce the effects of HGPS employing various techniques like gene correction, gene deletion, gene silencing, RNAi, CRISPR-Cas9, iPSCs etc. Development of diverse gene therapies is an outcome of exploration into biomolecules of the body, and study of molecular mechanisms of the involved pathways. In-depth concepts of genomic editing and genetic engineering may be exploited to add desirable and disease-free genes in the genomes of individuals suffering from the disease and give them a healthier life. The review would provide a detailed inspection into science of the disease, which would be helpful to establish a link between ageing and HGPS; along with various gene-therapy strategies with potential of treating HGPS and reversing ageing itself!

Keywords: Progeria, Gene-therapy, Genetic-disorder, CRISPR-Cas9, Genomic-editing, Mutation.

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MECHANISM OF ACTION IN ACUTE RESPIRATORY DISTRESS SYNDROME

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Abstract

The acute respiratory distress syndrome (ARDS) is a syndrome of hypoxemic respiratory failure associated with non-cardiogenic pulmonary edema. ARDS is a very prevalent disease worldwide. It is still a critical challenge having high mortality and morbidity rate. ARDS also increases healthcare costs and The ARDS is an acute condition characterized by bilateral pulmonary infiltrates and severe hypoxemia in the non-cardiogenic pulmonary edema. ARDS is still a critical challenge with high mortality worldwide. ARDS increases healthcare costs and weakens the quality of life seriously and hence it is important to understand the pathogenesis of ARDS. impairs quality of life seriously. Therefore, getting a better understanding of the pathogenesis of ARDS is important. This review mainly focuses on the pathogenesis of ARDS. The inflammation is caused due to which endothelial and epithelial permeabilities which eventually leads to the accumulation of pulmonary edema fluid. The immune system generates reactive oxygen species, leukocyte proteases, chemokines and cytokines that help to neutralize pathogens but this also results in deteriorating the lung injury. In lung injury, there is increase in concentration of thrombin, tumor necrosis factor-α, vascular endothelial growth factor and leukocyte signals in the lungs destabilize the VE-cadherin bonds, resulting in increases endothelial permeability and the accumulation of alveolar fluid.

Keywords: ARDS, Hypoxemia, Necrosis, VE-cadherin bonds.

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RECENT INTERVENTIONS CAUSED BY MONOCLONAL ANTIBODIES FOR THE TREATMENT AND DIAGNOSIS OF COVID-19

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Abstract

The immensely promising results of monoclonal antibodies (mAbs) in diagnosis of diseases and their therapeutics, have greatly encouraged its usage and production by scientists and industries. More than 80 mAbs have been approved for marketing and a lot more are currently under trial and will soon be up for marketing. These monoclonal antibodies are produced from a single clone of B-lymphocytes hybridized with cancer cells (hybridoma cells). Most of the mAbs treatment are currently focused on cancer therapy and diagnostics but now its uses are spreading onto other fields for example, bamlanivimab is being used for the treatment of mild-to-moderate COVID-19 in adults and pediatric patients, requiring high flow oxygen or mechanical ventilation. This approach of using mAb for the treatment and diagnosis, encapsulates the mAbs based therapeutic mediation against COVID-19 by contemplating the existing understanding about neutralizing mAbs against similar coronaviruses: SARS-CoV and MERS-CoV. The main target of these monoclonal antibodies is the surface spike glycoproteins of the virus that mediates viral entry into the host cells. mAbs possess two characteristics that prove to be very useful when it comes to diagnosis and as therapeutics for various diseases. First is their specificity i.e their ability to bind and attack to a specific antigen. Second, the continuity of the effect that is otherwise called the memory generated after the first encounter with the antigen, by which they continue to confer resistance against that disease on subsequent encounters. The various other types of mAbs also give an insight into their therapeutic and prophylactic application and are now being utilized as antiviral drugs against this newly emerging retrovirus. The present study explores the therapeutic interventions by recently made mAb against COVID-19.

Keywords: Monoclonal antibodies, Therapeutics, lymphocytes, Bamlanivimab, Prophylactic, Corona viruses, antigen.

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ROLE OF EPIGENETICS IN AGE-RELATED NEURODEGENERATIVE DISEASES

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Abstract

Neurodegenerative diseases are characterized by the progressive loss of neurons leading to decline in memory and cognitive functions in the brain. Consequently, complex disorders such as Alzheimer's Disease (AD) and Parkinson's Disease (PD) remain untreated till date. Of all the known risk factors for neurodegenerative diseases, ageing is known to have the most significant effect on its onset and pathogenesis. Epigenetic alterations, a primary hallmark of ageing, show a strong correlation with age-related disease progression. Epigenetic processes stably alter the gene expression patterns without any genetic changes but rather by mechanisms influenced by the environment. These mechanisms involve the reversible modification of DNA by addition or removal of methyl groups, post-translational modification of histone proteins, remodeling of chromatin and non-coding RNA based mechanisms. Recent studies have shown that epigenetic variations, including DNA methylation and histone modifications, influence a number of cell-specific processes like neurogenesis and DNA repair. Thus epigenetics-based treatments are crucial against age-related neurodegenerative diseases and are currently being explored for their therapeutic efficacy. This review summarizes the molecular mechanism of epigenetics associated with age-related neurodegenerative diseases, particularly AD and PD. In addition, the potential of epigenetic factors including histone and DNA modifications as therapeutic interventions in such diseases has also been discussed.

Keywords: Alzheimer's Disease, Parkinson's Disease, Epigenetics, DNA methylation, Histone modifications.

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DERMAL FILLERS FOR REDEFINING FACIAL STRUCTURE: TYPES, PROCEDURE AND EFFECTS.

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Abstract

Aging is a continuous process in any living being's life. In case of human being the skin epidermis structure changes as its gets thinner, paler and clearer and even the 3 dimensional view of human face keeps on changing with age due to depletion of fat and collagen protein in different compartment of face which may lead to eye bags, sagging cheeks and wrinkles. With the help of technology, we have already reached a point where one can minimize the sign of aging and redefine the facial structure, by inserting dermal fillers at different parts of the face. One of the most widely accepted fillers are Hyaluronic acid fillers, with least long term side effect, and occasional adverse outcomes ranging from chronic lymphoplasmacytic inflammatory reactions to classic foreign body type granulomatous reactions. It lasts between 6 to18 months, depending upon the metabolism of one's body. In the present study various old and advanced dermal fillers will be explored with deep discussion about different types, their effects on the body, their catabolism inside our body and the future prospects.

Keywords: Collagen protein, Hyaluronic acid fillers, Lymphoplasmacytic inflammatory reactions, Granulomatous reaction.

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GENETIC APPROACHES TO TREAT ALZHEIMER'S DISEASE

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Abstract

Degeneration of neurons is the key mechanism behind Alzheimer's disease (AD) which further leads to compromised neuronal function with gradual loss of memory. There are the two broad categories of AD: Familial Alzheimer Disease (FAD) and Sporadic Alzheimer disease (SAD). Major genes involved in FAD are found to be Amyloid precursor protein (APP), Presenilin1 (PSEN-1) and Presenilin 2 (PSEN-2) etc. On the other hand, the major gene involved in SAD is the APOE gene. Researchers are trying to understand the molecular mechanisms of these genes, how they affect the central nervous system and peripheral system so that the severity of Alzheimer's disease could be minimized by targeting specific targets. This review highlights two main hypotheses which might be helpful in designing therapeutic approaches for the disease. One of these hypotheses is Amyloid Cascade Hypothesis and other is Calcium Hypothesis. The present article emphasises on the pros and cons of the Amyloid Cascade Hypothesis and the relevance of new Calcium Hypothesis, in the process of designing the more specific therapeutic approach of the AD.

Keywords: Alzheimer disease, Familial Alzheimer disease, Sporadic Alzheimer disease, Amyloid Cascade Hypothesis, Calcium Hypothesis.

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AI IN NEUROSCIENCES: ROUTE TO PRECISION MEDICINE

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Abstract

The technological advancement, fostered by the necessity to develop a sustainable society with low disease burden had provided an impetus to explore the use of Artificial Intelligence (AI) in diagnostic, prognosis and treatment of varied diseases. With high morbidity and disease burden, neurological diseases obtrude as diseases requiring immediate intervention.

AI assists Neuroscience Techniques had increased Neuroimaging (Computer Aided Diagnosis-CAD) potential to acknowledge disease related prototype and brain behavior. AI-augmented health systems influence patient monitoring, clinical decision report, automating administrative tasks and drug discovery. Machine learning (neural network models) decrypts statistics from biological data. Some of the approaches that have seen integration of AI includes analysis of gene expression or methylation in genome assist exploration of histone revamping, analyses data and helps to uncover the patterns in brain activities which hurries up research.AI methods interprets large multimodal datasets, providing unbiased insights into fundamental principles of brain function, better-informed intervention protocols. ANN performs clustering, by finding structure in an unlabeled biological data, it discovers subtypes of disease, determining nuclei regions on images, using these regions into an algorithm that performs classification. Studies have shown how AI can effectuate early diagnosis of Alzheimer's(AD), employing probabilistic, optimization techniques permitting PCs to achieve from vast and complex datasets. CNN extracts functional biomarkers of AD{–42, total tau (t-tau), and phosphorylated tau-181 (p-tau)}. Abate levels of CSF Aβ1–42 and increased t-tau and p-tau indicates AD diagnosis. Inadequate levels of Glucose in the brain detected by Positron Emission Tomography (PET) scans, diagnose AD before symptoms become acute. Research in neurology results in promising Genotype-based personalized medicine, Biomarkers APOE4 surge risk of AD, APOE2 is defensive.

By developing a broad neural network and implementing it in images of cells using fluorescent tags, researchers can distinguish cell types explain conduction of electrochemical impulses.AI based health care would target on preventing disease instead of treatment, it might be more accurate, effective personalized medicine.

Keywords: Artificial Neural Network (ANN), Artificial Intelligence, Neuroscience, Diagnosis, Biomarkers.

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CRISPR/CAS9: A POWERFUL GENOME EDITING TECHNIQUE FOR TREATMENT OF BREAST CANCER

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Abstract

Cancer is referred to as a group of diseases involving abnormal cell growth with the potential to migrate to other parts of the body, for which various genetic and epigenetic factors are responsible. Globally, approximately 1 out of 4 cancers in women are diagnosed as breast cancer (BC). Despite the great advances in diagnostics and therapeutics, BC patients develop metastatic cancers which mostly relapse after the treatments. Hence, novel therapeutic techniques are required, which will selectively and efficiently kill malignant cells. Direct targeting of the genetic and epigenetic aberrations in the DNAs of BC development could be a promising strategy to beat the constraints of current therapeutics. The Cas system is grabbing a big attention of scientists these days for correcting the genetic defects. This Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR)/Cas system, composed of only an easily engineerable single guide RNA (sgRNA) sequence guaranteed to a Cas9 nuclease This could be a versatile technology that has the flexibility to feature or remove/correct DNA, within the genome in an exceedingly sequence-specific manner. CRISPR/Cas9 and its linked catalytically inactive dCas9 variants enables the knockout of overexpressed genes, correction of mutations in inactivated genes, and reprogramming of the epigenetic landscape to impair/prevent breast cancer growth. As immunotherapy has become an increasingly eminent source of cancer treatment, CRISPR/Cas9 can engineer the immune cells to redirect them against cancer cells and induce antitumor immune responses. Present study explores the DNA correcting potential of the Cas system against breast cancer and its mechanism of action with respect to its application of immunotherapy for breast cancer.

Keywords: Crispr/cas9, immunotherapy, Breast cancer, genome editing.

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METABOLOMIC INSIGHTS FOR IDENTIFYING CANDIDATE BIOMARKERS FOR DIAGNOSING AND MANAGING NAFLD

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Abstract

The term Nonalcoholic fatty liver disease (NAFLD) is mostly associated with chronic liver disease in patients without significant history of alcohol consumption and includes several pathological conditions such as simple steatosis without inflammation, nonalcoholic steatohepatitis (NASH) with inflammation, fibrosis of hepatic tissue and cirrhosis. Although perceived as a disease of the developed world, it is emerging as a major health problem of Asian continent as well. Despite data paucity, the reported prevalence in rural and urban India amounts to 9% and 32% respectively. The major obstacle is unavailability of non-invasive diagnostic techniques for monitoring pathological progression of NAFLD which follows a tentative 'three-hit' process namely steatosis, lipotoxicity and inflammation. The invasive procedure of biopsy needs to be carried out for diagnosing NAFLD. Recently, metabolomic analysis have been able to provide biomarkers that can distinguish healthy controls for NAFLD or NASH. Metabolomics is a powerful technique that is helping to develop treatment strategies also. This work aims to review newly found biomarkers for diagnosis as well as clinical management of the disease.

Keywords: NAFLD, NASH, Metabolomics, Biomarkers.

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Crispr-Cas9 GENE EDITING TOOL: ADVANCES AND CHALLENGES

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Abstract

Clustered regularly interspaced short palindromic repeats (CRISPR) and its associated nuclease 9 (CRISPR-Cas9) is a powerful gene editing tool that has won the 2020 Nobel Prize in Chemistry. The CRISPR-Cas9 system is essentially made up of two parts – 1. A guide RNA (gRNA) – Consists of a small piece of RNA designed complementary to the target gene. 2. The Cas9 enzyme – The Cas9 is an endonuclease enzyme which acts like a pair of molecular scissors, that is responsible to make the cuts in the genetic material. The gRNA binds at a specific location on the target gene and the Cas9 follows the gRNA to that location in the DNA. The Cas9 enzymes then make cuts on both the strands of the DNA. This protein system originally coded for an adaptive immunity in prokaryotic organisms to defend against infective genetic elements. Due to its simplicity and specificity, the CRISPR system has been repurposed into a strongly effective gene editing system that has revolutionized the field of molecular biology and generated excitement for new and improved gene therapies. It has been used to eliminate HIV from infected cells, modify the genome of cancer patients, treat Huntington's disease, reverse congenital blindness, etc, providing impetus in biomedical research. However, the technique faces multiple challenges, such as immunogenicity of therapeutic CRISPR-Cas9, fitness of edited cells, efficiency, specificity and translatability, that still need to be overcome to achieve effectiveness *in vivo* gene therapies. Also safe *in vivo* delivery of CRISPR needs to be taken into consideration. This work discusses recent advances and variants of the original technique for enhancing efficiency and minimizing off-target effects as well obstacles in this exciting technology.

Keywords: CRISPR, Cas9, Gene editing.

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RANDOM INSERTION TRANSPOSON MUTAGENESIS OF *Mycobacterium Fortuitum* IDENTIFIED ROLE OF ANTHRANILATE PHOSPHORIBOSYL TRANSFERASE (*trpD)* IN BIOFILM FORMATION AND HYPOXIC STRESS SURVIVAL

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Abstract

Mycobacterium fortuitum is an important rapidly growing NTM associated with a variety of nosocomial and post-surgical infections, majorly attributed to its biofilm forming capability. Transposon random mutagenesis was used to identify *M. fortuitum* membrane proteins required for biofilm formation, owing to significance of membrane proteins in colonization on substrate or tissue. Incorporation of transposon TnphoA based plasmid pRT291 into *M. fortuitum* ATCC 6841, constructed a mutant library with 450 mutants, of which 20 mutants showing highest alkaline phosphatase activity were shortlisted for analysis of their biofilm forming capability. One mutant namely, MT721 showed delay as well as defect in maintenance of its biofilm structure. Attenuation of MT721 was confirmed by microscopic analysis where MT721 showed scanty growth of biofilm forming cells relative to wild type strain. Analysis of mutant MT721 using genomic and bioinformatics approaches, identified homolog of anthranilate phosphoribosyltransferase of Mycobacterium abscessus in *M. fortuitum* (MftrpD) to be mutated. Computational functional interaction study of TrpD protein through STRING showed interaction of TrpD with chorismate utilizing proteins, majorly involved in aromatic amino acid and folic acid synthesis, suggesting that biofilm establishment and maintenance requires components of central metabolism. Mutant MT721 also showed defective growth under in vitro hypoxic stress conditions, indicating the probable role of MftrpD in resistance to in vitro hypoxic stress. Our study indicates the important role of MftrpD in hypoxic stress survival as well as establishment and maintenance of biofilm by *M. fortuitum*, which may further be explored for drug discovery studies against *M. fortuitum* and related pathogenic mycobacteria.

Keywords: Anthranilate phosphoribosyltransferase, Biofilm, *M. fortuitum*, Transposon mutagenesis, trpD.

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CHIMERIC DENGUE E PROTEIN ENHANCES SECRETION OF DENGUE VIRAL LIKE PARTICLES (VLP)

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Abstract

Viral like particles (VLP) are multiprotein structures that mimic the organization and conformation of authentic native viruses but lack the viral genome hence potentially yielding safer and cheaper vaccine candidates. DNA plasmids that express flavivirus structural proteins of premembrane/membrane (prM/M) and envelope (E) proteins result in generation of virus-like particles (VLPs). In this study we transfected HEK-293T cells with plasmid encoding for structural proteins of DENV-2 (prM and E) which resulted in its expression in cells but were not effective in VLP secretion in the medium. Previous studies have shown that region between 397-436 of DENV E protein contains endoplasmic reticulum (ER) retention sequence resulting in reduced secretion of Dengue virus. The membrane-proximal region of the glycoprotein (G) of vesicular stomatitis virus (VSV) has a high propensity to form alpha helices and mediate efficient VSV budding. We prepared 2 chimeric plasmids; TM chimera encodes DENV- E protein region from 1-451 and transmembrane (TM) region of VSV G protein from 492-511. A STEM chimera was generated containing DENV2 E protein from 1-395 and stem and TM region of VSV G protein from 421-511. Both TM and STEM chimeras were expressed in cells and underwent post translational glycosylation like wild type DENV-2 prM/E protein. Both chimeras resulted in 4-fold in VLP secretion as compared to wild type DENV-2 VLP. The VLPs generated by the chimeric plasmids showed efficient monoclonal antibody reactivity indicating the presentation of epitope on the E protein. Such chimeric vectors can be used for generation of high levels of DENV VLPs as vaccine candidates and also as diagnostics agents.

Keywords: Viral like particles (VLP), DENV, Envelope protein, VSV-G, Transmembrane, chimera.

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AMMONIUM SULPHATE, LITHIUM CHLORIDE, AND MANNITOL ENHANCE SOLUBILISATION OF THE CHIMERIC HUMAN INTERFERON REGULATORY FACTOR-1 (IRF-1) IN *Escherichia Coli*: A TUMOUR SUPPRESSOR PROTEIN

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Abstract

Interferon Regulatory Factor-1 (IRF-1) is a distinct member of the IRF family; a vertebrate transcription factor plays the vital role in prevention of neoplasm formation in the cell. High-level expression of recombinant IRF-1 in *Escherichia coli* (*E. coli*) leads to the formation of insoluble aggregates (insoluble fraction) at 37°C devoid of biological activity. In this study, we used chemical additives such as Ammonium sulfate, L-Arginine, Lithium chloride, Mannitol, Magnesium Chloride, Potassium Chloride, Proline, Sodium Dodecyl Sulfate (SDS) and CTAB (Cetyl Trimethyl ammonium Bromide) at the recommended concentration, during cell lysis to aid in solubility at 37°C. Use of additives resulted in the increased solubility of the recombinant IRF-1, with Lithium Chloride, Ammonium Sulfate and Mannitol being most effective. Although, we could get minimization of degradation products of chimeric protein with L-arginine only. Thus, we have developed an efficient procedure for the production of soluble IRF-1 by minimizing the formation degradation product and optimizing protein purification conditions. This result was further confirmed by western blot analysis with anti-GST and anti-IRF-1 polyclonal antibodies. The functionality of chimeric IRF-1 was attained by electrophoretic mobility shift assay (EMSA) study as a clear band shifting showed with VRE-IFN$_\beta$ promoter. We describe a straightforward strategy for the production of completely soluble and biologically active IRF-1 in *E. coli*.

Keywords: IRF-1, *E.coli*, Recombinant, Chimeric Protein.

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UNFOLDING THE CHIKUNGUNYA VIRUS-HUMAN PROTEINS INTERACTIONS

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Abstract

The chikungunya virus (CHIKV), an alphavirus, causing the recurrent epidemic worldwide with unavailability of vaccine so far. CHIKV has a positive sense single stranded RNA genome which encodes 5 structural and 4 non-structural proteins (nsPs). nsPs are responsible for viral replication while the structural proteins are mainly involved in viral encapsidation and budding. Cellular proteins play a crucial role during viral pathogenesis therefore, it is important to study the host-viral protein interactions. In the current study, the protein-protein interactions of one of the nsPs of CHIKV (truncated) and its human host were identified. The interactions were determined by the screening of a human cDNA library employing yeast two-hybrid technique. The interactions were further validated by GST pull-down assay. The network analysis was also performed which revealed that the identified host interactors were involved in the various cellular functions. Moreover, in-silico identification of the interacting residues between CHIKV and its human host were further predicted. The study will further assist in the development of host targeted antivirals.

Keywords: cDNA library, Pull down assay, Protein-protein interactions, Yeast two-hybrid.

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TRANSFER OF PHOBIAS AND MENTAL ILLNESSTHROUGH GENES

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Abstract

Phobias are common illnesses that cause a great deal of suffering to the individual and related ones. Gene-environment interaction research (GXE) have revealed a great deal about complex pathways underpinning the emergence of multiple mental disorders, but little has been discovered about phobias. It has been observed that lifetime records of irrational fears and phobias measured during intimate interviews are particularly inaccurate. Some of the features like: correcting for unreliability, blame for worries and their related phobias are shown to be mildly inherited. Individual-specific environmental interactions have also been shown to play a significant role in the production of phobias, although, family-environmental influences tend to be of little aetiological importance. Studying gene expression during brain development can lead us to understand the gene regulation and disease pathophysiology in this regard at genetic, cellular and systems level. Understanding Genetics of phobias can help us to develop new treatment strategies which can target the symptoms as well as the root causes of the disease. The present article explains the current understanding about genetic and environmental interactions which lead towards development of phobias and suggests that this knowledge could be used to optimise the likelihood of phobic detection and treatment.

Keywords: Gene-environment-interaction, Phobia, Mental disorders, Genetics of phobia.

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CRISPR cas9: THE LATEST TREND IN DESIGNER BABIES

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Abstract

CRISPR-Cas9 is being explored as a new therapeutic intervention for genetic disorders. Cas9 is an enzyme which acts as a pair of molecular scissors capable of snipping off the target deoxyribonucleic acid, and CRISPR is a collection of DNA sequences that tell Cas9 where to snip. It's a novel technology that permits geneticists and medical researchers to edit components of ordination by cutting out, replacing, or adding parts to the DNA sequences. In this way the two key components of CRISPR-Cas9 system can introduce the desired change into the target DNA., Once the DNA is cut at a particular location within the genome, bits of DNA can be added or removed. Basically a chunk of ribonucleic acid referred to as guide RNA (gRNA) consists of a little piece of predesigned RNA sequences which is meant to seek out and bind to a particular sequence within the DNA. A new concept of Designer babies is being popular these days using this technique. Designer babies are either created from an embryo selected by preimplantation genetic diagnosing (PGD) or genetically changed so as to influence the traits of the ensuing children. The primary aim of making designer babies is to avoid their having familial diseases coded by mutations in DNA. The present study describes the concept and mechanism of action of CRISPR-cas9 and evolution of the concept of designer babies in the modern era.

Keywords: CRISPR-Cas9, Designer baby, Familial disorders, Guide RNA.

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REGENERATIVE MEDICINE

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Abstract

At times people suffer from diseases which leads to tissue damage or in some cases complete organ failures. Possible solutions could be the use of biomaterials or an organ transplant but since there is scarcity of donors not everyone is lucky enough to receive an organ for transplant which ultimately results in death of many individuals'. Hence the need of the hour is to develop alternatives of organ transplant and prevention of immune rejection of transplanted organs. Organ and tissue loss through disease or injury requires the development of therapies that can regenerate tissues so that reliance on transplantations can be reduced.

Regenerative medicine is a branch of medicine that develops methods to regrow, repair or replace damaged or diseased cells, tissues or organs. It utilizes the principle of regeneration via use of therapeutic stem cells, tissue engineering and the production of efficient artificial organs. Stem cells are the cells which are able to self-renew and differentiate into mature cells.

Stem cells are capable of branching out in order to differentiate and become more specialized in function. The goal of tissue engineering is to assemble functional constructs that help in restoration, maintenance, or improvement of damaged tissues or whole organs. Artificial skin and cartilage are examples of engineered tissues that have been approved by the FDA; however, currently they have limited use in human patients. Production of artificial organs such as dialysis machines can be considered as a potential helping tool for the individual suffering from kidney failure or who is on the waiting list so that he can manage until someone donates. There are various focus areas of regenerative medicine including lung regeneration, cardiac regeneration, liver regeneration, neuro-regeneration etc. Regeneration of organs requires different approaches depending upon the cell type and regenerative ability of the cell. For example, the liver has the highest regenerative capacity than any organ which is not in the case of cardiac cells. Not only this regenerative medicine is also helpful in case of Parkinson's disease in which stem cells are taken as a source of neurons.

Keywords: ERT (Endogenous regenerative technology), Tissue engineering, cell therapy, artificial organs.

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FREEDOM TO OPERATE SEARCH: INTELLECTUAL PROPERTY ASSESSMENT OF PHARMACEUTICAL PRODUCTS

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Abstract

Developing a new drug and launching it successfully in the market is a risky, lengthy and expensive venture. It costs millions and takes 12–15 years to bring a new molecule from the laboratory to patients after clearing all clinical trials. With a humongous monetary investment, required to launch a novel drug or a unique drug delivery device design, no company would risk a total failure of a project and a filed lawsuit due to their product infringing on a pre-existing patented product. Freedom to operate search is a practice followed by a company to develop, produce, and market products without the risk of litigation for infringement of intellectual property rights (IPRs) held by third parties. FTO also provides an opportunity to modify the product and give an edge to it. Epilepsy is one of the most common chronic neurological disorders that affects around 50 million people worldwide and contributes to 0.5% global disease burden. It is estimated that up to 70% of people living with epilepsy could live seizure-free if properly diagnosed and treated. Due to multiple advantages of intranasal route of administration of drugs to treat epilepsy, this project entails to evaluate the market entry of intranasal, antiepileptic products into the US market by performing an FTO search. The aim of this project is to analyse a way of hassle-free entry of the chosen products in the US market, by determining to what extent do they infringe an already existing patented product and if there is a way to modify the chosen product so as to avoid any infringement.

Keywords: Patents, Infringement, FTO Search, Antiepileptic, Intranasal.

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ARTIFICIAL WOMB – THE FUTURE OF HUMANKIND

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Abstract

The present work, chronicles the research on "artificial wombs" – a sci-fi like concept but now an emerging technology projected to cater to healthcare issues such as the globally prevalent high female mortality and disruption of health and life due to childbirth, infertility, high mortality rate of preterm babies. The need for an artificial womb can be chronicled under two categories: mother based and fetus based. The scientific work on artificial womb started in 1954 with the diagrams of Greenberg (an inventor from USA). The next major milestone was the experiment conducted by Kuwabara (Juntendo University, Japan) and the next major milestone in the development of artificial womb came with the groundbreaking article published by Emily Partridge et al titled "An extra-uterine system to physiologically support the extreme premature lamb" (Philadelphia Children's Hospital, USA). It is this article that is the focus over here. The team successfully developed a system that supported fetal lambs that are "developmentally equal to the extreme premature human infant" for up to 4 weeks. Not only did this system break the 4-minute mile mark but also demonstrated that a healthy fetus can be sustained in an artificial environment or "bio bag" as they called it. The later examination of the lambs physiologically as well as post mortem showed that the time spent in an artificial womb did not affect the health negatively.

The technology has a few shortcomings that prevent its use on humans as well as the use of its full potential. However, there is plenty of scope for future research that can not only help save life of babies born preterm but also of all the mothers who die due to complications of childbirth

Despite the revolutionary nature of this technology, there also exist several ethical concerns ranging from the moral status of the embryo and the concern that a biological process will be commodified.

Keywords : artificial womb, healthcare, preterm babies.

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IDENTIFICATION OF DRUG CANDIDATES FOR BREAST CANCER-DRUG REPOSITIONING

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Abstract

Prevalence of breast cancer remains one of the major causes of death among women worldwide. Various new treatment modalities are available in markets like biological agents, immunotherapies which have great results and promises to deliver better treatment, but this treatment imposes financial constraints on the low- and middle-income countries. Drug repurposing is an alternative novel approach relating new clinical indications for old, clinical approved off patent drugs with known targets. Repositioning of drugs benefits us from data available on safety, efficacy, dosages, and clinical trials which are recorded for their primary indication. The advancement in genomics, proteomics and computational biology has simplified the process of repurposing. This novel pathway along with speeding up the process of drug development provides effective, safer and less side effects. Various research has been carried on the drug having the properties of CDK4/6 inhibition, cell cycle inhibition, mTOR inhibition and mitotic cell state inhibition for repositioning for breast cancer therapy. This review focuses on some of drugs under classes of Antidepressants (Imipramine), Antiepileptic (Phenytonin), Anti diabetics (metformin), antipsychotic (chlorpromazine) which have been reported to show the secondary indication of toxicity against the cancerous cells

Keywords: Drug Repositioning, Breast cancer, Secondary indication, Cytotoxic activity, Non cancerous drugs.

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HEALING OF NATURE DURING THE LOCKDOWN COVID-19

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Abstract

The climate is an important aspect of the protection of people and wildlife. COVID-19 in the 21st century poses a public safety threat. The SARS-CoV-2, which originated in December 2019 in Wuhan, China and spread to the area and to over 210 countries in the world today, is the first ever coronavirus pandemic. The pandemic COVID-19 has a major impact on most human activities, economics and health systems. The pandemic has culminated in a reduction in air emissions attributed to lockdowns, quarantines and boundary restrictions through decreased travel and development. Such positive environmental impacts are possibly only transient, but they can show how improvements in the way we live will contribute to direct positive environmental outcomes and indicate that steps to minimize transport, such as transportation, are useful. Recognizing that COVID-19 is mainly an environmental catastrophe, it will encourage potential actions with beneficial impact on the climate.

Keywords: COVID-19, Nature, Food supply, Diversity, Coronavirus, Biodiversity.

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NANOMEDICINE IN BRAIN CANCER TREATMENT

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Abstract

Glioblastoma is a malignant tumour of the brain. It is a fast-growing and hostile form of brain cancer. Delivering chemotherapeutic drugs to the brain is a challenging task due to the presence of the Blood-Brain Barrier (BBB). Nano-medicine provides a solution by virtue of its small size, the drug encapsulated drug particles can cross the BBB more effectively. Besides, it offers a number of other advantages pertaining to drug delivery to the brain. Through drug-loaded nanoparticles which offer high tumour specificity, increased drug loading capacity, and less toxicity that increases the efficacy of drugs. PLGA is a US FDA approved polymeric nanoparticle and due to its biodegradable nature and high biocompatibility, it can be safely used in humans. Delivery of drugs to treat brain tumours is mainly done by active targeting of the nanoparticles as it is more specific and can deliver a high concentration of drugs to the tumour site. Nano medicine has shown better survival rates and decreased side-effects in in-vitro cell line and in-vivo glioma bearing mouse models. It is still a developing field and is being seen as a next-generation therapeutic in the field of cancer.

Keywords: Blood Brain Barrier (BBB), Nanoparticles (NPs), Poly Lactic-co-Glycolic Acid (PLGA), Tumour specificity.

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MUCORMYCOSIS: FUNGAL INFECTION RE-EXPLORED

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Abstract

Mucormycosis is viewed as a deadly fungal infection happening in patients with hindered resistant immune response. These contaminants are getting dynamic, yet the endurance remains poor. A more profound knowledge of the pathogenesis of the sickness may incite future therapy. The mediation of mucormycosis, as Rhino-orbito-cerebral, aspiratory, scattered, cutaneous, or gastrointestinal is more in the patients who are having conditions like blood loss, low active bone marrow, neutropenia, solid organ transplantation, diabetes mellitus with or without ketoacidosis, corticosteroids, and deferoxamine haemochromatosis treatment. Mucormycosis is commonly found in immunocompromised hosts. Depending upon the state of the patient and the type of mucormycosis, infection rates could arrive at 100%. Basic therapy for ailment includes treatment with antifungals like amphotericin B drug. The primary unbiased and key focal point of examination of mucormycosis is related with the review and etiopathogenesis of mucormycosis, Management of Mucormycosis is drew on a multimodal system, including the modification of factors, the early usage of dynamic antifungal agents at appropriate levels, to prohibit harm to affected tissue and the utilization of various alternative medicines. . The ongoing advancements in indicative and remedial methodologies prove to be promising strategies to combat the disease. The current exploration and endeavors in for this infection quickens the identification of ligands and drug targets.

Keywords: Mucormycosis, Pathogenesis, Diagnostic, Drug target.

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NANOMEDICINE FOR THE TREATMENT OF BRAIN DISORDERS

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Abstract

Parkinson's disease (PD) is one of the most common neurodegenerative disorder which brings about the deficiency of dopaminergic neurons and a decrease in motor functioning. Most pressing issues while dealing with neurological disorders is the efficient delivery of drugs to the brain. Although the conventional oral route associated with the highest patient compatibility, brain bioavailability is often compromised due to presence of blood–brain barrier (BBB). The intranasal route has attracted an incredible deal of attention as a potential drug delivery pathway for the treatment of brain disorders. Polymeric nanoparticles, particularly the ones incorporating biodegradable polymers, have set the way forward for nasal drug delivery systems. The advantages of such polymeric nanoparticles are their small size, better uptake by cells, and the accumulation of drugs at the targeted sites. Drugs like Levodopa and Carbidopa are brought into treatment when severe symptoms are observed. It works when the brain cells convert it into dopamine. On the other hand, a drug called Amantadine is used when mild symptoms are shown. Non-steroidal anti-inflammatory drugs (NSAIDs) and Pramipexole dihydrochloride loaded chitosan nanoparticles are also majorly used in the treatment of the disease. However, Pramipexole dihydrochloride loaded chitosan nanoparticles displayed superior qualities than other formulations for brain targeted delivery through non-intrusive nasal route for treatment of Parkinson's disease. Nano medicines have proven better target delivery to the brain thereby reducing side effects indicating a promising future prospect for the treatment of brain disorders.

Keywords: Neurological disorder, Chitosan nanoparticles, Dopamine, Intranasal, Nanomedicine.

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NANOPARTICLES FOR THE TREATMENT OF ALZHEIMER’S DISEASE

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Abstract

Alzheimer’s disease (AD) is an irremediable and progressive neurodegenerative disorder, accounting for 60-80% of the total dementia cases. Around 5.8 million people in the United States age 65 and older live with Alzheimer's disease. The inability of most of the drugs to cross the BBB has resulted in slower development of new drugs for the treatment of CNS disorders. Nanoparticles provide better target delivery, increase the therapeutic efficacy, and reduce the incidence of side effects by restricting their localization in healthy tissues.Polymeric nanoparticles stand out as a key tool to improve drug bioavailability or specific delivery at the site of action. Cheng developed a stable curcumin loaded polyethy-leneglycol-polylactide (PEG-PLA) nanoparticle formulation using nanoprecipitation method, administered orally in order to improve bioavailability of drugs in the brain. Curcumin prevents aggregation by binding to Amyloid beta (Aβ). Curcumin nanoparticles' ability to penetrate the blood brain barrier to treat Alzheimer’s disease determines its therapeutic effects. This novel nanocurcumin may have great potential for AD therapy and can be a promising reference for future studies on formulation of drugs as nanoparticles. Biocompatible nanomaterials with increased magnetic and optical properties can act as excellent alternative agents for an early diagnosis. With the high volume of research coming in support of the effective usage of NP based drug delivery in the critical environment of CNS, it is quite likely that this approach can end up providing remarkable breakthroughs in early stage diagnosis and therapy of AD.

Keywords: Nanoparticles, Alzheimer’s disease, Polyethy-leneglycol-polylactide (PEG-PLA), Curcumin.

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DEVELOPMENT AND VALIDATION OF A SENSITIVE AND RUGGED METHOD FOR BIOANALYSIS OF RAMIPRIL AND ITS METABOLITE IN PLASMA SAMPLES

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Abstract

Bioanalytical techniques are being widely applied for quantitative estimation of xenobiotics and biotics in biological matrices such as blood, serum, plasma, proteins or urine. They are crucial for supporting new drug applications or biologics license applications. LC–MS/MS has become an important tool in pharmaceutical industry as it offers reduced analysis times, improved selectivity, and increased throughput in drug bioanalysis.In the present work attempt has been made to develop a novel bioanalytical method for estimation of antihypertensive drug Ramipril and its metabolite Ramiprilat in the plasma samples, by a hyphenated technique which includes fluid chromatography combined with mass spectrometry[LC-MS-MS],using Enalapril and Enalaprilat as internal standards.The developed method was validated as per the guidelines of InternationalCouncil for Harmonisation(ICH M10) for Selectivity, Specificity, Matrix Effect, Calibration Curve and Range, Accuracy and precision, Dilution Integrity, Stability etc. It exhibited a sensitivity i.e., Limit of Quantification of 1.09ng/mL for Ramipril and1.08ng/mL for Ramiprilat.The analytes, Ramipril and Ramiprilat were extracted from plasma by Liquid Chromatography-Tandem Mass Spectrometry using solvents mixture comprising of acetonitrile, methanol and 0.2% trifluoro acetic acid as mobile phase and Chromolith Speed Rod RP 18e Gold (50 x 4.6) column as stationary phase.The validated parameters were within the acceptance criteria as per the regulatory guidelines and the validated calibration curve (CC) exhibited r^2 value greater than or equal to 0.98 with high recovery.Hence it can be concluded that the developed method was specific,accurate,sensitive,and reliable to quantify Ramipril and its metabolite Ramiprilat in biological samples and can be potentially applied for Pharmacokinetic and bioequivalence studies.

Keywords: Liquid Chromatography-Mass Spectroscopy (LC-MS), Hyphenated techniques, Bio-analytical technique, Ramipril , Ramiprilat, ICH M10 guidelines.

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HYDROXYCHLOROQUINE INDUCED CARDIOTOXICITY

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Abstract

Hydroxychloroquine (HCQ) is a common antimalarial drug which has also been effectively used in the treatment of various rheumatic and auto-immunity diseases. Although the major side effects and drawbacks associated with this drug, such as Retinopathy, have been vastly studied and understood. However, the dimension of HCQ-induced cardiotoxicity has been generally overlooked due to its low frequency of occurrence. Several studies have shown that the occurrence of hydroxychloroquine-associated myopathy and hydroxychloroquine-mediated cardiotoxic effects, include rhythm disorders and the development of cardiomyopathy which have been exhibited in multiple clinical case studies. Furthermore, it is seen that Myocarditis is less common (estimated clinical prevalence is 3% to 15%) but has the potential to cause dilated heart failure. Subclinical left ventricular dysfunction is found in up to 71% of patients and has a broad differential diagnosis. Moreover, the increasing prevalence and duration of HCQ use make it increasingly important to understand the range of potential toxicities, however this has become increasingly difficult due to lack of common consensus on its mechanism of action, as well as the sudden exponential increase in its use in the treatment of COVID-19 has particularly highlighted the occurrence of much more complex forms of cardiac toxicities reported via extensively screening the patients. Therefore, a dire need arises to study the available case reports of cardiotoxicity to understand the mechanisms associated with cardiotoxicity and develop a thorough framework for efficient treatment which minimizes the occurrence of any HCQ-induced toxicity.

Keywords: Hydroxychloroquine, Cardiotoxicity, Cardiomyopathy, COVID-19.

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PHARMACOLOGICAL INDUCTION OF AUTOPHAGY AS A POTENTIAL THERAPEUTIC TARGET FOR JAPANESE ENCEPHALITIS

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Abstract

Japanese encephalitis (JE) is the leading global cause of viral encephalitis with a significant disease burden in India. One-third of JE infections are fatal, and one-third develop permanent neurological sequelae. Our research has established that the cellular homeostatic process– Autophagy, becomes dysfunctional during JE infection. Our studies suggest that autophagy enhancement can be neuroprotective in JE infection. Recent studies have shown the promise of using autophagy modulators to treat disease conditions. Several FDA approved drugs have been shown to enhance autophagy, and have the potential to be repurposed for treatment of diseases where autophagy upregulation is likely to be beneficial. Here we propose to check novel compounds and FDA approved drugs for their potential to modulate autophagy. One of the critical aspects of studying autophagy is measurement of autophagic flux (rate of degradation) is important to identify novel autophagy inducers and inhibitors. Here, we have established a stable mammalian cell line expressing the fluorescent probe GFP-LC3-RFP to evaluate autophagy flux using a high throughput imaging platform. We have utilized this assay to screen a drug library comprising 2560 compounds to identify autophagy modulators. In addition to known autophagy effectors, we have identified several novel autophagy inducers and inhibitors. These are currently being tested for their effect on JEV replication, neuronal cell death, and inflammatory responses.

Keywords: Japanese encephalitis, Autophagy, Fluorescent probe.

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ADIPOSE-DERIVED MESENCHYMAL STROMAL CELLS IN REGENERATIVE MEDICINE: NEW PERSPECTIVES AND CHALLENGES

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Abstract

Stem cells have been the subject of extensive research which introduces new possibilities for the treatment of various diseases. Mesenchymal stromal cells (MSCs) are multipotent cells with efficient immunomodulatory properties due to which they are considered as a promising source for externally grown tissue replacements and also for various metabolic disorders management. To increase the efficiency and resolve the several issues related to MSC, their biology and functions need to be studied and well clarified. Several studies have explained that the sources from which MSCs are isolated are diverse and might affect their properties. Main sources for MSC harvesting are bone marrow, adipose tissue and umbilical cord blood. Adipose derived mesenchymal stromal cells (AD-MSCs) are now being used to a much greater extent in clinical trials for regenerative medicine and for the real validation, randomized trials must follow strict guidelines such as (CONSORT) statement. Due to the paracrine activity and the multipotent nature of AD-MSC, it has potential to cure various degenerative and inflammatory diseases. AD-MSC serves as an excellent candidate for allogeneic treatments due to high proliferation capacity and easy access. The effectiveness of AD-MSC therapy depends on the robustness of the biological functions of AD-MSCs, which involve control of the heterogeneity and production process of source, and synthesis of biomarkers that predict desired responses. In future, studies need to be done to explore how AD-MSC therapy can be used to treat difficult to-heal wounds, pain, tissue scarring and standardization of preparation processes are needed. All these aspects related to the functional and technical understanding of MSCs and AD-MSCs and their potential,applications and current clinical trials will be discussed and summarized in this review.

Keywords: MSCs (Mesenchymal stem cells), Immunomodulatory, Adipose-derived MSC.

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PANCREATIC CANCER: BIOMARKERS FOR EARLY DIAGNOSIS

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Abstract

Current review presents the current scenario of biomarkers and biosensors for diagnosis of Pancreatic adenocarcinoma (PDAC). PDAC is the fourth leading cause of death worldwide. Diagnosis of cancer in the early-stage is essential for improving survival rates. We present the advantages of biosensors based on specific biomarkers as opposed to other time consuming and invasive conventional methods like biopsy etc. Various PDAC biomarkers are presented such as CA 19-9, CA 494, CA 242, MUC1, MUC4, MMP7, CEACAM1, MMP-9, TIMP-1,macrophage inhibitory cytokine (MIC), osteoprotegerin (OPG), ICAM-1, osteopontin (OPN), thrombospondin-2 (THBS2), carboxypeptidase A and haptoglobin. Amongst these, CA 19-9 has shown promising results in terms of early diagnosis. In addition to these, circulating miRNAs biomarkers for PDAC have also been discussed like miR-21, miR-155, miR-210, miR-938, miR-196a, miR-205, miR-210, miR-492, and mi-1427. However, specificity and sensitivity of individual biomarkers is poor, which is a major hurdle in development of diagnostic tools. Combination of protein, protein-miRNA, and only miRNAs could improve the specificity and sensitivity of PDAC diagnosis.

Keywords: miRNA, MMPs, PDAC, Biomarkers.

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MULTIPHASE CFD ANALYSIS OF SEPARATION OF BLOOD CONSTITUENTS IN A CENTRIFUGE

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Abstract

In this work, we perform three-dimensional computational fluid dynamics (CFD) simulation on a tube containing whole blood to analyze the serum-plasma separation process and its efficiency in a centrifuge. The CFD simulation is being carried out in ANSYS-Fluent software using its multiphase solver, wherein the blood is assumed to be composed of two phases serum and plasma in the ratio 7:3 by volume. The transient simulation using adaptive time-step for a sufficiently longer time is run such that the simulation attains a quasi-steady state at the end. Based on commercially available blood collection tubes, the length of the tube is taken as 12 cm inclined at a fixed angle of 40^o with the base of the centrifuge plate. The centrifuge is rotated about the vertical axis at a fixed rotational speed of 3000 rpm. The results of volume fraction of serum and plasma will be obtained with different diameters of the tube starting with a diameter of 1.7 cm. The outcome of this study will help us to find the optimum diameter of the tube for the best possible separation of the serum and plasma.

Keywords: CFD, Blood separation, Centrifuge, ANSYS-Fluent.

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PROTEOMIC ANALYSIS OF CARDIAC MYOBLASTS UNDER HYPERGLYCAEMIC CONDITIONS

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Abstract

Dysregulation of stress responsive proteins is considered as one of the early mechanisms initiating diabetic cardiomyopathy. In the present study we performed the proteomic analysis of glucose induced H9C2 cardiomyoblasts to assess the dysregulation of proteins and their implications in cardiac cell survival. H9C2 cells were treated with 25 mM dose of D-glucose and total cell protein was extracted. After estimating the protein concentration through Bradford assay, the samples (Control and glucose treated) were subjected to proteomic analysis through LC-MS/MS. Mass spectrometric analysis of peptide mixtures was performed using EASY-nLC 1000 system coupled to a Q Exactive HF mass spectrometer equipped with nanoelectrospray ion source. All samples were processed and raw files generated were analysed with Proteome Discoverer (v2.2) against the Uniprot Rattus norvegicus reference proteome database. A total of 2891 Proteins; 1351 Protein Groups; 4381 Peptide Groups were identified. The abundance ratio of proteins in cells treated with glucose as compared to untreated cells suggested that several proteins were downregulated with log2 value varying from -6 to +6. The most important of them were heat shock proteins (HSPs), enzymes regulating glucose metabolism such as pyruvate kinase, phosphoglycerate kinase, glyceraldehyde 3 phosphate dehydrogenase, fructose bisphosphate aldolase, ATP synthase etc. We also observed high abundance of Tropomyosin alpha-3 and Actin alpha cardiac muscle that regulate hypertrophic cardiomyopathy and dilated cardiomyopathy. This study provides in-depth information about the protein dysregulation that may be useful for interconnecting molecular networks regulating diabetic cardiomyopathy.

Keywords:*Diabetes mellitus*, Diabetic cardiomyopathy, Proteomic, LC-MS/MS.

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IDENTIFICATION OF MIRNAS UNDER HYPERGLYCAEMIC CONDITIONS IN CARDIAC MYOBLASTS

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Abstract

Diabetes mellitus (DM) is one of the major socioeconomic health problems around the globe, presently affects >180 million people and anticipated to rise to 450 million by 2030. Cardiovascular dysfunction is an important manifestation of DM and accounts for increased morbidity and mortality in diabetic patients. Moreover, mortality from cardiac diseases is approximately two-to four-folds higher in patients with diabetes than in patients without diabetes having similar manifestation of vascular diseases. Recently miRNAs have emerged as critical regulators of diverse aspects of cardiac function and dysfunction. The present study is designed to identify the miRNAs that depict differential expression when cardio-myoblast (H9C2 cell line) cells are cultured under hyperglycaemic conditions. H9C2 cells were treated with three different doses of D-glucose to mimic pre-diabetic, diabetic, and high-diabetic under optimal culture conditions. Small RNA libraries were generated and high throughput next generation sequencing was performed using Illumina NextSeq 550 sequencer. Data analysis revealed that a total of 373, 401, 379, and 395 known miRNAs were detected from untreated, and three treated samples respectively. The most abundant miRNAs found were let-7, miR-10, miR-154, miR-17, miR-30, and miR-181. Differential expression analysis revealed a large number of miRNAs as up-regulated as well as down-regulated. Target prediction, gene ontology and KEEG analysis revealed the potential role of these miRNAs in key molecular pathways such as insulin secretion, heat shock protein and others. In future, this study may provide a direction for specific miRNAs based studies as therapeutic targets for diabetic cardiomyopathy.

Keywords: Diabetes mellitus, diabetic cardiomyopathy, microRNAs, Next generation sequencing.

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ANTICANCEROUS DRUG INDUCED CARDIOTOXICITY: A MAJOR CONCERN

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Abstract

Cardiotoxicity is one of the serious toxic side effects associated with several types of drugs specially antineoplastic agents. Anthracyclines cause irreversible (type 1 drug-induced cardiotoxicity) cardiomyocytes necrosis and apoptosis. Reversible (type 2) cardiotoxicity is caused by biological drugs targeting proteins and regulating cancer cell proliferation. These proteins are also necessary for maintenance of cardiovascular homeostasis thus causing toxicity. Doxorubicin, an anthracycline drug causes ROS mediated DNA damage by intercalating thus preventing DNA synthesis.

With increasing cardiac patients day by day, there is an urgent need to develop safe and effective therapies with long-term relief and no associated side-effects. Natural products hold a great potential in preventing drug induced cardiotoxicity. Many herbal products have been identified with cardiotonic actions.Supplementing drugs with natural products may increase the therapeutic index of drugs in addition to various protective effects. The synergistic potential of drug and natural products may also be beneficial for developing future cardiovascular therapeutics. Medicinal herbs having both anti-cancerous, as well as cardioprotective effects may hold a great potential in drug induced toxicity.

Keywords: Cardiotoxicity, Anthracyclines, Natural product, Synergy, Medicinal herbs, Therapeutic index.

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ACE-2& CCR4 RECEPTORS: CRITICAL TARGETS TO COMBAT CARDIOTOXICITY

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Abstract

Different types of receptors can be targeted to treat cardiotoxicity. Some of these are ACE-2 receptor and CCR4 receptor. ACE-2 is found on lung cells and also on heart muscle cells which lines the blood vessels.CCR4 receptor(C-C chemokine receptor type 4) is a seven transmembrane G protein coupled receptor (GPCR) expressed throughout the human body with highest expression level in the bone marrow and lymphoid tissue. It shows both beneficial and deleterious effects in immune response. In recruiting immune cell to the site of infection it shows beneficial effect triggering immune response. CCR4 also plays deleterious role negatively impacting wound healing and causes sepsis. Drugs such as Hydroxychloroquine, targets ACE-2 and CCR4 receptor there for inhibiting their actions. Modulation of the receptor function by natural herbal products can significantly combat drug induced cardiotoxicity.

Keywords: Cardiotoxicity, ACE-2 receptor, CCR4 receptor, Immune response.

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APPLICATION OF OPTIMIZATION METHODS IN MENTAL HEALTH

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Abstract

Mental health is an indicator of emotional, psychological and social well-being of an individual. The optimization methods are applied in theory to solve the disease prediction accuracy problem in the early diagnosis of the mental health. The mental disorders are of many types such as depression, schizophrenia, bipolar disorder, post trauma stress disorder, anxiety. With high-throughput technologies, the amount of data generated has increased, generating complex and massive heterogeneous datasets, for many tools and methods have been developed for the data integration and its interpretation. The optimization methods can both be applied to both machine learning approaches as well as graph based-approaches. In semi-supervised learning method, the laplacian regularization constraints are applied to increase the accuracy performance of the machine learning methods. Similarly, the graph laplacian regularization is used to find the functional relation and the co-expression between the gene networks in the early survival prediction analysis. The other optimization methods includes the laplacian regularization, Elastic-net, lasso regression, and other integrated methods such as random walk laplacian regularization. Network-based analytics has been applied to the precision medicine. In this review article, we have reviewed the research articles that focused on the application of the optimization constraints in the early disease survival prediction in mental disorders.

Keywords: Optimization methods, mental disorder, integration methods, Laplacian regularization.

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COVID- 19 TRANSMISSION FROM MOTHER TO THE CHILD DURING PREGNANCY: A REVIEW

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Abstract

The Coronavirus Disease 2019 (COVID19) is a pandemic faced by humans all over the world. According to WHO, till December 2020, globally there are 76,382,044 confirmed cases with 1,702,128 deaths. The major mode of transmission of the virus include respiratory transmission, transmission via respiratory droplets, surface to human transmission and in some cases transmission through air was also seen. In this study, transmission of the SARS-CoV-2 (Severe Acute Respiratory Syndrome Corona Virus 2) from mother to the child has been studied. This also covers the effects of COVID-19 on the mother and new born child. It has been reported in Turkey that the age of approximately 1% of the total COVID-19 patients ranges between 1 day to 17 years. Out of this 1% cases, it was found that 50.4% were showing mild symptoms and around 0.8% had sever complication. The transmission of the virus from mother to child can be via vertical transmission or mother to fetal interaction at the time of parturition. Respiratory swabs of the child after the birth are used for checking the viral presence in the infant. Amniotic fluid, umbilical cord blood, and blood samples from the new born can be used to find where the transmission of the virus took place before or after birth. Among 33 neonates, 9% of them (3 infants) were tested positive for SARS-CoV-2 after 1 day of the birth. Various complication, like preterm births, low birth weight and fetal distress, has also been seen in the pregnancy based on the exposure of the virus and the stage of the pregnancy at which the mother is tested positive for the COVID-19. This study will be focused on all the aspects of the transmission from mother to child before the birth and after the birth.

Keywords: COVID-19, Viral transmission, COVID-19 in fetus, SARS-CoV-2.

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EXPLORING OF ANTICANCER POTENTIAL OF MOSAMBI (*Citrus limetta*) PEEL EXTRACTS

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Abstract

Citrus limetta particularly called known as Mosambi have been identified as an agent with utility in the treatment of different cancers. There are numerous strategies available in the market for the treatment of cancers but unfortunately apart from their benefits these methods have harmful side effects as well. Effective measures in the form of plants and herbs for the treatment of cancers are preferred as the peel extracts composition is inversely related with reduced cancer incidence and mortality rate due to the phytochemical content. Historical studies have identified that the mosambi peel contain flavonoids that possess cell proliferation, cell cycle regulation, increasing apoptosis, and metastasis. The peel has the biological properties for modulating the intercellular key pathways involved in the degenerative processes leading to the formation of cancer cell. The mechanism of action of the mosambi peel extracts inhibits cell proliferation by down regulation of oncogenes and cell cycle dysfunction by limiting the growth of signalling pathways. Polymethoxyflavones present in the peel induces cell cycle arrest instructions that medicate the signals to live or die by apoptosis. Thus mosambi peel extract acts as chemo preventive agents, anticancinogenic, antitumor. The present study focuses on exploring the anticarcinogenic effect of mosambi peel extract in cancer treatment, together with the underlying important molecular mechanism mediated by various mechanism mediated by various phytochemical compounds.

Keywords: *Citrus limetta,* Cancers, Peel extracts, Phytochemical, Anticancinogenic.

Session II

FOOD AND MICROBIAL BIOTECHNOLOGY

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MODULATION OF *STREPTOCOCCUS MUTANS* BIOFILM GROWTH BY *Lactobacillus rhamnosus*

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Abstract

Streptococcus mutans is facultative anaerobic coccus commonly found in the human oral cavity being highly efficient at forming biofilms contributing significantly to cariogenesis. Previous studies have suggested use of *lactobacillus* and *bifidobacteria* as probiotics preventing the of antimicrobial compounds produced by *Lactobacillus rhamnosus* on *S. mutans* biofilm formation. For this, rhamnosus was screened by coculturing with *S.mutans* and static biofilm of *S. mutans* was seeded with *L. rhamnosus*. Crystal violet quantification method was used for biofilm quantification. Our results show inhibitory effect with *L. rhamnosus* cells when co cultured with *S. mutans*. Use of cell free supernatant of *lactobacillus* on *S. mutans* showed similar inhibitory effect. *Lactobacillus* species are known to produce organic acid causing pH reduction, which might be the cause of biofilm inhibition. To eliminate we used pH adjusted conditional medium, which also recapitulated the phenotype. Phase separation of cell free supernatant was performed. Organic phase showed increased antibiofilm activity in comparison to aqueous phase. To understand which genes are being affected by our metabolite, gene expression studies were performed by qPCR with *lactobacillus* treated and untreated *S. mutans* cells. The expressions of genes involved in TCSTS, quorum sensing, EPS formation and cell surface adhesins was down regulated in rhamnosus treated *S.mutans* cells. Our data indicates that *lactobacillus* species is probably producing a small organic molecule which may be responsible for biofilm suppression of *S. mutans*.

Keywords: *Streptococcus mutans*, Biofilm inhibition, Lactobacillus rhamnosus, antibiofilm, qPCR.

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SYSTEMATIC ANALYSIS OF THE INDICA RICE PHD-FINGER GENE FAMILY AND THEIR RESPONSE IN SALINITY STRESS

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Abstract

The PHD finger family proteins are universally distributed among eukaryotes and involved in a variety of biological functions. In the present study, we identified 44 putative PHD finger proteins by genome wide analysis and found their distribution on all chromosomes except on 10. Multiple sequence alignment analysis showed the presence of conserved domain sequence in all the PHD finger proteins. These identified 44 PHD proteins were further classified into 10 subfamilies based on the phylogenetic relationship. Gene structure analysis showed large variation in the number of exon-introns but their organization were relatively similar for each group. Further, to study the expression of 44 PHD finger genes under salinity, RT-PCR was performed. The expression profile of 8 genes was found to be differentially regulated, among them two genes were significantly upregulated i.e., *OsPHD6* and *OsPHD12*. To decipher the possible role of both the genes under salinity stress, we have used the STRING database to perform *in silico* protein-protein interaction analysis. The interactions of both the proteins with other protein partners are directly or indirectly involved in development and abiotic stress tolerance. In conclusion, our study provides valuable information about indica rice PHD finger family and their response under salinity stress.

Keywords: PHD transcription factor, Abiotic stress, Rice, RT-PCR, STRING.

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ADDRESSING THE NON-SPECIFIC AMPLIFICATION IN RCA: A COMPARISON OF THREE DIFFERENT LIGATION TECHNIQUES FOR PREPARING CIRCULAR DNA

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Abstract

Rolling circle amplification or RCA is a sensitive, isothermal amplification technique used to detect a wide range of biomolecules, small molecules, and molecular pathways such as endonuclease and methylation assay. However, non-specific amplification originating from the choice of ligation process and the subsequent exonuclease treatment is a well-documented problem for RCA-based assay. In this research study, three types of ligation processes are investigated, namely, self-annealing ligation, splint-padlock ligation, and sticky end ligation for their role in non-specific amplification. It was found that the latter two, even after treatment with exonuclease I and III, showed a variable amount of non-specific amplification. Incidentally, splint-padlock ligation is also the classical way of circular DNA synthesis and continues to remain the most popular method. On the other hand, self-annealing ligation after exonuclease I and III digestion showed no trace of non-specific amplification. The absence of non-specific amplification is possibly due to its independence from the interaction of two or more DNA fragments for circular DNA synthesis. Through this quantitative study, we have hypothesized the mechanism for the non-specific amplification and have brought to light the advantages of adopting the relatively under-utilized circular DNA synthesis approach to avoid the non-specific amplification. The proposed method is robust, cost-effective, and accommodates broad future application, and is believed to improve the RCA based detection assay results.

Keywords: Amplification, Biomolecules, Endonuclease, Ligation.

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NEED FOR PROBIOTIC PRODUCTS

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Abstract

Probiotics are live microorganisms like bacteria and yeast, which proclaim to provide a healthy well-being by restoring and enhancing gut flora. It is usually believed that bacteria, yeast, or any other microbe can only cause infection and be harmful. But some microbes like *Lactobacillus*, *Bifidobacterium*, *Saccharomyces boulardii*help to cure various infections like diarrhea, inflammatory and irritable bowel, skin disease, oral health and many others. Antibiotics have been the first choice of treatment for infectious diseases over many years. Rampant usage of antibiotics and non-compliance amongst patients have led to the development of drug resistance bacterial strains. At times, these resistant strains can pose a significant health hazard. Probiotics can rebalance the microbial flora in the gut. They can reduce the chances and duration of infection. Both phenotypic and genotypic characteristics of probiotics are studied for the accurate surveillance and epidemiological studies. The microbes present in probiotics can restore the balance of gut, block pathogenic activities, improve barriers' function and can alter the immune response of the host. There are few disadvantages associated with the excessive use of such products like gas, bloating, allergy, discomfort in the gut. Overall, probiotics offer tremendous health benefits.

Keywords: Antibiotic resistance, *Bifidobacterium,* Gut microbiome, *Saccharomyces boulardii.*

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CLOVE (*Syzygium aromaticum*) AND BLACK PEPPER (*Piper nigrum*) AS PROMISING ANTIMICROBIAL AGENTS AGAINST COMMON FOOD BORNE PATHOGENS

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Abstract

Infectious diseases caused by pathogens, and food contamination caused by microorganisms, are compromising human health. The efficacies of antimicrobial agents and antibiotics, which are currently being used, have been weakened by microbial resistance, while antibiotic toxicity is another known challenge. This arises the need of natural antimicrobial agents. Spices and herbs have been used for centuries, to enhance the aroma of food, and for their antimicrobial and antioxidant activities. In this study, antimicrobial activity of aqueous and ethanolic extracts of five Indian spices i.e., Black pepper, Carom, Cinnamon, Clove and Cumin, was explored against *Esterichia coli* and *Staphylococcus aureus*, by agar dilution method and disk diffusion method. For agar dilution, aqueous and ethanolic extracts, with concentrations ranging from 0.5mg/ml – 8mg/ml, were used. Whereas for the disc diffusion method, varying concentrations of the ethanolic extracts (50%, 75% and 100%) were used. The results indicated an inhibitory effect on the growth of the microbes when using higher concentration of the extract. Clove and Black pepper showed best antimicrobial effects amongst all the tested spices. Amongst the tested spice extracts, Clove also had the biggest zone of inhibition (16mm), using 100% ethanolic extract, while Black pepper had a zone of inhibition of 20mm against *S. aureus,* using 100% ethanolic extract. Therefore, spices and particularly Clove and Black pepper extracts have great potential to be further tested and developed as novel safe antimicrobial agents.

Keywords: Antimicrobial activity, Spices, Agar dilution, Disk diffusion, MIC, Zone of Inhibition.

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QUORUM SENSING AND ITS ROLE IN VIRULENCE

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Abstract

We find ourselves facing a significant moment in modern health care where many antibiotics have lost their effectiveness in treating life-threatening and debilitating diseases. It brings up various difficulties for humans, animals and even plants to tackle with these new pathogens. With the ongoing emergence of antibiotic-resistant pathogens, there is a current need for development of alternative therapeutic strategies that will provide sustainable, long-term effectiveness against bacterial pathogens. This review focuses on a similar strategy which aims to interfere with the coordinated regulation of virulence factor production, rather than the virulence factors themselves, and summarizes the development and current status of strategies that target bacterial communication known as quorum sensing. Cell-cell communication, or quorum sensing, is a widespread phenomenon in bacteria that is used to coordinate gene expression among local populations. Its use by bacterial pathogens to regulate genes that promote invasion, defense, and spread, is a natural thing which can be used to our own advantage, against our competitors. The fact, they commonly benefit from social interactions and intercellular signaling, presents an opportunity to interfere with their ability to coordinate efforts to invade their hosts, whether human, animal, or plant. An antivirulence approach by which quorum sensing is impeded has caught on as a viable means to manipulate bacterial processes, especially pathogenic traits that are harmful to human and animal health and agricultural productivity. Compounds such as phenols, quinones, saponins, tannins, and alkaloids are able to override bacterial signaling. Herein we discuss the signaling mechanisms, potential anti pathogenic drugs like erythromycin, tobramycin, azithromycin and natural extracts like fungal extracts, plant extracts, oils that specifically target quorum-sensing systems. Techniques like, quorum sensing signal degradation, inactivation and inhibition of signal detection are reviewed here.

Keywords: Quorum sensing, Virulence, Pathogen, Host.

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GOAT MILK-A NECTAR BEHIND THE POISON

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Abstract

Goat breeding and farming is an important contributor to the economic growth of nations, especially the Mediterranean and middle east regions. One of the reasons is the awareness and analysis of the vital constituents and their therapeutic benefits. The impact and benefits of goat milk are known for around a century now and public health analysis of goat milk and its positive impact on infant mortality had been reported even before the nutritional components and their properties were explored. The metabolic conversion of all the carotene to vitamin A, enriches goat milk with significantly higher amounts of vitamin A than cow milk, equivalent to human milk. It is also a richer source of vitamins like Thiamin, Riboflavin and Niacin than cow milk.

Last decade had seen an exploration of the use of goat milk for developing probiotic products. The symbiotic fermented goat milk had shown good probiotic viability, sensory acceptance, good nutritive value in terms of Calcium and Potassium level and protein content and higher acceptance. The awareness and exploration of prebiotics in dairy products have been attracting the attention of the global scientific community and the story is not different for goat milk. Recent studies have explored around fourteen oligosaccharides with prebiotic potential and ability to modulate the growth of *Bifidobacterium* sp., and *Lactobacillus* sp., a peculiar property of prebiotics. Moreover, five of these oligosaccharides resemble those in human milk. Anti-pathogen properties analysis of such oligosaccharides had revealed their ability to reduce the adhesion of *E.coli* and *S.typhimurium* on human epithelial cells (Caco 2), thereby minimizing competition among pathogenic and probiotic bacteria in gut.

The exploration of the detailed mechanism of the bioactivity and anti-pathogenic properties of the recently discovered oligosaccharides will pave the way for developing a fortified formulation with higher nutritive value and efficacy

Keywords: Goat milk, Vitamins, Oligosaccharide, Prebiotics, Probiotic, Oligosaccharide.

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AGEING, DAIRY PRODUCT CONSUMPTION AND PROSTATE CANCER RISK

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Abstract

Prostate cancer is the second most common cause of cancer deaths in men in most developed countries, and the incidence has increased significantly over recent years. It is estimated that less than 5% of all prostate cancer is hereditary. The risk of prostate cancer is increased by a factor of 1.3 if there is an affected father in the family, and by a factor of 2.5 if there is a brother who has prostate cancer.

Age is the most important risk factor. Prostate cancer is rare under the age of 40, and its incidence increases exponentially with age. There is a varied geographical incidence. The age standardised mortality rates vary from country to country ,it being 0.1 per 100 000 in Thailand to 30 per 100 000 in some parts of the West Indies. Studies of migrant populations have suggested that environmental factors are at least as significant as race. Environmental factors implicated in prostate cancer include a high intake of saturated fat and low level of dietary selenium, vitamin E, and vitamin D.

An ongoing controversy exists regarding the effect of dairy products on prostate cancer risk in observational studies. After calculating pre-diagnostic intake of individual or subgroups of dairy products using a validated food frequency questionnaire, it was estimated that the hazard ratios (HR) and 95% confidence intervals (CI) for pathologically-verified cases of incident prostate cancer among men, overall, or stratified by severity. Among 49,472 men, 4134 were diagnosed with prostate cancer during an average follow-up period of 11.2 years. The median total dairy intake was 101 g/1000 kcal. Consumption of total, individual, or subgroups of dairy products was not statistically significantly associated with prostate cancer risk overall or stratified by severity, except for regular-fat dairy product intake with late-stage prostate cancer risk and 2%-fat milk intake with advanced prostate cancer risk.

Keywords: Hazard Ratio, Confidence Interval, Pathologically verified, Dietary selenium.

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EFFECT OF UV-B IRRADIATION ON BIOACTIVES OF EDIBLE MUSHROOM POWDER

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Abstract

Utilizing food as a medicine in the traditional system was very popular and one such traditional cure comprises using medicinal mushroom having therapeutic value. The present research is an attempt to enhance the vitamin D_2 content in the dried powder of xylotrophic edible mushrooms using Ultraviolet (UV-B) irradiation at different time points (0 h - 2.5 h). HPLC studies depicted a significant augmentation in vitamin D_2 concentration after an irradiation period of two hours. The enhanced vitamin D_2 enriched dried mushroom powder exhibited an elevated level of Total Phenolics and Flavonoid contents. GC MS analysis was performed to further explore the impact of UV irradiation on the bioactive profiles of UVB irradiated and non-irradiated samples of dried mushroom extracts. Color changes were evaluated using the Hunter color system. The study demonstrates the use of a sustainable approach for enriching the nutraceutical quality (vitamin. antioxidant etc.) of mushrooms which play an important place in human nutrition especially during the current pandemic of COVID-19.

Keywords: Nutraceuticals, Vitamin-D_2, Mushrooms, Sustainable approach, UV-irradiation.

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EXTREMOPHILES: MEDICAL POTENTIALS EXPLODE

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Abstract

Biotechnology has unimaginable potential which can greatly affect our lives in very interesting ways and to make our lives easier while upgrading our standard of living. We have various kinds of industries like food, medical, laundry detergent industry etc. Chemical reactions take place during production at highly extreme conditions like very high or low temperature or pH or pressure or salinity. These chemical reactions require catalytic enzymes to catalyze the reaction and traditionally we have been using enzymes from mesophilic origin. But researchers have found extremophiles as most suitable for these reactions. These are more tolerant and are designed to thrive in extreme environmental conditions. Due to the study of extremophiles, researchers were able to understand the process of evolution more clearly. Extremophile term is given based on the extreme environmental condition in which the organisms can optimally grow. The systems by which various life forms adjust to outrageous conditions, give an exceptional point of view on the key qualities of organic procedures, for example, certain macromolecules balance out in one or more lethal environmental conditions. These organisms have adapted biomolecules and peculiar biochemical pathways, also its property of stability and activity at one or more extreme conditions is appropriate to use them as alternatives to different molecules. Few extremophiles have found their way into large scale use in the field of Biotechnology. Microorganisms have been killing each other for their own survival. So humans took advantage of this natural phenomenon to cure many diseases. If some of these microorganisms were pathogenic then some were also used to produce antibiotics, anti-fungal. Extremophiles have largely contributed to the medical industry from producing bio-plastics (PHAs-polyhydroxyalkanoates) to generating alternative vaccine delivery systems.

Keywords: Extremophiles, Extreme conditions, Tolerant, Medical industry, Polyhydroxyalkanoates.

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STUDY THE DETECTION OF AFLATOXIN B1,B2,G1,G2 IN COMMERCIALIZED INFANT FORMULA

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Abstract

Occurrence of aflatoxins contamination are worldwide concern in food products. Food security is a multifaceted aspect covering nutrition, availability, sufficiently, accessibility and safety. The biggest hindrance in attaining food security was less productivity due to lack of enough resources. In order to increase the availability and produce sufficient food, malpractices like growing food on contaminated land or using untreated wastewater for irrigation came into play. Such practices have led to transfer of toxic heavy metals and harmful toxins Aflatoxin in food crops. Baby milk products and cereal products are available in pharmacies, in the local market are important for newborns and infants that are not breastfeed. Aflatoxins were investigated in some baby food product samples obtained from the local market in India. The study shows a test for the presence of harmful carcinogenic Aflatoxins B1, B2, G1, G2 by HPTLC at under fluorescence light 366nm in formula milk aged for 6 month to 12 months baby and their levels within or beyond standards limit. The study shows that the samples analysed, do not represent harmful aflatoxins for newborn and infants. The result also indicated negative for the presence of aflatoxin levels that complies within the permissible limit in baby food products. This study is important because of concern around the complex risk assessment of baby food products available in pharmacies.

Keywords: Aflatoxin, Heavy metals, Baby food.

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INSIGHTS INTO BACTERIAL CELLULOSE BIOSYNTHESIS

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Abstract

There has been a surge in the demand of bio based polymeric materials owing to environmental, safety and economic issues associated with the synthetic polymers. This has shifted the research paradigm to explore new sources of biomaterials which are sustainable and eco-friendly. In this context, Bacterial cellulose (BC) has gained attention worldwide owing to its network structure and excellent physicochemical properties such as biocompatibility, biodegradability, improved mechanical strength etc. This polymer has been recognized for a wide range of industrial applications in various biological and non-biological sectors. BC is a significant common biopolymer delivered by different bacterial strains and *Komagataeibacter xylinus* has been used as the model organism for the production of BC.

Bacterial cellulose biosynthesis is particularly regulated by a multi-step reaction mechanism which involves membrane-integrated cellulose synthase (*CeS*) complexes activated by c-di-GMP. Improvement in molecular cloning techniques resulted in determining the bacterial cellulose synthase (bcs) operon for the cellulose synthase. The structure of bc operon consists of several genes (*bcsA, bcsB, bcsC, bcsD*) at upstream promoter sequence which combinedly operate the formation of cellulose microfibrils. These functional subunits play key roles in determining the quantity and structure of derived biofilms with the process of substrate recognition (initiation), step wise elongation and translocation. This study focuses on current knowledge in genetic organization of cellulose synthase operon, function and cellulose biosynthesis regulation.

Keywords: Biocompatible, Biodegradable, Biomaterial, Bacterial cellulose, Cellulose synthase.

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FUNCTIONAL PROPERTIES OF BIOACTIVE PEPTIDES DERIVED FROM MILK

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Abstract

There are many health perks that are link with the dairy products. They are good originator of nutrients such as lipids, minerals, carbohydrates, protein (bioactive peptides) and vitamins, which are basic requirement for development, alignment and growth of human body. In human diet, milk acts as essential protein source. Hence, they are most focus compound present in contrasting dairy products. Some of the most sufficient milk proteins are β-lactoglobulin, α-lactalbumin, α-casein, β-casein, and κ-casein. These proteins are main birthplace of bioactive peptides which constituent milk. Dairy bioactive compound can be analyze as immunomodulant, antihypertensive, antimicrobial, anti-mutagenic, anti-obesity, mineral-binding agents and opioid build on their biological functions. These bioactive peptides can be easily extracted from their native structure by enzymatic hydrolysis, gastrointestinal digestion and during fermentation. Hence, many fermented dairy products like cheese, yogurt and sour milk which are used worldwide are treated as admirable source of dairy peptides. They are also related with the lowering the risk of stroke, cancer and hypertension. The current review article is an attempt to propagate the information of dairy peptides and their health benefits.

Keywords: Milk, Bioactive peptides, Fermentation, Protein.

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MILLETS: AN EMERGING NEW TREND IN FUNCTIONAL FOOD

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Abstract

In the last few decades, the progress witnessed in nutritional science has highlighted the value of food as a source of personalized therapeutics. Food acts as a natural matrix that delivers not only nutrients but also certain biologically active constituents that have important health implications. Therefore, it becomes necessary to look out for potential food sources that can offer a range of these compounds and thus act as preventive medicine for human well-being. Millets are emerging as one promising candidate in this endeavor. Millets have been known to mankind for many years. They are easy to grow and require less amount of water. It has also been recognized that incorporating millets in mainstream agriculture can ensure diversity and sustainability of the food supply chain. A growing number of scientific publications suggests that millets harbor many compounds with antioxidant, anti-cancerous, antihypertensive, and many other functionalities yet to be completely characterized. Millets are also a good source of prebiotics and various processing strategies applied to millets have been shown to drastically improve their nutritional and biological properties. However, functional millet-based food product development is still in its infancy. Therefore, a concentrated effort is needed to develop and investigate this valuable resource for its role in human health and bring to our daily diet.

Keywords: polyphenols, anti-oxidant, fermentation, malting, germination.

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URBAN INLAND WATER BODIES AND MICROBIAL SHIFT

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Abstract

Inland water systems are aquatic environments enclosed within land boundaries containing freshwater for human consumption. They are of the utmost economic and ecological importance. These water bodies hold a dynamic range of micro-organism which are regulated by the local environment. These micro-organisms occupy the lowermost position in the hierarchy of the aquatic ecosystem; thereby they are the major executor in nutrient cycling and the food chain. However, these microbial ecosystems are under adversity due to urbanization. An aggressive increase in population has not only led to significant demographic changes but increased ecological footprint as well. But, the structure and pattern of the microbial community remain underexplored than those of higher-level organisms. In this review, we aim to document the effects of urbanization on the structure and functioning of inland water microbiology. With a progressive urban ecosystem, there is a critical need for understanding the microbial community shift. Simultaneously, the identified microbial community can further be used for commercial and environmental benefits.

Keywords: Inland water bodies, Population growth, Wastewater treatment, Urbanization, Microbial shift.

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EVALUATION OF THE LICHEN *Parmelia sp*. FOR MOLECULES OF HIGH MEDICINAL VALUE

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Abtract

The increase in antimicrobial resistance (AMR) has led to the exploration of new and unexplored flora and fauna for obtaining new antimicrobials that may contain novel chemical pathways to counter AMR. Bioprospection from niche habitat or species can elaborate promising new molecules. Lichens have been less studied for their antimicrobial properties. *Parmelia saxatilis*, known as the salted shield lichen or crottle, is a type of foliose lichen, with a greenish-gray to somewhat bluish gray thallus. It normally grows on stone, but also on bark or wood sometimes. It is utilized to make dyes with rusty orange tones. Various literature have reported the medicinal properties of *Parmelia sp.* This research focuses on evaluation of those compounds that have been reported in *Parmelia saxatilis* and can act as potential drug molecules in future. The compounds reported in Parmelia were studied for their medicinal properties and their drug likeliness was evaluated using ADMET analysis. The medicinally potent compounds were evaluated using the Lipinski's Rule of Five and were shortlisted on the basis of given criterias. The results stated that out of 17 reported compounds, five showed the potential to be drug molecules in future.

Keywords: Lichens, Antimicrobials, Antimicrobial Resistance (AMR), ADMET Analysis, Lipinski's Rule.

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METABOLIC INTERVENTIONS OF GUT MICROBIOTA IN DIABETIC CARDIOMYOPATHY

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Abstract

Diabetes and its associated complications are contributing great major concern globally by increasing the burden of diseases and mortality rate per year. Diabetes associated structural and functional changes in heart known as diabetic cardiomyopathy. It correlates with the adaptation of poor life style, genetic disorder, polluted environment and unhealthy diet. Although, many medicinal treatments are available to treat diabetes and its associated cardiac complication like cardiomyopathy, still death rate is reported to increase drastically. Recent studies have found the link between the human microbiota especially gut microbiota with various human pathologies and could be proposed a natural way to treat the chronic diseases such as diabetes and cardiac diseases. In this article, we reviewed how the gut microbiota and their metabolites can modulate human health and also discusses about the disease specific dysbiotic conditions as a new way of therapeutic strategies. We also propose use of prebiotics to improve the dysbiotic conditions.

Keywords: Diabetes, Diabetic Cardiomyopathy, Gut Microbiota, Dysbiosis, Metabolites.

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GENETICALLY ENGINEERED MICROORGANISMS FOR THE DEGRADATION FOR ENVIRONMENTAL POLLUTANTS

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Abstract

Rapid advances in urban and industrial activities has a major impact on the environment due to discharge of hazardous waste into the immediate surroundings. The traditional remediation technologies namely physical and chemical technologies are being applied extensively but these methods show certain limitations. Thereby, it is essential to look for alternative technologies which are relatively safer and cost effective. Microbial biotechnology assisted technologies, including those using genetic engineering can prove to a promising strategy and can provide efficient engineered micro-organisms with increased remedial abilities with greater adaptability to the surrounding conditions. Genetically modified organisms (GMOs) are inserted with particular genes which can alter a specific mechanism, thereby increasing resistance towards a particular compound, metabolizing and remediating the pollutant. The present study would critically discuss in detail the role of GMOs in bioremediation of environmental pollutants along with the challenges and future perspectives.

Keywords: GMOs, Pollutants, Remediation.

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MICROBIOME

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Abstract

Microbiome is the community of microorganisms living together in a particular habitat. It is like a complex ecosystem of all life forms. All plants, animals and human beings have their own unique microbiome. For example human gut microbiome is essential for digestion and nutrition but it also plays a major role in cancer.The skin is the human body's largest organ colonized by a number of microorganisms most of which are harmless or even beneficial to their host. Microbiome also play an important role in food security particularly related to crops and livestock. Microbiome research is still going on but with modern technology it is possible to sequence the DNA of entire microbial community and study the thousands of genes and proteins that microbiome contains. In the future the more wide understanding of microbial life could help us to treat diseases, protect environment and harness the power of earth's ecosystem. The human microbiome project initiated by the national institutes of health in 2007 has identified microbiota at various surfaces of human body. However microbiota changes with the changing environment during maturation. The microbiome develop early in life may affect the development of chronic lung disease for example asthma and atopy in later life. Further research is needed to unfolds the mechanisms underlying the health benefits of probiotics. Now, the microbiome has become a hot topic in the world of science. It provides a new understanding of human health and disease.

Keywords: Microbiome, Microbiota, Probiotics, Atopy.

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MINING FOR NONRIBOSOMAL PEPTIDE SYNTHETASE AND POLYKETIDE SYNTHASE OF *Burkholderia* SPECIES GENES WITH EXTENSIVE POTENTIAL FOR BIOTECHNOLOGICAL USE

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Abstract

Burkholderia is a significant genus that includes several species, including both pathogenic strains and strains that promote plant growth. While a rich secondary metabolism is shown by the *Burkholderia* metagenome, the genes have not been investigated yet.The diversity of nonribosomal peptide synthetases (NRPSs) and polyketide synthases (PKSs) genes in *Burkholderia* was investigated by in silico data mining to analyse NRPS and PKSs with the aid of whole genome-related gene analysis. The biosynthetic pathway of NRPS sequences resemble to that of the *Protebacteria* phylum, whereas PKS sequences resemble with *Actinobacteria*. Analysis revealed the number of nonribosomal peptide synthetase (NRPS) clusters with the ability to synthesise at least 11 novel products, the majority of which are siderophores or lipopeptides, two product groups with potential biocontrol applications. The strategy led to the identification, for the first time, of the cluster for Isariin compound that matches the peptide monomers obtained. As microbes gradually demonstrate resistance to the current classes of antibiotics, peptides will play a very significant role in drug production. In peptide-based drug preparation, the use of NRPS studies will also play a crucial role, as it will be easy to recognise endophytes with the ability to generate peptides.

Keywords: Metagenomics, Endophytes, NRPS, Comptaional NRPS-PKS analysis, *Burkholderia*, genome mining.

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CURRENT TRENDS IN FUNGAL CHITOSAN PRODUCTION AND APPLICATIONS

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Abstract

Environmental problems associated with the use of synthetic polymers has raised public awareness and increased demand for safer and sustainable substitutes, resembling synthetic properties in terms of the characteristics. Polysaccharide based biopolymers possess material properties relevant to various industrial and biomedical applications such as pharmaceutical, cosmetics, biomedical, biotechnological, agricultural, food and non-food industries such as paper, textile and water treatment., making them an excellent candidate for replacing synthetic polymers. Chitin and chitosan are natural biopolymers, found in the exoskeletons of insects and crustaceans and as a cell wall component of fungi. Chitosan has been receiving wide attention worldwide due to its versatile nature and excellent physicochemical properties such as biodegradability, bioactivity, biocompatibility, bioresorbtivity, non-allergenic, non-toxicity and good adsorption properties. Chitin is a polymer of acetyl-D-glucosamine residues. Chitosan is the deacetylated derivative of chitin formed by alkaline treatment, further adding to environmental pollution. Recent focus has shifted towards the role of chitin deacetylase for enzymatic deacetylation of chitin. Fungal biomass generated as the major byproduct of most industrial fermentation processes, can be effectively utilized for production of fungal chitosan. A sustainable biorefinery approach could result in effective utilization of industrial fungal waste and production of biopolymer. Current production strategy focuses on utilization of low cost agro industrial residues for cost effective production of fungal chitosan. This review focuses on recent developments in the production and application areas of fungal chitosan.

Keywords: Fungal chitosan, Chitin, Deacetylation, Biocompatible, Bio refinery, Sustainable, Biopolymer.

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BACTERIAL CELLULOSE COMPOSITES: AN ADVANCED BIOMATERIAL

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Abstract

Past few decades have witnessed increased interest in development of bio-based polymeric products which are sustainable and environmentally safe. Various types of biopolymers are reported to be produced by microorganisms. In this context, Bacterial cellulose (BC) also known as microbial cellulose, is a microbial extracellular polysaccharide, which has gained attention as an emerging advanced biomaterial. BC is produced by bacterial from widely known genera including *Gluconacetobacter, Agrobacteria, Aerobacter, Rhizobium, Sarcina* by oxidative fermentation. BC possess excellent physicochemical properties such as high purity, porous network structure, high crystallinity, improved mechanical strength, high degree of polymerization, high water retention ability, compared to plant cellulose. This versatile nature of BC has resulted in increased demand in various industrial and biomedical applications including paper and pulp, food, waste water treatment, pharmaceutical, cosmeceuticals etc. Despite of excellent properties, pristine BC exhibit lacks of flexibility and bioactivity which limits its application in various fields.

To enhance the physicochemical properties and the application potential of bacterial cellulose, Bacterial cellulose composites are synthesized. Currently, there are several synthesis techniques used for synthesis of BC composites, based on the nature and properties of the reinforced material. Till date, BC composites have been successfully synthesized using chitosan, alginate, collagen, graphene oxide to improve biological and conductive properties. etc. BC composites have shown improved performance in wound healing and have also been successfully employed in biosensors, display, electrochemical devices, loudspeaker membranes, bone tissue regeneration and enzyme immobilization. This review summarizes various synthesis strategies for BC composites and their applications.

Keyword: Bacterial cellulose, Biopolymer, Sustainable, BC-composites, Enzyme immobilization.

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IN-SILICO DRUG SCREENING STUDIES OF POTENT INHIBITORS AGAINST MAIN PROTEASE (MPRO) FOR COVID-19.

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Abstract

Covid-19 has emerged as a global outbreak which has affected the lives of many and also challenged the health care sectors in different countries. Several *in-silico* researches have already been done by different researchers for screening of different products be it natural or chemical based for the possible treatment of COVID-19. SARS-CoV-2 structure is very recent, and the development of novel drugs are in recent needs. Currently, there is no successful treatment available which can directly cure this viral disease by directly inhibiting the main viral protein that is main protease Mpro. *In-Silico* drug screening serves as a good tool to screen drugs before their synthesis in labs. Molecular docking has always been a successful and easy platform to conduct *in-silico* docking for several drug candidates. The screened ligand which showed good potency to inhibit Mpro were quercetin with binding energy -5.96, epigallocatechin gallate with binding energy -6.57, curcumin with binding energy -5.79 and eucalyptol (1,8 cineole) with binding energy -5.94. Among these four ligands, two ligands which exhibited better potency by displaying the least energy were quercetin and epigallocatechin gallate. So, quercetin and epigallocatechin gallate could be used as an option to treat coronaviruses. This work paves a way for inhibiting Mpro that can possibly suppress the infection and serve as a drug candidate.

Keywords: Covid-19, SARS-COV-2, viral disease, Mpro, in-silico screening, molecular docking, ligand, binding energy, drug candidate.

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AN INTEGRATIVE BIOINFORMATICS ANALYSIS FOR IDENTIFYING HUB GENES IN HUMAN IMMUNODEFICIENCY VIRUS

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Abstract

The inability of modern medicine to find a cure for human immunodeficiency virus (HIV), the causative agent of acquired immunodeficiency syndrome (AIDS), has made HIV as one of the most dreadful pathogens of this century. The present study retrieves the putative drug targets and biomarkers of HIV using *in-silico* analysis. Microarray data analysis of datasets that involve HIV cases vs controls was done in order to scrutinize the differentially expressed genes (DEGs). From this data a total of 57 up-regulated DEGs and 108 down-regulated genes were obtained. The functional annotation and pathway analysis of the DEGs was done in order to get the enriched biological processes and pathways. The significant genes that were obtained for HIV datasets were 'Protein Kinase C Alpha (PRKCA)', 'Signal Transducer and Activator of Transcription 5B (STAT5B)', 'Krupple Like Factor-6 (KLF6)', 'Granzyme K (GZMK)', 'T-cell Immunoreceptor With Ig and ITIM Domains (TIGIT)', 'Ectonucleoside Triphosphate Diphosphohydrolase 1 (ENTPD1)', 'Regulator of G protein signaling 1 (RGS1)', 'CD48 Molecules (CD48)', 'Cytotoxicity and Regulatory T-cell Molecule (CRTAM)', and 'Neutrophil Cytosolic factor 4 (NCF4)'. The network and topological analysis was done for these genes for better understanding of their interaction. The present study suggests that the significant DEGs and the associated biological processes and pathways may have the potential to be utilized as possible drug targets and biomarkers in the prognosis, diagnosis as well as treatment of HIV and warrants for further experimental validation.

Keywords: HIV, microarray analysis, PPI interactions, functional annotation, pathway analysis, topological analysis.

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GENOMIC ANALYSIS OF CIPROFLOXACIN INDUCED *Salmonella typhimurium* MUTANTS

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Abstract

Nontyphoidal *Salmonella* is one of the food-borne pathogens and treated with ciprofloxacin. The evolution of drug resistance was studied by subjecting the wild type strain to ciprofloxacin 10 times its minimal inhibitory concentration (MIC) for 20 cycles. The mutants obtained had 100 fold of the initial MIC. The whole genome sequencing showed 40513 SNPs distributed in 3843 genes and in that pool, 2124 were non-synonymous. Out of these 80% were transitions and 20% transversions with a ratio of <1 indicating a positive selection. The SNPs were distributed throughout the genes with <50 mutations in some genes while only 1-2 alterations were observed in others. The location of SNPs covers the chromosome as observed for the genes *dnaE*, *gyrA,iroC*, *metH* and *rpoB* point mutations. Many biological pathways were affected by mutation, the affected pathways were mapped to Gene Ontology (GO) Biological Processes at both David and Panther ontology databases. Both the databases showed that most affected pathways were transcription regulation, transmembrane transport, cell adhesion, pathogenesis, pilus assembly, oxidation-reduction mechanisms, phosphor-relay signal transduction and LPS biosynthesis. Besides the common results, DAVID database showed that pathways involved with DNA replication, amino acid transport and ion transport had more than 5 genes mutated while Panther database showed that proteolysis, methylation and chemotaxis had several genes mutated. We propose that development resistance to ciprofloxacin is due to the mutations in these genes. The 3D structure of *gyrA* shows Ser83 is replaced by phenylalanine, the most common cause of quinolone resistance.

Keywords:*Salmonella*, MIC, whole genome sequencing, SNP, non-synonymous, mutation.

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IN SILICO CHARACTERIZATION OF POTENTIAL BIOMARKERS IN PROSTATE CANCER ADENOCARCINOMA

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Abstract

Prostate adenocarcinoma is the most common type of prostate cancer found among men of all ages. The commonly used biomarker for testing prostate cancer like prostate specific antigen (PSA), has its shortcomings like low specificity, which leads to the overtreatment or over-detection of prostate cancer. Therefore, the need for new potential biomarkers arises for better diagnosis and therapeutic interventions. Protein-protein interactions are relevant in cancer and can be used to find biomarkers as their differential expression indicates the ability of a protein to bind to its protein-binding partner. The bioinformatic analysis of mRNA differential databasesavailable at EMBL-EBI Expression Atlas, was used to create a protein-protein network on Search Tool for the Retrieval of Interacting Genes/Proteins (STRING). The data generated 177 nodes or proteins at a medium confidence interaction score of 0.4 along with a clustering coefficient of 0.668 and a Protein-Protein Interaction (PPI) enrichment p-value lesser than 1.0e-16. The identified genes, further characterized through Gene Ontology (GO) revealed their involvement in apoptotic, calcium ion trans-membrane and cell migration pathways, that are highly significant in prostate cancer progression. The use of Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways tool highlighted that certain common proteins were involved in pathways of prostate cancer and that of type II diabetes, colorectal cancer, pancreatic cancer, cardiomyopathy, and viral myocarditis. Further, the CYTOSCAPE analysis, a confirmation of reported mutated genes from The Cancer Genome Atlas (TGCA) database, and through Gene Expression Profiling Interactive Analysis (GEPIA), the potential biomarkers were characterized.

Keywords: Differential expression; Gene Expression Profiling Interactive Analysis (GEPIA); Gene Ontology (GO); Kyoto Encyclopedia of Genes and Genomes (KEGG); Search Tool for the Retrieval of Interacting Genes/Proteins (STRING).

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BIG DATA ANALYSIS OF ALZHEIMER'S DISEASE FOR EARLY PREDICTION

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Abstract

The devastating condition of Alzheimer's disease (AD) affects up to 50 million of humans globally. The biggest risk factor for AD is age and for the first time in history, there are more people over the age of 65, than there are under the age of five, making AD one of the greatest challenges of our time. Dr Alois Alzheimer discovered the disease over 120 years ago nevertheless, the current worldwide recovery rate for AD patients is zero percent. Enormous amounts of data that is generated by healthcare transactions and AD research on a daily basis. Researchers collect this health data from patients to determine the amount of cognitive decline and if it is significant it leads to dementia. Thus, the data obtained is too complex and voluminous to be processed and analyzed by traditional methods. Data mining provides the methodology and technology to transform this complex data into useful information for decision-making. This paper explores data mining applications to make a data-driven machine learning model which is based on large-scale administrative health data in AD risk prediction. By applying a sorting model to the big data available on the databases, we first sorted the data accordingly, to determine the functional parameters. We trained and validated random forest, support vector machine and logistic regression to predict the incidence of AD in a patient. Then we applied logistic regression for parameter estimation and a dynamic prediction framework for predicting the future outcome trajectories and risk of dementia of patients, based on the functional parameters. By this model, we can predict in advance the possible chances of developing AD in an individual, by using functional parameters selected by the sorting of big data.

Keywords: Alzheimer's Disease, Computational analysis, Functional Data analysis, Logistic Regression, Prediction model.

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BINDING ENERGY COMPARISON OF ANTIBODY-ANTIGEN INTERACTION IN SARS-COV-2 WITH RESPECT TO ANTIBODY DEPENDENT ENHANCEMENT

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Abstract

Antibody Dependent Enhancement (ADE), is a phenomenon where premature, non-inactive or inadequately neutralizing antibodies enhance the ensuing viral entry into the cells due to which infection is increased. There are some viruses where the impact of ADE has been shown to be valid for ex.- Ebola, Dengue, Zika virus, and most importantly coronavirus (CoVs), etc. In the case of SARS-CoV-2 as we know that SARS-CoV-2 is a quickly spreading infection that represents a significant weight on worldwide human wellbeing and the economy. Presently, there is no immediate proof of the event of ADE in patients with SARS or with COVID-19. So, it is essential to create immunotherapeutics against SARS-CoV-2.

In this study, we examined the binding energy of antigen-antibody interaction which includes a sophisticated reaction of the immune system. The binding antibodies and antigens have high selectivity and affinity. In ADE binding, antibodies bind the viruses on the surface of immune cells with the help of receptors. It enables the entry of the virus and enhances the infection instead of protecting. In our current work, we have investigated the protein-antibody complexes of different viruses that are involved in ADE or without ADE mechanism with the help of PDB database. Further, we have tried to compare the binding energies of both types of complex proteins with ADE or without ADE using the docking method. Various docking techniques have been created in the past for the underlying assurance of protein-peptide buildings. Basically, there are many types of methods of docking but here we are using Protein-Protein docking to compare the binding energies of antigen-antibody. We used tools to perform docking like HADDOCK, HEX 8.0.0, etc. These findings may help guide rational vaccine design.

Keywords: ADE, SARS -CoV-2, HADDOCK, Antigen-Antibody interactions.

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MUSIC PREFERENCE AS A PREDICTOR OF MENTAL HEALTH: DEVELOPING SPOTIFY MOOD ANALYSER TO PREDICT MENTAL HEALTH

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Abstract

COVID health crisis has affected the health and well-being of individuals. Extensive research in disaster mental health has established that emotional distress is pervasive in affected populations-a phenomenon which is echoed among people during this Covid-19 pandemic.

Social scientists using interaction theories have established a relationship between music and mental health. Listening to music that induces sadness may lead to higher levels of prolactin, that leads to poor mental health. Access to various music streaming apps is increasingly becoming popular among music lovers. Spotify is one such peer-assisted music streaming app-based service that offers instant access to a vast music catalogue.

This paper proposes a model to predict the moods of the music lovers using massive amounts of user activity data. The study analyses the user's choices on the dimensions "acousticness', 'danceability', 'energy', 'instrumentalness', 'liveness', 'loudness', 'speechiness', 'tempo', 'valence', 'popularity') and creates a data frame encapsulating all these, to judge the mood of the listener. In addition, Natural Language processing was carried out on the lyrics that were extracted using VADER (Valence Aware Dictionary and Sentiment Reasoner) to probe the sentiment of the listener.

The study has vital implications for the healthcare industry. The rich individual -level information provides social scientists to understand the sentiments of the listeners and provides cues about mental health of the listener and thus identifies opportunities for probable intervention.

Keywords: Spotify, Mental health, NLP, Music preference, Sentiments, COVID -19, Mood Analyser

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VIRTUAL SCREENING OF COMPOUNDS FROM *Aureobasidium* STRAIN TD-062 OBTAINED FROM THE THAR DESERT OF INDIA

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Abstract

Computational tools facilitate screening of small molecules for high throughput screening (hits). Virtual screening has huge demand in the pharmaceutical industry due to time, cost and resource effectiveness and shortening the lead time. ADMET represents Absorption, Distribution, Metabolism, Excretion and Toxicity. The forecast of the ADMET properties assumes a significant part in light of the fact that these properties represent the failure of about 60% of all drugs in the clinical phases. On the basis of different parameters, ADMET score study can help in prediction of drug activity, identification of compounds or modification of lead compounds for drug designing. A black coloured yeast-like micro colonial fungus, TD-062, was obtained from red soil of Thar Desert. GC-MS analysis of extracts from this isolate showed the presence of eighteen compounds. Application of ADMET scores showed that one of the compounds, 1-H-indole, 5-methyl and 1-H-beta-pregna, is promising with reference to its toxicity profile, and can be selected for further drug designing.

Keywords: Computational tools, Virtual screening, ADMET score, molecular docking, drug likeness, drug discovery

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EFFECT OF NATURAL COMPOUNDS ON GLIOBLASTOMA MULTIFORME PATHWAYS

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Abstract

Glioblastoma is one of the most debilitating forms of brain tumour. It accounts for 17% of all the brain tumours and has resulted in 251,329 deaths in 2020 itself. Several studies performed on patient profiling have revealed that many genes tend to be overexpressed or mutated in many GBM patients and hamper the signalling and growth pathways. Additionally, there is a requirement to explore supplementary or alternative treatment that can aid in overcoming the resistance caused by standard care treatment (Temozolomide with radiation). The preliminary analysis on potential of certain phytocompounds on the critical genes involved in GBM have been studied *in silico* through several plugins of Cytoscape software like BiNGO and MCODE. The network of the genes has been analysed based on factors such as degree, closeness and betweenness. The ERBB4 and TP53 were identified as seed nodes for cluster 1 and cluster 2 implying their correlation with genes in their specific clusters. The BiNGO plugin gave out gene ontology data telling about the functions of the genes of a single cluster. Additionally, the properties of ligands were studied by PharmaGist servers and 3D patterns of shared features by all or most input ligands were analysed. Alignment of three ligands resulted in the best pharmacophore with scores of 19.29, 18.83, 18.37, 16 and 15.6 as the top 5 alignment. Apart from these, several compounds have been analysed *in vitro* for their cytotoxicity effect on GBM cell lines.

Keywords: Gene; Inhibition; Proliferation; Signalling pathway; Temozolomide; Tumor Microenvironment

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EVOLUTIONARY GENOMICS OF OLFACTORY GENE FAMILY IN *Drosophila*

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Abstract

The differential patterns of food choices can be studied by exploring genetic differences of chemosensory traits via chemosensory pathways. This behavioural development of food choices incorporates the complex association among biological, social and environmental regulators or the influencers. The olfaction - sense of smell- serves the most prime sensation towards food detection, enhancement of one's appetite, regulation of potential towards mating partners and identification of danger or enemies. Literature confirms that olfactory systems of mammals and insects work on common principle. With regard to experimental accessibility and tools, including repertoire for molecular, genetical, cellular, physiological and behavioural assays at varying levels and conditions, the fruit fly *Drosophila* proves to be an excellent model system. The *Drosophila* olfactory system is regulated by two organs: antenna and maxillary palp and their family comprises about 60 odorant genes which showcase their expression within the subset of odorant receptor neurons. The evolutionary genetic studies on olfaction have significance in understanding sensory abilities, important interconnections with respect to memory, learning, behaviour and affiliations with their social groups. The present work focuses on the evolutionary aspect of 7 Odorant genes (Or42a, Or71a, Or33c, Or85e, Or46a, Or59c and Or85d) located in the maxillary palp region in genus *Drosophila*. Each of these genes belong to a particular olfactory sensory neuron and works as a sole or prime detector for specific active compounds with high sensitivity emphasizing the independent and important functions of maxillary palp. Here, we retrieved the gene sequences of these 7 Odorant genes found in different *Drosophila* species from NCBI database and performed the comparative and phylogenetic study. Multiple Sequence alignment for each gene was done through the MUSCLE tool of MEGA-X and maximum likelihood phylogenetic trees were constructed using MEGA-X with a bootstrap value 100. Our results indicate that most of these genes have been evolved through the "speciation" event. However, more population studies need to be done in order to obtain a clear insight on olfactory adaptation processes.

Keywords: *Drosophila*, Chemosensation, Olfactory odorant genes, Evolutionary relationship

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SUBSTRATE SPECIFICITY OF PARABEN TOWARDS LIVER ESTERASE: A BIOINFORMATICS APPROACH

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Abstract

Parabens, esters of para-hydroxybenzoic acid, have so far been "safely" used in our daily life as a preservative in most of the commercial products including cosmetics. It is the relatively inert, non-reactive, odorless nature and easy miscibility with the majority of the products that make it a suitable choice as preservative. However, recent studies have explored the dark side of the uses of this compound, as a potential environmental hazard due to its impact on humans as endocrine disruptor and carcinogen. Current *in-silico* study explores the interaction between one such most extensively used paraben (methyl paraben) and with esterase from pig liver, to explore the compound as potential substrate, a strategic approach used to explore potential methods of biodegradation of the enzyme. The bioinformatics analysis revealed the existence of around 27 binding sites with amino acid count in the binding site ranging from 3 to 21. Further the docking of Paraben, analyzed using bioinformatics tools, have revealed comparatively better binding energy of paraben with the enzyme than the substrate. Based on the analysis it can be proposed that Paraben can be a potential substrate for pig liver esterase. The study will open the avenue of using enzymes for designing analytical tools for detection of Paraben.

Keywords: Paraben, Preservative, docking, Esterase, binding energy.

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MUTATIONAL ANALYSIS IN BACTERIA USING COMPUTATIONAL TOOL - MUTANET

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Abstract

Mutation is a significant idea in science today that prompts varieties in genes. A mutation is a lasting adjustment in the grouping of nitrogenous bases of a DNA molecule. The consequence of a transformation is commonly an adjustment in the finished result determined by that gene. Now and again, a transformation can be useful if another metabolic action emerges in a microorganism, or it tends to be hindering if a metabolic action is lost. Transformations cannot be constrained, or initiated by a mutagen in the climate. Mis-pairing is likely due to cell cycles, for example, Tautomeric move of bases, oxidative harm to DNA, Depurination and Deamination or brought about by "climate", i.e., synthetic compounds, radiation, infections, diet and way of life (Mutagens). Replacement of a nucleotide and Deletion or addition of them is two systems of change. Change in microscopic organisms has a few outcomes, for example, missense, nonsense, quiet, frameshift, deadly, silencer and deadly transformation. And the Recognizing these mutations requires identification techniques. Techniques such as Replica plating, Penicillin enhancement, Ames test, Use of chromogenic substrate and novel tests, for example, Polymerase chain response (PCR) and Gel electrophoresis, Gene tests and Southern blotching, DNA sequencing and DNA microarray are a portion of these strategies. And the MutaNET, is an effective and efficient in-depth mutation analysing tool which comes with the Next Generation Sequencing (NGS) pipeline calling for paired-end NGS read mutations, an automated mutation analysis tool, and a number of file converters and mergers. And basically it was designed to determine the possible effect of mutations on gene expression and protein function of the genome. And suitable to use on almost all the operating systems and available free of cost and it is designed using Python programming language and can be accessed through Github.

Keywords: Mutation, Spontaneous and induced mutation, detection methods, MutaNET, Antibiotic Resistant Subnetwork.

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TRANSFER LEARNING-BASED ATTENTION GATED SIAMESE NETWORK FOR HUMAN AND SARS-COV-2 PROTEIN INTERACTIONS

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Abstract

For the past year SARS-CoV-2 has affected the lives of people around the globe. Therefore, the research community is continuously putting in their best efforts to find a solution to curb and cure the disease. SARS-CoV-2 is a 29.9k bp long sequence genome consisting of 25 different proteins among which it was discovered that spike glycoprotein plays a vital role in interaction with the host cells. Hence majority of the recent works were focused towards targeting the spike region for the vaccine design against the contagious virus. Thorough study of protein-protein interaction between human and virus can help us in better understanding and management of this disease. For this purpose, an Attention gated Siamese framework is utilized from which a consensus of prominent features and contextual information is taken into account to identify the influence of protein sequences. Moreover, to obtain the pattern of interacting pairs of human and SARS-CoV-2 proteins, a transfer learning-based approach is opted from the proposed network through which we obtained an accuracy of 85%. Additionally, by using this model, we identified that there were 30 human proteins with spike, 13 having a nucleocapsid and 17 with membrane having predictive interaction of above 90%.

Keywords: Virus, SARS-CoV-2, Attention gated Siamese framework, Proteins.

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GENOME-WIDE IDENTIFICATION AND CHARACTERIZATION OF METAL BINDING GENE FAMILIES IN LEGUMES: METHOD AND STRATEGIES

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Abstract

In the present date, thirteen species of legume i.e. have been completely sequenced. This data has a starting point to understand the evaluation of legumes corps. Additionally, comprising the heavy metal accumulation in legume at the whole genome level based on the metal binding genes families evolutionary changes. This study offers advice on the heavy metal toxicity in the soil. The HMM-based method can be used to identify heavy metal salinity and drought-stress tolerant genes. Full-length sequence is used to describe the evolutionary relationship of heavy metal binding genes. Understand the molecular function for the bio-transporter and bio-observant and evolutionary mechanism of heavy metal in these legume crops. Gene expression datasets used to compare inter-specific analysis genomic resources become available across the legume family and comparative analysis of the heavy metal binding gene between legume species uncovered several evolutionary changes between the tropical legume species from the Phaseoloid clades and the other legume species. The study will be continued by using in-silico approaches and provide the theoretical foundation for the improvement of the identification, characterization of heavy metal-binding proteins in legume crops. Altogether, this study will provide interesting new features on the evaluation of heavy metal binding gene families and also provide valuable clues to identify the additional heavy metal binding gene families from non-sequenced species.

Keyword: Heavy Metal, Gene family, expression

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PRODUCTION OF THERAPEUTIC ANTIBODIES FOR DISEASE TREATMENT

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Abstract

It has been more than three decades since the United States Food and Drug Administration (US FDA) approved the first monoclonal antibody in 1986, and antibody engineering has significantly advanced during this period. Due to their elevated specificity, new antibody drugs have increasingly less adverse effects. As a consequence, in recent years, therapeutic antibodies have become the predominant class of new drugs created. Antibodies have been the pharmaceutical market's best-selling products over the past five years, and eight of the top ten best-selling drugs worldwide were biologics in 2018. In 2018, the global demand for monoclonal therapeutic antibodies was estimated at approximately US$115.2 billion and is projected to produce revenue of US$300 billion by 2025. Thus, as new medicines have been approved for the treatment of numerous human diseases, including several tumours, autoimmune, metabolic and infectious diseases, the demand for therapeutic antibody drugs has experienced exponential development. As of December 2019, the US FDA has approved 79 therapeutic mAbs, but there is still considerable potential for development. The present article analyses the current market developments and describes the leading techniques in antibody engineering used in the production of therapeutic antibody drugs, such as monoclonal antibody humanization, phage show, human antibody mouse, technology for single B cell antibody, and maturation of affinity. Finally, there are also potential applications and viewpoints explored.

Keywords: Monoclonal Antibody, Therapeutic drugs, Treatment of human diseases.

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APPROACHES TO ENHANCE APTAMER SUBSTRATE BINDING

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Abstract

Aptamer that binds specifically to the target molecules are produced by a specialized method known as in vitro (SELEX) selection. In order to obtain high affinity aptamers, SELEX may not always result in achieving the desired affinities. There may be various factors for limitation in the SELEX process pertaining to the binding affinities of aptamers viz., the restriction of molecular variability in the initial library, or the loss of potentially high affinity aptamers while the PCR process.

Since high target affinity is a primary requirement of aptamers development process, there could be several ways to enhance the aptamer affinity. Developing multivalent aptamers by attaching different short stretches of aptamers that recognize very specific epitopes is an easy and highly probable method to increase the aptamer's binding affinity. It has been found that inserting LNA (Locked Nucleic Acid) into double stranded regions of aptamers increases the affinity constants. Increase in the number of interactions between an aptamer and a target also results in increased affinity. Connecting different binding motifs of aptamers greatly aids to increase interaction zones between aptamers and target molecules for improving the binding affinities of aptamers. Recent Study has proved that in silico maturation (ISM), shows much higher affinity on its multimerization. With advent of newer in silico search tools namely- stochastic tunnelling, basin hopping and discrete molecular dynamics, one can predict the very stable aptamer/target molecule complex. Hence, to obtain high affinity aptamer, optimization using a combination of in silico approaches and in vitro methods are critical.

Keywords: Aptamers, SELEX, LNA (Locked Nucleic Acid), in silico Maturation (ISM).

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COMPUTATIONAL APPROACH FOR IDENTIFICATION OF POTENTIAL GENES AGAINST COLORECTAL CANCER

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Abstract

Colorectal cancer (CRC) is one of the deadliest diseases, affecting 8% of all cancer deaths. The disease progression depends on different factors including genetic, age, alcohol consumption and abnormal lifestyle. The selective symptoms of CRC are change in bowel habit, abdominal pain, a change in stool form, Rectal bleeding, blood in the stool and eventually intestinal obstruction usually observed in small and large intestine inner membrane which become malignant and spreaded across the other body part. Currently available treatment strategies for CRC viz. surgery, Radiation therapy, Chemotherapy, Immunotherapy but patients respond to these therapies remain challenging. The International Agency for Research on Cancer (IARC) estimated 36 types of cancer and 43.8 million peoples are suffering over the past 5-year prevalence, in disease indication chart CRC raised to 2nd most cancer disease (WHO-2018). The available treatment for CRC is not so effective and emerging multidisciplinary area research on genomics proteomics clinical science and soft computing technologies have raised good hope to reach the best treatment. In the present study, the objectives were aimed to identify differentially expressed genes from available biological and clinical databases and network prediction to identify the potential genes involved in CRC treatment sensitivity by the application of R, Bioconductor, biocLite, Affimetrix, NGS and Cancer data analytics. In this study, Out of 800's GEO datasets, 40 datasets of TMA CRC expressed gene datasets (CEL files) were selected from different sources. The raw data files are extracted from all sources into R-Cran and the data was normalized to make array image plots. To select the differentially expressed genes, the normalized data was performed with linear Models for Microarray Data (Limma) by concatenating experimental and functional t-test p value<0.05. All differentially expressed genes were taken for functional annotations by Database for Annotation, Visualization and Integrated Discovery (DAVID) v6.7. The network analysis by String and Cytoscape are under progress to select the differently expressed potential genes for treatment of colorectal Cancer.

Keyword: Colorectal Cancer, differential gene expression, bioinformatics analysis, hub genes, application of R.

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IN SILICO APPROACHES TO INVESTIGATE CARDIOPROTECTIVE PHYTOCONSTITUENTS AS TMAO INHIBITOR

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Abstract

Cardiovascular diseases are becoming a major health problem throughout the world but it is highly affecting developed and developing countries. Diet and lifestyle are strongly responsible for the various chronic diseases such as obesity, diabetes, inflammatory bowel diseases, cardiac diseases etc. Numerous studies have suggested that gut microbiota plays significant jobs in human health and diseases. Gut microbiota reside in the human body in a symbiotic nature, but the composition of microorganism is crucial for maintaining the healthy state of an individual. Dysbiotic conditions of intestinal microbiota may cause various diseases and release many bad metabolites such as trimethylamine, uremic toxins, bile acids and lipopolysaccharides. Emerging evidence have shown that interaction between gut microbiota and herbal products give potential therapeutic effects with no or less side effects in comparison to synthetic medicines. Herbal products may help to inhibit the production of toxic microbial metabolites and imay also modulate the composition of bad microbiota.

In this study, Phytochemical screening and antimicrobial testing were performed on gut negative microbiota such as *Salmonella typhimurium* by using various assays to obtain therapeutically enriched herbal formulations as Trimethylamine-N-Oxide (TMAO) inhibitor. Furthermore, co-interaction studies were performed to check the affinity of selected herbal formulations against TMAO by using bioinformatics approaches.

Keywords: Gut microbiota, Metabolomics, Trimethylamine-N-Oxide, Herbal Formulations, *In silico* testing.

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EFFECT OF PHYTO-COMPOUNDS ON SARS-COV2

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Abstract

The severe acute respiratory syndrome coronavirus 2 (SARS CoV2), better known as COVID-19 has become the current health concern to the entire world. The medical facilities of all, developing as well as well developed nations failed in front of the novel Corona Virus and a huge loss of human life has been faced by the world. Various researchers are still working on to develop the drugs against this deadly incurable disease. It has been reported in various theories that many compounds found in nature holds the potential to treat these diseases. Current research was performed aiming to find the compounds that can treat both COVID-19. It has been found that Hydroxypanduratin A, 2-(2ethoxyethoxy)ethanol and Eugenol are some of the compounds that these compounds are the potent drug candidates. It has been reported that the Main protease of SARS CoV2 is associated plays a pivotal role in viral gene expression and replication and spike protein of SARS CoV2 is responsible for the receptor recognition and cell membrane fusion process which makes these proteins the potential drug target for the inhibition of infection. With the help of in-silico studies performed by AutoDock tool it was reported that these compound have sufficient binding energy to state that these compounds holds the potential to prevent and cure this disease. However, more in-vitro should be performed on these compounds to confirm their potential and gain more knowledge about the mechanism of prevention.

Keywords: SARS-CoV2, phytocompounds, protease.

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NUTRITIONAL PROFILING OF *DESI* AND *KABULI* CHICKPEA GENOTYPES AND ASSESSMENT OF PROTEIN QUALITY BASED ON ESSENTIAL AMINO ACID SCORE AND IN-VITRO PROTEIN DIGESTIBILITY

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Abstract

Malnutrition affects more than 600 million people across the globe and India houses most of the undernourished children. Since animal-based protein isn't preferred by many due to socio-economic reasons, supplementing the diet with plant-based proteins is the need of hour. A study to determine nutritional profile in terms of total protein content, amino acids content, Essential Amino Acid Score (EAAS) and the in-vitro protein digestibility of 12 *Desi* and 12 *Kabuli* chickpea genotypes was conducted. The quality of proteins was assessed by in vitro protein digestion where with pepsin, trypsin and chymotrypsin followed by Ninhydrin assay. Among chickpea genotypes, *Desi* types showed highest protein digestibility of 42 to 86% with most cultivars showing a score >0.5. The amino acid profile showed balanced EAAS and Daily Value (DV%) for all except for methionine, and thus, chickpeas can contribute 45%–100% DV for a 60 kg adult of various essential amino acids. Since the genotypes showed higher protein content (14-23 %), which is more than egg (13 %), and milk (3.4%), chickpeas can be good alternative to egg and milk. Chickpea also contain bioactive compounds which may provide health benefits through their antioxidant activity (AOA) which was determined through DPPH and FRAP assays. Since pulses are not consumed raw, the effect of boiling and canning on protein digestibility and AOA was also studied in 2 contrasting desi & kabuli genotypes. The generated holistic information will help in identifying promising chickpea genotypes with high nutritional quality and aid in future breeding programmes.

Key words: Quality Proteins, Chickpeas, Digestibility, Amino acid, Antioxidant.

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STRUCTURAL CHARACTERIZATION OF *KLEBSIELLA PNEUMONIAE* CYSTEINE SYNTHASE COMPLEX USING INTEGRATIVE STRUCTURAL BIOLOGY APPROACH

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Abstract

De novo cysteine biosynthetic pathway finds its significance in several organisms, especially plants and microbes due to its role in assimilating inorganic sulfur and biosynthesis of sulfur containing amino acid - L-cysteine. Its documented importancein facilitating microbial adaptation to selective pressure inside the host, toxin inactivation, biofilmformation, and antimicrobial resistance, coupled with its absence in humans, makes the enzymes involved in the pathway promising targets for developing novel therapeutics.In addition, CysE and CysK,the two enzymes of the pathway associate to form Cysteine Synthase Complex (CSC) that is a major route for regulating production ofL-cysteine from L-serine. Although industrial and therapeutic importance of CSC has been long recognized, unresolved structure hinders its molecular investigations for optimal exploitation of its potential. This study reports purificationand characterization of recombinant CSC of Klebsiella pneumoniae, as an essential first step in understanding its structure and biochemical function. Purified recombinant CSC was obtained and subjected to -(i) gel filtration chromatography to separate and estimate molar massof the complex, (ii) dynamic light scattering for determining hydrodynamic radius and verifying homogenous population, and (iii) negative stain electron microscopy to visualize the purified complex. At the same time, techniques of integrative structural biology were used to predict 3-dimensional structure of CSC and identify residues contributing to protein-protein interface stabilization.However, heterogeneity in the CSC preparation and flexible/dynamic nature of the association between the two interacting proteins pose considerable challenges. We aim to contribute to understanding of useful molecular recognition inferences within CSC, which presently are far from being well-understood.

Keywords: CSC, CysE, CysK, protein-protein interaction, purification, gel filtration chromatography, DLS, Homology modelling.

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EVALUATING MULTIPLE PHYTOCOMPOUNDS OF *Carica papaya* LEAVES EXTRACT FOR BACTERIAL SKIN INFECTIONS BY COMPUTATIONAL AND EXPERIMENTAL VALIDATION

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Abstract

The quotidian form of bacterial and fungal skin infections such as impetigo, cellulitis, folliculitis or mycosis, ringworm etc. are frequently found in people of all ages and gender. These infections are well catered by the antibiotic or antifungal regimen but due to the ever-increasing resistance against these infections by the antibiotics, more focus towards the existing phototherapeutics have garnered and gained support in the scientific community. And contemporary research exploring therapeutic altercations against conventional pharmaceutics have observed a significant raise in recent times. Amongst other solutions, *Carica papaya* (Papaya) has been reported as one of the most efficacious and potential phytocompound demonstrating anticancer, anti-oxidative, anti-inflammatory, anti-bacterial, and many more therapeutic effects. Thus, a detailed study exploring as well as elucidating such attributes of *Carica papaya* is necessary for developing a potential breakthrough phytocompound for therapeutic application. The primary aim of this research study was to illustrate and explore a detailed phytochemical evaluation of *C. papaya* fruit extract along with antioxidant and antimicrobial analysis. In silico studies further validated its therapeutic potential by investigating the active site molecular docking and ADMET analysis. Further, evaluation was done by preparing the sample with crude ethanolic extract and aqueous fractions, then these sample solutions were analysed for the presence and absence of important secondary metabolites such as alkaloids, flavonoids, phenolic, and tannins. Thereafter, comparative analysis was sketched employing antioxidant activity by DPPH and ABTS assays to provide comprehensive free radical scavenging results. Lastly, pathogenic bacterial strains of *Micrococcus luteus, Bacillus licheniformis* and fungal strains *Rhizopus oryzae, Aspergillus niger*, and *Trichoderma* were screened to determine antibacterial and antifungal activity of the extracts using agar well diffusion technique. The results unveil all the present phytocompounds, flavanone, dicoumarol and terpenes which were inferred as the prominent compounds based on their binding affinity, drug likeness, ADMET property, toxicity, and bioactivity. Furthermore the free radical scavenging and antimicrobial activity of extract was found to be equivalent to the standard antibiotic, suggesting the significant therapeutic efficiency by the *C. papaya* fruit extract. Thus the research study enables us to propose the utilization of the extract further in the pharmaceutical industry.

Keywords: Antioxidant, Antimicrobial, Bioactivity, Binding affinity, Free radical scavenging.

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THERAPEUTIC AND NUTRITIONAL IMPORTANCE OF *Cordyceps sinensis*

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Abstract

There are different types of ecological associations, seen among diverse microbiota that inhabit the earth. Most of these associations are primarily for sufficing nutritional requirement, protection and survival in adverse conditions or for growth without harming each other and the associated organism often complement each other. It may be mutualism, parasitism or commensalism.

A unique saprophytic association exists between the medicinally important fungi *Cordyceps Sinensis* and the larvae of insect *Lepidoptera spp*. The blade shaped fungi belongs to the familyClavicipitaceae. According to some recent studies, the fungus has been re-named *Ophiocordyceps Sinensis*. The fungi are unique due to the "entomopathogenic fungus-host larva complex" which is formed when fungus grows in the larvae of insect and after filling their hemocoelom, the stroma, bearing the fruiting body, break the cuticle and comes out from the head region of dead larvae. The fruiting bodies then again produce ascospores which further infect other insect larvae.

The fungal or the fungal dead insect complex had been used for more than 2000 years in Chinese herbal medicine due the therapeutic properties associated with the bioactive compounds of the fungal system. The fungal system is a rich source of nucleosides including a group of compounds called 'cordycepin' (3′-deoxyadenosine). Cordycepin usually targets the cell division and apoptotic cycle. It is also reported for neuroprotective potential with ability to prevent injuries in cerebral ischemic brain and thus prevent myocardial infarction. Cordycepin had also been explored for its analgesic, anti-inflammatory and anti-cancer properties. The anticancer activity is attributed to the potential of cordycepin to induce steroidogenesis via various intracellular signal transduction pathways (such as PLC and MAPK pathway) which induces apoptosis in tumor cells. It also regulates the immune system by inducing the production of cytokines. Not only this, the compound had also shown the bactericidal, antiviral and insecticidal properties. Apart from Cordycepin the fungal system also produces other nucleoside, carbohydrate and fatty acids which have been explored in recent past for nutritional and therapeutic properties

However, one of the major constraints is the complicated life cycle which is a major bottleneck in cost effective cultivation of the fungal system. High demand and low production obtrudes *Cordycep* sp. as one of the costliest fungal systems in the world.

Studies underway are exploring the optimization strategies for developing a cost-effective cultivation strategy for mass production of the fungal system and bioactive compound profile.

Keywords: Cordycep, anticancer, cordycepin, nucleoside, nutritional.

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THE CORRELATION OF GUT MICROBIOME WITH PERSISTENT DEPRESSIVE DISORDER AND MDD IN POPULATION

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Abstract

Depression affects more than 21% of the global population yet is highly undiagnosed and left untreated for various reasons. Depression presents with a persistent low mood and is a common psychiatric disorder that faces the obstacles of social stigma, lack of effective therapies, and inadequate mental health resources. Major depressive disorders (MDD) - the common clinical presentation of depression, is widely researched to expand our understanding of its molecular and physiological manifestations.

An exciting area emerging to be of potential therapeutic value in MDD is examination of the gut-microbiota of the depressed subjects. A bi-directional communication between the central and the enteric nervous system, and the role of our gut microflora in influencing neurological functions is gaining ground. Studies have shown that a healthy gut microflora helps transmit brain signals through the pathways involved in neurogenesis, neural transmission, microglial activation, and behavioral control while undergoing stress and anxiety inducing experiences ; moreover the genes involved in synapse formation between neurons in the brain and neurons in the GI tract are similar, and any mutation could possibly lead to both brain and GI abnormalities. An important aspect which has emerged is the differential composition of MDD patients' gut microbiota - increased abundance of the genus *Bacteroides, Firmicutes, Actinobacteria* and decrease in presence of the genera *Blautia and Eubacterium*. Further, interesting revelations have also been made when the use of anti-depressant drugs and diversity of the gut microbiome was studied – number of undesirable microbes was limited in the long run. Additionally, probiotic formulations stimulating the growth of intestinal microbiota having a positive influence on central nervous system functioning are also being investigated.

Keywords: Depression, Gut Microbiome, Gut-Brain axis, anti-depressants, Probiotics.

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STUDY OF THE GENETIC VARIATIONS IN DIFFERENT VARIANTS OF *Tribulus terrestris* L. (GOKSHURA) THROUGH DNA RAPD ANALYSIS.

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Abstract

Tribulus terrestris (Family – Zygophyllaceae) is a well known medicinal herb, commonly known as palleru, which is found in all over the India and is used in various systems of medicine such as diuresis, chronic cystitis, calculous affection, incontinence of urine, impotency, gonorrhoea, gleet, spermetorrhoea, phosphateurea. *Tribulus terrestris* is one of the components of Dashamoola (compounds of 10 drugs) and chyavanprash widely used in Ayurveda. In the present study 8 different regions of *Tribulus terrestris* plant leaves were collected which is further subjected to molecular characterization by RAPD analysis. RAPD analysis found various mild variations with respect to different regions of Kurnool district, Rayalaseema region of Andhra Pradesh. It was observed that all 15 primers were found to generate clear and polymorphic bands. A total of 223 bands were generated of which 159 were polymorphic. The percentage of polymorphism obtained by 15 primers was 71.3%. Polymorphism was high enough to enable discrimination of all varieties, though none of the primer discriminate all accessions independently. This deduced that these primers employed in the study returned a high degree of confidence in the identification.

Keywords: *Tribulus terrestris*, Genetic diversity, RAPD analysis, medicinal herb.

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MOLECULAR DOCKING OF RESVERATROL & PIPERINE NATURAL COMPOUND WITH SEROTONIN TRANSPORTER (SERT)

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Abstract

Neuropsychiatric disorders are one of the leading threats to global health which includes disorders such as depression, anxiety deficit hyperactivity disorder (ADHD), anxiety, bipolar disorder etc. These disorders are characterized by low and sad mood, loss in interest in daily activities. For treating depression and anxiety, inhibition of serotonintransporter (SERT) can be considered as an effective way by the inhibitory ligands. Some of the commercially used drugs such as paroxetine, fluoxetine and sertraline and many more work on the similar principle of inhibiting the SERT receptor. These days scientists and researchers are more inclined towards the use of natural compounds for developing therapeutics for such diseases. Certain natural compounds such as curcumin, quercetin, EGCG (Epigallocatechin gallate), resveratrol etc have been reported to show antidepressant effects with minimal side effects. In the present study, we selected two natural compounds and explored their therapeutic potential by predicting its binding score through the method of computer aided technique such as molecular docking. Docking was performed between the selected natural compounds (resveratrol & piperine) and SERT. Results showed the binding affinity score of (-6.60 and -6.80 kcal/mol). Results predict that these compounds can be equivalently used as chemically synthesized in form of certain drug formulation against the treatment of psychiatric disorders after further experimental studies.

Keywords: Neuropsychiatric disorder; Serotonintransporter; resveratrol; piperine; molecular docking.

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MOLECULAR PATHWAYS IN VULVAR SQUAMOUS CELL CARCINOMA: IMPLICATIONS FOR TARGET THERAPEUTIC STRATEGIES

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Abstract

Squamous cell carcinoma (SCC) accounts for approximately 95% of the malignant tumors of the vaginal vulva and has a high propensity to occur in elderly women. Patients with vulvar SCC are expected to rise in the future, mainly because of the proportional increase in the average age of the population. The vulvar SCC can develop via two different pathways. The SCC can be mediated by infection with a high-risk-type Human Papillomavirus (HPV). The integration of the DNA of HPV into the host genome leads to the development of a typical vulvar intraepithelial neoplasia (VIN), accompanied with overexpression of two genes p14ARF and p16INK4A. This lesion subsequently forms a warty- or basaloid-type squamous cell carcinoma. Another pathway is dependent on autoimmune response, which leads to tumor progression inside vagina. Many therapies have evolved recently like surgical treatment, radiotherapy, chemotherapy and targeted drug delivery to suppress the development of vulvar cancer. In the recent years, targeted drug delivery has shown a competent response by exploring the mechanism of action of the tumor progression and genes involved in the pathway. Furthermore, in a recent study Oxymatrine, herbal medicine has inhibited the proliferation of SW962 and A431 VSCC cells in a time and dose-dependent manner. Also, CHK1 and Cofilin-1 activity are also known as potential therapeutic agent in different cancer related research studies.

Keywords: Autoimmune, Human papillomavirus, Oxymatrine, Tumor.

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GENETIC TRANSFORMATION AND ECTOPIC OVER EXPRESSION OF CYTOCHROME P450 MONOOXYGENASE (P450) GENE (CYP88D6) IN *Glycyrrhiza glabra*

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Abstract

Glycyrrhiza glabra is one of the most important and well-known medicinal plants which produces various triterpene saponins such as glycyrrhizin. Glycyrrhizin, a major bioactive compound derived from the underground parts of *Glycyrrhiza* (licorice) plants, is a triterpene saponin that possesses a wide range of pharmacological properties and is used worldwide as a natural sweetener. Beta-amyrin 11-oxidase (CYP88D6) plays a key role in the metabolic pathway of glycyrrhizin production and converts an intermediate beta-amyrin compound to glycyrrhizin. CYP88D6 catalyzes the sequential two-step oxidation of β-amyrin at C-11 to produce 11-oxo-β-amyrin, a possible biosynthetic intermediate between β-amyrin and glycyrrhizin. In this study, pBI121:CYP88D6 construct was transferred to *G. glabra* using *Agrobacterium tumefaciens* EHA 105. The quantitation of transgene was measured in putative roots of transgenic plants using qRT-PCR. The amount of glycyrrhizin production was measured by HPLC in transgenic plants. Gene expression analysis demonstrated that CYP88D6 was over-expressed by eight folds. The amount of glycyrrhizin metabolite in the over-expressed line was more than or similar to that of control. According to the obtained results, it would be recommended that CYP88D6 of glycyrrhizin biosynthetic pathway be transferred to leaf explants of *Glycyrrhiza glabra* in order to increase glycyrrhizin content in transgenic plants.

Keywords: Glycyrrhizin, β-amyrin, HPLC,Triterpene saponin, Gene expression.

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Azadirachta indica AND ITS POTENTIAL USES AGAINST SARS-COV-2

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Abstract

Coronavirus Disease 19 (COVID-19) is a disease caused by the Severe Acute Respiratory Syndrome Coronavirus-2 (SARS-CoV-2) that infects the respiratory tract of humans and spreads from human to human via droplets. The recent breakdown of the COVID-19 pandemic has become a global concern. Finding a treatment for this disease to combat the pandemic is the necessity of the hour. Currently, researchers worldwide are looking for potential solutions against COVID-19 and several vaccines across the world are on trial phase. Several methods for control of COVID-19 such as drugs, vaccines, interferon therapies, plasma therapies have been predicted. However, these interventions need months to develop. Also, the existing treatments may face challenges of viral resistance and possible side effects. In view of these, several scientists have focused their research on finding natural solutions for combating COVID-19. Literature review revealed a huge number of potential antiviral compounds present in nature that can be harnessed and used for effective COVID-19 treatment. For the present study, secondary metabolites of *Azadirachta indica* like nimbin, nimbiol etc. were chosen and were docked against helicase protein of the SARS-CoV-2 and the results obtained showed that it may have a promising potential to fight against COVID-19. *Azadirachta indica* or commonly called Neem is vastly used in Ayurvedic formulations against various infections, inflammations and for treating other diseases like: cardiovascular disorders, diabetes, gum disease, liver problems and stomach problems etc. Thus, this study is focused on exploring secondary metabolites present in Neem that have potential antiviral properties against the COVID-19 disease.

Keywords: Coronavirus Disease 19 (COVID-19), Severe Acute Respiratory Syndrome Coronavirus-2 (SARS-CoV-2), Interferon therapies, Plasma therapies, *Azadirachta indica*

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THERAPEUTIC POTENTIAL OF THE PHYTOCOMPOUNDS FROM *Vateria indica*

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Abstract

The wide acceptance of herbal products and formulation, due to their comparable efficacies, easy availability and minimal side effects, had revolutionized the ethno-pharmacological sciences throughout the world. One such medicinal plant, which is gaining the interest of researchers, the world over, is a plant commonly found in South east Asia, *Vateria indica* L.

Vateria indica L., belonging to the family Dipterocarpaceae, is well exploited for timber, tallow and aromatic resin apart from medicinal and therapeutic properties. According to IUCN red list, the plant is categorized as vulnerable plant due to the overexploited harvesting of the plant from the wild habitat, for its therapeutic properties.

Different parts of the plants are analysed to be rich in various phytocompounds that have been explored for their therapeutic potential. The analysis of the therapeutically important phytocompounds in the bark of the stem revealed the presence of polyphenols (of stilbenoids group), that is a combination of two phenyl rings linked to each other by an ethylene moiety. Around 12 different types of stilbenoids exist in the plant bark and leaves. Other phytocompounds explored in aqueous extract of various plant parts are tannins, phytosterols, flavonoid, alkaloid, saponins and carbohydrates, to name a few. Though the molecular mechanism associated with therapeutic potential of plant extracts had not been studied in detail in most of the reports, but some reports have highlighted the anti-inflammatory activity of the varying concentration of plant extract analysed using inhibition of protein (albumin) denaturation and anti-lipoxygenase activity along with other assays.

Studies have also shown the anti-tumor effect of the orally administered *V. indica* aqueous extract, rich in bergenin, hopeaphenol, vaticanol B, vaticanol C, and epsilon-viniferin against subcutaneously allografted sarcoma cells in DDY mice model. Studies have also compared the anticancer properties of the aqueous and non-aqueous extract of the plant bark on cancer cell lines *viz.* C6 and EAC cells.

In the light of existing reports, the role of phytocompounds from *V. indica* is paramount and the detailed analysis of phytocompounds and their therapeutic potential, along with the detailed mechanism of bioactivity, needs to be analysed for higher efficacy of the formulation.

Keywords: Phytocompounds, anti-tumor, anticancer, stilbenoids, *Vateria indica.*

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PLANT SECONDARY METABOLITES: EFFECT OF STRESS AND DEFENSE RESPONSES IN THEIR PRODUCTION

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Abstract

The plant kingdom produces secondary metabolites, which regulate plant–environment interactions and play a major role in overcoming stress constraints. Ecosystems consist of varieties of microbes, mites, insects, mammals and other herbivorous animals, which cause reduction in crop productivity. Secondary metabolites are classified into three categories:-terpenes, phenolics and nitrogen sulphur containing compounds. They act as a defense mechanism against herbivores and many pathogenic microorganisms as well as for various kinds of abiotic stresses.

Various research studies have shown that secondary metabolites are also used for medicinal,nutritive and cosmetic purposes, and significant in plant stress physiology. During the growth of plants, various secondary metabolites are produced by them to perform a variety of cellular functions which are crucial for physiological processes, and recent studies showed that stress and defense response signaling affect the production of secondary metabolites. During growth, various environmental, genetics and physiological factors affect the production of secondary metabolites. Nowadays, scientists focus on studying abiotic factors that influence secondary metabolism during *in vitro* and *in vivo* growth of plants. This review presents an overview about defence mechanisms by which plants protect themselves against various abiotic stresses and important secondary metabolites and discuss the role of stress and defense responses in plant secondary metabolites production.

Keywords: microbes, herbivorous, metabolites, terpenes, phenolics, nitrogen and sulphur.

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A STUDY ON THE ANTIOXIDANT, ANTIDIABETIC AND CYTOTOXIC PROPERTIES OF A POLYHERBAL FORMULATION

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Abstract

Herbal drugs are of vital importance from prehistoric periods. The basis of these practices is to clear the root cause of the disease and to restore balance to lead a healthy life. The concept of Polyherbal formulation is to achieve a greater therapeutic efficacy. When combining herbs having different potential qualities in a particular ratio, it will give a much better therapeutic result and there by forms the basis of remedy. This led to the polyherbal formulation constituting extracts of seven plants namely. The studies were carried out to find out the therapeutic potential of the Polyherbal formulation. The results of the study proved that the extract can yield a good quality drug which was found to have antioxidant, hypoglycemic, and cytotoxic properties. The study can further be extended to evaluate and isolate metabolites from the extract which helps in controlling the blood glucose level. The isolated metabolite can then be formulated as a drug and can be taken for clinical trials as an antidiabetic drug.

Keywords: Polyherbal formulation, antioxidant, antidiabetic, cytotoxic, antidiabetic.

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ANTI-PROLIFERATIVE EFFECT OF PHYTO-COMPOUNDS IN HUMAN GLIOBLASTOMA MULTIFORME CELL LINES

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Abstract

Glioblastoma multiforme (GBM) is a lethal high grade brain tumour with median survival around 15 months and recurrence with current treatment. Temozolomide (TMZ) is used as a standard drug along with radiation therapy to treat GBM. The treatment for brain tumour is still challenging due to its heterogeneous nature, suggesting that more novel therapeutics should be explored for effective treatment to enhance the survival rate. The natural compounds are known to suppress the cancerous growth due its multipronged mechanism of action. The selected phyto-compounds were studied for anti-proliferative effects against GBM cell lines. Vanillin is used as a food flavoring agent; ellagic acid is present in various fruits like cranberries; carvacrol and thymol are derived from terpene, and hesperetin is found in citrus fruits. The anti-proliferative effect of phyto-compounds was determined using 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (MTT) assay after 48h of treatment with compounds. The results showed that vanillin, carvacrol, thymol and ellagic acid significantly reduced the cell-proliferation while hesperetin was not effective in U87MG and LN229 cell lines. Thus, these natural compounds with anti-cancer effect might be a possible substitute for the treatment.

Keywords: Brain tumour; Carvacrol; Ellagic acid; MTT.

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GINSENOSIDES: A TRANSPIRING NUTRACEUTICAL

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Abstract

Ginsenosides are the major bioactive components of plant genus Panax (ginseng) and has been used as the natural medicine worldwide. These are the natural compounds and come into the category of triterpenes saponins. These can be isolated from the plant roots, stems, leaves, fruits or flowers. Majorly their teleology is to provide defense to the plants, since these are bitter tasting and helps to keep insects away from the plant. These natural compounds are frequently used dietary supplements and convey the benefit to the host after getting absorbed by gut microbiota. This chapter discusses the biosynthesis pathway of Ginsenosides which has been formed from the precursor compound – Squalene. Apart from this, the production of Ginsenosides using the biotechnological strategies and biotransformation processes has also been mentioned. Also certain important health benefits of Ginsenosides in cancer prevention, modulation of the immune system, lowering the risks of diabetes, hypertension, atherosclerosis and others, have been discussed in detail too. Studies show that these compounds have great diversity of their chemical structures and hence are responsible for versatile applications. Ginsenosides also exhibit nutraceutical properties as in case of Parkinson disease, it plays an important role in regulating certain pathways and maintain iron levels. Besides many uses of this plant natural compound, future prospects must include - more studies of its molecular mechanisms, finding of new potential therapeutic applications and searching for the other ways to boost its production to meet increasing demand, hence helping to understand Ginsenosides in an explicit and a better way.

Keywords: Natural medicine, Triterpenes, Parkinson Disease.

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PHARMACOLOGICAL IMPORTANCE OF SECONDARY METABOLITES FROM PLANTS

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Abstract

Phytochemicals hold boundless therapeutic properties in curing several diseases. Large numbers of medicinal plants have antibiotic, antioxidant, antimicrobial, and wound healing properties due to which they are vastly used in traditional medicinal plants. Phytocompounds like alkaloid, terpene phenolic, tannin, steroid, flavonoid, glycoside, and fatty acid are responsible for scavenging free radicals, fighting infection and promoting the faster wound-healing process. Secondary metabolites are a wide range of active compounds which are derived from primary metabolites. Scientific research for new products for the pharmacological purpose can help in getting cost effective drugs for various diseases. In the present review secondary metabolites from plants of medicinal importance have been studied.

Keywords: Phytochemicals, Secondary metabolites, Pharmacological, Drugs.

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ROLE OF FLAVONOIDS AGAINST COVID – 19

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Abstract

COVID-19 is an infectious disease caused by coronavirus-2 (SARS-CoV-2). The first human cases due to the novel coronavirus were first reported in Wuhan City, China, in December 2019. A devastating pandemic started in February 2020 which led to an urgent need to provide rapid, efficient and cost-effective solutions against COVID-19 and forced the scientists, immunologists, epidemiologists, mathematicians, physicists and engineers globally to discover solutions and drugs to inhibit the viral spread which resulted in the development of many vaccine trials and antivirals such as remdesivir, ribavirin or herbacetin. Flavonoids are bioactive compounds which have gained attention due to their antibacterial, anti-cancerous, antifungal and antiviral properties. They are promising tools for targeting different life cycle steps of SARS-CoV-2. The main highlights of the study are to see the potential use of flavonoids against the (+) ssRNA viruses such as coronaviruses. There are some reported computational studies done by using docking techniques that mainly focused on inhibiting the coronaviral proteins such as 3CL protease, the spike protein and finally, by using synthetic biology pipeline and industrial biotechnology DBTL (Design, Build, Test, Learn) principle, to rationally design, construct and screen various libraries of antiviral properties of this family of natural bioactive compounds.

Keywords: COVID-19, pandemic, vaccine, antiviral, flavonoids, bioactive compounds, phytochemicals, synthetic biology.

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IN VIVO EVALUATION OF WITHACOAGULIN IN EXPERIMENTALLY INDUCED HYPERTENSION AND MYOCARDIAL INFARCTION IN ALBINO RATS.

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Abstract

Objective:Withacoagulin is an isolated natural product from *Withania coagulans* fruits and studied to evaluate the cardioprotective and antihypertensive effect in albino rats.

Methods: Myocardial infarction in rats was induced by isoprenaline (85 mg/kg; s.c.). Assessments of myocardial infarction in rats were done using biochemical estimations and histopathology of myocardial tissues. Hypertension in rats was induced by DOCA (10mg/kg; i.p.) and a diet rich in sodium chloride salt. Noninvasive tail blood pressure amplifier (NIBP200A) was used to measure blood pressure of conscious rats every day for four weeks.

Results: Biochemical assessment showed withacoagulin having similar antioxidant activity to Vit E. Withacoagulin significantly ($*P < 0.05$) improved glutathione level. Highly significant decrease ($P<0.01$) in the level of superoxide dismutase, catalase, creatinine phosphokinase and lactate dehydrogenase has been observed. Withacoagulin (25 mg/ kg) showed a strong cardioprotective effect in isoprenaline-induced myonecrosis in rat. A significant decrease ($P< 0.05$) in the blood pressure of withacoagulin treated group was observed. Withacoagulin at 50 mg/kg dose produced highly significant antihypertensive effect ($P< 0.001$) as compared to standard verapamil.

Conclusion: Biochemical and histopathology assessment showed strong cardioprotective effect of withacoagulin in experimental rats. Augmentation of endogenous antioxidants and maintenance of the myocardial antioxidant status may contribute to its cardioprotective effect. Antihypertensive effects of withacoagulin may be linked to blocking of calcium ion channels and vagus stimulation in the experimental animal.

Keywords: Withacoagulin, *Withania coagulans*, Cardioprotection, Antihypertension.

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SUPPRESSION OF PATHWAYS OF BRAIN INFLAMMATION BY FISETIN IN PTZ-INDUCED KINDLING IN MICE.

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Abstract

Introduction: Epilepsy is a complex neurological disorder, characterized by frequent electrical activity in the brain regions. Inflammation and apoptosis cascade activation are the serious neurological sequelae of seizure events during epilepsy. Fisetin (3,3′,4′,7-tetrahydroxyflavone), a natural occurring flavonoid molecule, is considered by its effective anti-inflammatory and anti-apoptotic properties. Accordingly, the objectives of the present study were to investigate its potential neuroprotective effect in models of epilepsy in experimental mice. In addition, the plausible neuroprotective mechanisms, especially those related to the neuronal inflammation, were also explored.

Methodology: For acute study, increasing current electroshock (ICES) test and pentylenetetrazole (PTZ)-induced seizures were used to evaluate antiseizure activity of fisetin. For chronic study, the kindling model was established by intraperitoneal (i.p.) administration of subconvulsive dose (25 mg/kg) of chemoconvulsant, PTZ. Animals were treated with fisetin (5, 10 and 20 mg/kg) to study its probable antiseizure effect and mechanism. The kindled mice were evaluated for seizure scores, neuronal damage and inflammatory mediators in the hippocampus and cortex.

Results: Our results showed that fisetin pre-treatment increased the seizure threshold current (STC) in ICES test in a dose-dependent manner. Furthermore, the fisetin administration increased the latency for myoclonic jerks (MJ) and generalized seizures (GS) in PTZ-induced seizures.In chronic study, fisetin treatment attenuated seizure activity and the associated neuronal damage in kindled mice. Also, fisetin treatment attenuated kindling-induced neuroinflammation evident from decreased levels of interleukins and tumour necrosis factor-α (TNF-α) levels in the hippocampus and cortex of kindled mice.

Conclusions: Overall, these findings suggest that fisetin might show a promising adjunct to antiepileptic agents in epilepsy .

Keywords: Pentylenetetrazole, Fisetin, Interleukin, Epilepsy.

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RAW AND AGED GARLIC EXTRACT: A COMPARATIVE ANALYSIS

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Abstract

Aging of Garlic *(Allium sativum L.)* for twenty months convert its reactive organosulfure compounds into odourless, non-irritating, safe sulphur compounds is called Aged Garlic Extract (AGE). The newly formed allyl compound like SAC, DADS, SAMC believe to have exceptional therapeutic benefit as of the raw garlic but their comparative antioxidative and organo-protective

potential is still under acknowledged. The present study was designed to perform a comparative analysis between the raw and aged garlic extracts for their antioxidative efficacy.

Phytochemical screening for raw and aged garlic extract was determined by qualitative methods. For antioxidative activity; DPPH, ABTS, Nitric oxide, Hydrogen peroxide activity was tested. Further, FRAP assay and lipid Peroxidation activity by FTC and TBA was also performed. To determine the cardioprotective effect, cytotoxic dose of aged and raw garlic was optimized by MTT assay. Morphological analysis on below and above the cytotoxic dose was also done and cell viability was observed by trypan blue assay. Our study suggests that aged garlic extract has higher antioxidative and cardioprotective activity compared to raw garlic.

Keywords: Aged garlic extract**,** Garlic, Antioxidants, Cardiovascular system, Oxidative stress.

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HYDROGEN SULFIDE IN CARDIOPROTECTION

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Abstract

ydrogen sulfide (H2S), is the third endogenous gas along with nitrogen oxide (NO) and carbon monoxide (CO) synthesized in cardiovascular system. H2S, which was originally considered as a highly toxic gas outside the body has now been emerging as signaling pathway with potential molecular mechanism to protect the heart against myocardial dysfunction, hypertrophy, IR injury and heart failure. Some mechanisms, like antioxidative action, protection of mitochondrial function, reduction of apoptosis, anti-inflammatory responses, angiogenic actions, regulation of ion channel, and interaction with NO, have been found to be responsible for the cardioprotective effect of H2S. Though, the mechanism of H2S mediated cardioprotective and homeostasis is not fully elucidated and need further research. The present review focuses on the recent insight of protective H2S molecular mechanism in various physiological and pathological cardiac conditions which can lead to new therapeutic target based on exogenous H2S donors.

Keywords: Hydrogen Sulfide**,** Cardioprotection, Homeostasis, Molecular Mechanism, Gasotransmitters.

Session V

AGRICULTURE, ENVIRONMENT AND INDUSTRY

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NOVEL MECHANISM OF ACTION OF ARSENATE REDUCTASE FROM ARSENIC RESISTANT BACTERIUM *Deinococcus indicus* DR1

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Abstract

Natural processes and anthropogenic activities release toxic pollutant Arsenic (As) into the environment. In nature, two ionic forms of arsenic are found. The trivalent form arsenite [As(III)] is considered more toxic but less abundant than the pentavalent form arsenate [As(V)]. To combat the widespread distribution of arsenic, many organisms such as bacteria and fungi have acquired resistance over time by developing pathways that degrade As(V) to As(III) using enzyme Arsenate reductase (ArsC).

Deinococcus indicus DR1 (Accession no. NHMK00000000) is a Gram-negative, rod shape, pleomorphic bacterium that has additional resistance toward highly toxic forms of arsenic. The key enzyme, arsenate reductase (ArsC), which converts pentavalent form to trivalent form of arsenic is not functionally characterized in *D. indicus*. Although it shares homology with the well-studied ArsC of *E. coli* having a catalytic cysteine (Cys 12) and arginine triad (Arg 60, 94, and 107), the active site of *D.indicus* ArsC contains four residues Glu 9, Asp 53, Arg 86, and Glu100, and with complete absence of structurally equivalent residue for crucial Cys 12 (PubMed:30610463).ArsC of *D. indicus* was able to complement the function in arsenate hypersensitive strain *E. coli* WC3110 (ΔarsC), thus proving that it is a functional enzyme. We report that ArsC of *D. indicus* is able to detoxify As(V) using a mix of positively- and negatively-charged residues in its active site, unlike the residues of *E. coli.*

Keywords: Arsenic bioremediation, *D. indicus* DR1, Molecular modelling, arsenate reductase.

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SECOND GENERATION BIOETHANOL PRODUCTION FROM RICE STRAW RESIDUES

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Abstract

Rice is one of the most major food crops for people in India. It is estimated that every kilogram of grain harvested produces ~1-1.5kg of rice straw. Rice straw is one of the abundant lignocellulosic waste materials and easily available. However, the rice straw is completely a waste and is removed by burning. As a result, this practice causes pollution and thus affects human health and many life forms. An alternative method to solve this waste problem without affecting the environment is to convert the rice straw into bioethanol. In this study, bioethanol was produced from rice straw feedstock by the fermentation process using *Saccharomyces cerevisiae* by maintaining its favourable temperature, pH and incubation period at 30°C, 5 and 28 hrs respectively. After 7 days of fermentation with *Saccharomyces cerevisiae*, ethanol concentration was measured and the highest yield of ethanol was found to be 18.2%. In this investigation, one major challenge we have faced is the selection of an appropriate pre-treatment technique for the feedstock. The present study also discusses the use of available pre-treatment technologies such as the physical treatment and chemical treatment (NaOH, HCl, H_2S0_4, Chloroform) for bioethanol production using rice straw and it was found that 8% NaOH treatment was the best available option for releasing maximum cellulose.

Keywords: Rice straw, bioethanol, fermentation, *Saccharomyces cerevisiae*, pre-treatment.

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RESIDUAL EFFECT OF HERBICIDES ON SOIL MICROFLORA OF BAJRA (*Pennisetum glaucum* l.)

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Abstract

A field experiment was designed to study the residual effect of herbicides (Pendimethalin, Phenaxoprop Ethyl, Pendimethalin + Propaquizafop Ethyl, Oxyfluorfen, Imazethapyr and Pendimethalin + Imazethapyr) applied for previous chickpea crop on soil microflora of succeeding Bajra crop. Herbicides applied to soil may persist for a long time and affect the microbial community. To analyze this residual effect, Bajra was grown in the field which was previously treated with herbicide for chickpea crop. Bacterial, fungal and actinomycetes populations decreased upon application of herbicides when compared to the control. Results indicated that soils treated with Oxyfluorfen, Imazethapyr and Pendimethalin + Imazethapyr recorded the lowest bacterial, fungal and actinomycetes population.

Keywords: Actinomycetes, Bajra, Herbicides, Imazethepyr.

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PURIFICATION OF CELLULASE ENZYME FROM PEEL OF *Colocasia esculenta*

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Abstract

Peel of *Colocasia esculenta* is considered as waste. In this study, our aim is to extract the cellulase enzyme from agrowaste. Crude enzyme was extracted from the peel *of Colocasia esculenta*, commonly known as taro. Fractionation of an enzyme is done using ammonium sulphate precipitation and further purified. Enzyme activity was seen in dialysed fraction of 0 to 60% ammonium sulphate precipitate. Presence of enzyme activity was also confirmed by Congo red diffusion test that involved incubation of 0 to 60% ammonium sulphate dialysed fraction on congo red infused agar plates for 24 hours at 50°C. The optimum temperature, pH, incubation time, substrate concentration for both Carboxymethyl-cellulase (CMCase) and Filter-paperase (FPase) enzyme activity assay was also determined by DNS method. The total protein concentration of crude and dialysed samples was 590.41ug/ml and 14.2ug/ml respectively. The specific activity of crude and dialysed was 1.165 U/min/ml of enzyme, 0.388 U/min/ml of enzyme. Cellulase from agrowaste can be of potential use in textile, dyeing, food industry. Purification and application of enzymes isolated from waste would be economically viable.

Keywords: Cellulase; Peel; ammonium sulphate precipitation; Congo red plate diffusion; Carboxymethyl-cellulase (CMCase); Filter-paperase (FPase) enzyme activity assay.

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HEAVY METAL INDUCED NEURONAL TOXICITY SERVING AS A PRECURSOR TO NDDS

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Abstract

Physiological integrity of the Central Nervous System (CNS) is essential for the healthy functioning of the brain and any disruptions in its physicochemical conformity results in irreversible neuronal damages like – cognitive impairments, proteinopathies etc. Such irreversible changes also occur in Neurodegenerative Diseases (NDDs) that are concerned with continuous loss of clustered neuronal cells and are associated with aggregates of protein. This will result in Alzheimer's disease, Parkinson's disease Amyotrophic Lateral Sclerosis (ALS), etc. Approximately 56 Million people are suffering from Alzheimer's disease and estimated to reach 88 Million by 2050. Certain reactive species which tend to react with various elements and molecules to activate neuronal cell death via an array of different signaling pathways which further contributes in the formation of toxic species such as ROS , Cholesterol Oxide, Peroxides and RNS.Out of the many sources responsible for causing oxidative stress and neurodegenerative pathologies, the human system interaction and intoxication with heavy metals is one of the leading causes, originated from industrial processes, ground water, contaminated foods, herbal components, etc. Epidemiological studies have shown that these heavy metals cause degeneration of neurons in various ways via DNA damage, Amyloidogenesis, disturbing Brain enzymes activities, etc. Heavy Metals targets processes and proteins which are involved in early onset of any disease such as, DNA and genotoxic damage, LPO, protein sulfhydryl's depletion, thiol degradation, cell differentiation and cell cycle regulation. This Metal toxicity engenders dysfunction of mitochondria and infers with normal functioning of cells.

Keywords: Alzheimer, proteinopathies, neuronal, herbal.

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NEGATIVE IMPACT OF COVID-19 ON THE ENVIRONMENT

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Abstract

Many papers have been published in the medical community related to the spread of Covid-19, which has surrounded the planet and killed many people. However its environmental and energy implications have not been properly examined. Some reports contend that the Covid-19 epidemic lowers environmental emissions, while others suggest that we are facing substantial environmental harm. On the other hand the concern is how the global scalable renewable energy market can react to the Covid-19 outbreak. In this report, the environmental and clean energy implications of the Covid-19 outbreak in the literature were analysed in depth and the results were presented.

It creates serious environmental pollution as a result of patient versatility in the environmental sense. On the other hand it often results in a decline in household waste, as people who are removed from reception are fearful of waste due to their sociological issues. On the other hand, decreases in carbon emissions have been observed due to a substantial decrease in public travel, decreased manufacturing, educational and other practises, but it has been seen that this is not enough to minimise contamination for all pollutants. The epidemic created very severe problems in the green energy industry, such as shortages in the supply chain, difficulties in the tax capital markets and thus the possibility of not being able to benefit from government subsidies ending this year. Investors are unstable because of the sector's instability. Thus, countries have had to show very serious incentives for renewable energy.

Keywords: COVID-19 outbreak, Renewable energy sector, Environment-Air pollution, Water pollution, Air Quality Index.

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EXPLORING PHYTOREMEDIATION POTENTIAL OF *Vigna radiate* AND *V. aconitifolia* UNDER CR(VI) INDUCED STRESS IN HYDROPONICS

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Abstract

A global concern regarding environmental pollution has gathered and among this Chromium contamination of agricultural soil has set up a critical challenge as its accumulation causes adverse effects on food safety and marketability and is noxious for human consumption. Toxicity of Cr to plants relies on its valence state where Cr (VI) is highly toxic. Therefore, present study investigates the phytoremediation of hexavalent chromium by leguminous plants; *Vigna radiata (RP3)* and *Vigna. Aconitifolia (RP2)* as a potential tool for reduction of Cr (VI) load hydroponically. The study was designed to compare the growth parameters of both the species on varying concentrations of chromium ranging from 100 mg kg^{-1} – 800 mg kg^{-1}. The seeds of *RP3 & RP2* were germinated and grown hydroponically for a period of 3 weeks and were assessed for toxicity parameters and remediation potential under hexavalent chromium stress. A significant decrease in root and shoot lengths were observed with increasing concentration in both the species with higher percentage decrease in *RP3* as compared to *RP2*. Percentage decrease in root length was recorded as 17.31% & 78.85% and shoot length as 26.39% & 72.22% in *RP3* at 100 mg kg^{-1} and 800 mg kg^{-1} respectively. Whereas; in *RP2* it was found to be as 9.26% & 72.22% in root as well as 18.67% & 68% in shoot at 100 mg kg^{-1} and 800 mg kg^{-1} respectively. Translocation factor > 1 was observed in both the plants with maximum as 2 in *RP2* at 600 mg kg^{-1} which makes it a better phytoremediator than *RP3*. Certain morphological aberrations such as necrosis of leaves and discoloration of roots and shoots were observed at 600 mg kg^{-1} and 800 mg kg^{-1} concentration of chromium. Therefore based on these observations it can be concluded that *V. aconitifolia can be* considered as a potential phytoremediator and hyperaccumulator of Cr(VI) over *V. radiata*.

Keywords: Cr(VI) stress, phytoremediation, leguminous plant, hyperaccumulation, phytotoxicity.

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MICROBIAL DEGRADATION OF PLASTIC WASTE

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Abstract

Global warming and climate change are the leading environmental challenges, World is facing these years. Plastic pollution is one of the major causes of climate change. Plastic are reported to have both environmental and public health related issues. Owing to the recent surge in the demand and disposal of plastic based products, the threat of plastic pollution to the global climate has now become a matter of concern. Plastic waste management strategies include landfills, incineration and recycling. Most plastic waste becomes a part of the landfills which further leads to problems like emissions of greenhouse gases, deterioration of land quality and water pollution. Recycling of plastic waste releases a significant amount of greenhouse gases too. Presence of micro plastics in the oceans interferes with the natural carbon fixation capacity of the oceans and also poses a serious threat to marine flora and fauna. It is estimated that release of greenhouse gases during the life cycle of plastics will reach approximately 1.34 gigatons per year and is expected to reach 2.8 gigatons per year by 2050. This comes as a threat to efforts put forth worldwide to limit global temperature increase to 1.5-2 degrees C by 2100. Therefore, the need of the hour is to look for after approaches for management of the plastic waste.

Microbial degradation of plastics is a cost-effective and eco-friendly approach for the management of plastic waste without causing damage to the environment. Different microorganisms are reported to possess the ability to degrade various types of commonly used synthetic plastics including polyethylene terephthalate (PET), polypropylene (PP), polyvinyl chloride (PVC), polystyrene (PS), polyurethane (PUR), and polyethylene (PE). Microbial degradation of plastics is an enzymatic process involving hydrolysis and oxidation reactions, resulting in cleavage of polymeric structures into small monomers. The observed changes in the polymer involves changes in the chemical structure and shape, mechanical strength, colour, and molecular weight of plastic polymers. Researchers have also done the sequence analysis of the various types of bacterial colonies living as biofilm on the plastic's surface obtained from the abandoned landfills. Recently, PETase (plastic eating enzyme) has been isolated that has potential to degrade PET.

Keywords: Climate change, Synthetic plastics, PETase , Greenhouse gases, Biofilm, microbial degradation.

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ENVIRONMENTAL IMPACTS OF CORONAVIRUS

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Abstract

In December 2019, an unknown coronavirus was detected to cause pneumonia-like disease in humans. It was related to the SARS-COV of 2003 and has caused tremendous loss to socio-economic life forms. It started spreading massively and affecting people globally. Extreme measures of partial-to-total shutdown might have influenced the quality of the global environment because of decreased emissions of atmospheric pollutants and water pollutants since the industries and factories had also been shut. This study aimed to understand its direct and indirect impacts on the environment. Reports on changes in the Air quality, water quality and Renewable energy sources were analyzed. It was seen that the air quality and water quality had increased whereas there was a decrease in the sources of renewable energy such as windmills and solar plants. This had direct effect and impact on environment which made coronavirus prove out to be a silver lining in the dark sky with increase in quality of air and water

Keywords: Coronavirus, Air Quality, Water Quality, global environment.

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POLYMER BIOSYNTHESIS PATHWAYS IN MICROORGANISMS

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Abstract

Microorganisms can biosynthesize a diverse range of polymers that with their biological functions and unique characteristics can serve as a suitable raw material for numerous industrial and medical applications. To improve economic-production efficiency and to produce tailor-made polymers with highly applicable material properties, one needs to understand the fundamental metabolic biosynthesis of the polymer inside the microorganism. Bacteria efficiently convert different carbon sources into various polymers with varying chemical and material properties. Bacteria produce four major classes of polymers: polysaccharides, polyamides, polyesters and inorganic polyanhydrides. Among these classes, polysaccharides is commercially more significant as it provides overwhelming diversity with respect to polymers formed. Bacterial polysaccharides include: glycogen, alginate, xythan, dextran, K30 antigen, cellulose, hyaluronic acid etc. Among these, cellulose is the most abundantly available polymer major source of which are plants. Plant cellulose has impurities like lignin and hemicellulose in it and also it is not an eco-friendly process. Therefore, bacterial cellulose proves to be a better alternative to fulfill the raw material availability. Pathway tools and Model SEED will be employed for analysing the molecular mechanisms and regulatory processes underlying the synthesis of bacterial cellulose that are capable of efficient and inexpensive biopolymer production exhibiting unique material properties for specific high-value applications.

Keywords: Bacterial cellulose, Biosynthesis, Polymers, Pathway tools, Model SEED.

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ANTIBIOTICS IN SOIL AND WATER AND ITS IMPACT ON LIVING ORGANISMS

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Abstract

In recent year's antibiotic use has gained immense popularity leading to their increased usage in human and veterinary medicines. They play an important role in providing treatment to the infectious diseases caused in humans, animals, and livestock. Due to antibiotic's excessive usage it has emerged as a major contaminant all over the world and causes its release to water and soil creating a major threat for all the life forms including microorganisms, humans, plants and animals. It has been observed that one of the major sources of antibiotic pollution is wastewater treatment plants. Up till now there is no availability of any technique or equipment which can help in remediating the compounds like antibiotics before discharging the effluent into water sources. Contamination of water sources such as lakes and streams leads to contamination of various other environmental sources. Occurrence of various antibiotics were reported in the sludge, manure, soil, plants, and animals across the globe. It affects the overall growth and functioning of the plants and inhibits the growth of soil microorganisms. Lately, India has emerged in the list of top countries having increased usage of antibiotics in the food-animal sector, leading to the rising rates of antibiotic resistance (ABR). There are various traditional remediation methods such as filtration, Ozonation, chlorination, adsorption, and photolysis, although any of the above mentioned techniques are not applied due to their expenses and conditions. Whereas, the biological remediation methods such as phytoremediation, and bioremediation have received immense popularity in recent years, over all other methods and technologies. Remediation using plants and microbes has various advantages, such as they don't require any specific conditions and they are not expensive.

Keywords: Antibiotics, Bioremediation, Contamination, Phytoremediation, Ozonation.

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IMPACT OF INFORMAL E-WASTE RECYCLING ACTIVITY ON SOIL

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Abstract

IT and communication sectors are causing an upshot of demand for electronic equipment exponentiallyand this rise in usage of electronic products has rocketed the E-waste discharge. E-waste is the cast-off of electronic products that has reached its end of life. It comprises more than 1000 different substances which are hazardous or non-hazardous.Chemically it is composed of various heavy metals (Pb, Sb, As, Cd, Ni, Hg, Cr, Cu, Zn), plastics and polychlorinated biphenyls (PCB). Due to the presence of such chemical components which are non-biodegradable, E-waste is globally associated with environmental contamination and health issues, therefore, there is a dire need for particular treatment and recycle practices for E-waste. If it is not disposed of properly, it will accumulate in the natural environment, which leads to adverse impact on environment and human health. Our country ranks third among E-waste producing countries. It is reported that India can only recycle 17.4% of its total E-waste, sustainably. In India solid waste management is a burdensome task and a large volume of such waste is handled in the informal sectors and recycled without any environmental safeguard. No proper mechanism or method are followed, to manage or recycle this waste and a lot of this ends up accumulating in landfills or traveling down in informal markets. Most of these unregulated sectors retrieve valuable metals, present in E-waste and sell them in the market for their profit and dump the rest. This can have a detrimental effect on the soil of a region it is dumped on. E-waste will then break down and releases toxic heavy metals which will leach into the soil and bioaccumulate in tissue and are biomagnified along with the tropic levels which influences the plants and trees that are growing in this soil, from plants and trees these toxins can reach the complete food chain and can harm all living organisms directly or indirectly.

Keywords: E-waste, Heavy metals, Soil, Recycle, Impact.

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VETIVER GRASS: POTENTIAL TOOL FOR PHYTOREMEDIATION OF HEAVY METALS

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Abstract

Heavy metal contamination in soil has become a worldwide concern and usually it occurs due to the various reasons such as improper management of agricultural leaching, sludge, metallurgical and electronic industry waste, and other chemical waste materials. . The soil of various regions around the world which are located near refinery and manufacturing industries contains high levels of various heavy metals (such as Pb, Mn etc), which possess health risk to humans and the surrounding environment. Also, Use of polluted water from rivers, and the water table for irrigation purposes leads to soil contamination with heavy metals and due to the less solubility and the carcinogenic heavy metals has made the condition worse. There are various physical and chemical conventional methods to remediate polluted soils contaminated with metals but these methods are expensive, time-consuming although they are efficient. Therefore it is important to develop new technologies that are less expensive and environmentally friendly. Phytoremediation is a cost-effective method, and safe for the environment, in which plants are used to remove complex contaminants from terrestrial or marine habitats. Recent research studies showed that Vetiver considered as a refining plant and remediation using this is considered as an effective and promising technique for removing contaminants in polluted water because of its vegetative characteristics, cost-effectiveness and high adaptation to environmental conditions. Vetiver is a tropical grass and non-invasive plant, which can survive and thrive under mild temperate conditions. It has a deep and complex root system. Recent studies showed potential of vetiver grass in phytoremediation for heavy metals removal and suggest that metals uptake is generally higher in root than in shoot. The aim of this review is to describe the potential of Vetiver grass for the phytoremediation of soils contaminated with heavy metals.

Keywords: Carcinogenic, phytoremediation, Pb (Lead), Mn (Manganese), Vetiver grass.

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MICROBIAL REMEDIATION FOR EXPLOSIVE CONTAMINATED SOIL: RECENT ADVANCEMENT AND FUTURE PROSPECTS

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Abstract

Environmental contamination with explosives has been posing a threat to human health and ecosystem. Explosives are highly reactive and energetic chemicals which are capable of self oxidation and classified as hazardous due to their toxic and recalcitrant nature. They can easily penetrate into the groundwater and soil which lead to harmful effects to human life and the environment. Explosives are mainly used in industries and demilitarization operations and due to their improper handling and disposal cause contamination of detonation sites and environment. Various methods have been developed for the remediation of explosive compounds such as physical, chemical and biological methods. Although physical and chemical methods fast, they lead to phase transfer of pollutant and inhibit mineralization which cause secondary pollution and to combat all these drawbacks biological treatment methods have gained importance due to their eco-friendly nature and effectiveness. Microbial remediation, a type of biological treatment plays a vital role in remediation of explosives by utilizing the ubiquitous nature of microbes. This method is sustainable and inexpensive and acts as an alternative to physical and chemical methods. Variety of different microbes such as *Bacillus, Pseudomonas, Simiduia, Salegentibacter* showed potential in biodegradation of explosives. This review summarizes information on the biodegradation and biotransformation pathways of several important explosives and assesses the various microbial treatment technologies, both in situ and ex situ available for remediation of explosive contaminated soil. Also, it discusses the potential of *T. viride* as a biological agent to eradicate the toxicity of the TNT explosive environmental impact and explore the future prospects of microbial remediation for soil explosive contamination.

Keywords: Microbes, *Bacillus, Pseudomonas, Simiduia, Salegentibacter, Trichoderma viride.*

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LAUNDRY DETERGENTS: A BRIEF OVERVIEW

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Abstract

Here we present a brief overview of advancements in the detergent industry. The Major driving force behind evolution of detergent formulations being – 1) Need to minimize energy and water consumption, 2) Raw material cost, 3) Green movement, 4) Advancements in appliance Technology and last but not the least 5) Safety regulations. Liquid as well as powder detergents have been formulated based on usage in textile or other surface cleansing purposes. In addition to above driving forces the basic criteria governing research advancements in detergent formulation have been washing temperature, fabric quality, time of cleansing and amount of water. Early formulations were harsh on fabric as well as skin. Further advancements incorporating enzymes were able to achieve efficient cleansing at the same time protect the fabric quality. However, the remnants of detergent formulations, leading to allergic reactions of skins are a major problem. Finally, we present currently used formulations that address this problem by using safer enzymes from genetically modified organisms.

Keywords: Detergent, Enzymes, Formulation, Genetically modified organisms, Technology.

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REGIONAL WASTEWATER CHARACTERIZATION SURVEY

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Abstract

The Basic principles and details on assessment of wastewater characterization are reviewed and reported for metropolitan areas with significant and powerful industrial activities, with great capacity for future development. The various human activities and iseeingndustries are playing a very important role offering tremendous environmental hazard. The conceptual approach related to the evaluation of pollution in terms of various important parameters is defined both for domestic & industrial sources. The present study elaborated upon wastewater survey and the physico-chemical characteristics of waste water discharge from industry such as COD, BOD, TDS and pH. The characteristics of the wastewater treatment practices in various regions of Uttarakhand are analyzed, where we analyzed the various procedures that take place to clean the water to supply that into the local household. From the available data reviewed and originated from the study it depicts the present pollution scenario at various regions and the local awareness among the general public about the wastewater treatment.

Keywords: Wastewater, COD, BOD, TDS, pH.

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EVALUATING THE PARAMETERS AFFECTING AIR QUALITY INDEX: CASE STUDY APPROACH

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Abstract

Pollution is the adulteration of atmosphere with substances that intervene with nature and hence affect the health of humans as well as animals. This study aims at assessing the rate of air pollution in Lucknow and Delhi with the prime focus on Particulate Matter 10, Particulate Matter 2.5, Sulphur Dioxide and Nitrogen Dioxide. Worldwide spread of COVID-19 in a short time has brought about a dramatic decrease in industrial activities, road traffic and tourism. Restricted human interaction with nature during this crisis has appeared as a blessing for nature and environment. A thorough analysis study of quality of air in Delhi-NCR and Lucknow with the help of certain research papers has been done by us for certain areas, and broadly, the analysis results of air quality data has revealed that the Air Quality Index was low during the lockdown period as compared to pre- and post-lockdown time. This paper also focuses on the October and November crop burning season which brings about a massive increase in AQI in the northern parts of India. It focuses on the factors leading to such a dramatic change in the air quality and also the various ways in which this situation can be tackled. It includes the data collected over the month of November to highlight how stubble farming is very harmful for our environment and can cause major health risks.

Our analysis reveals that there are various factors that affect AQI, mainly the particulate matters. The approach clearly identifies that there is a clear decrease in the AQI level during the lockdown months of 2020 and its level again reached the peak value in stubble burning season.

Keywords: Air Quality Index (AQI) , Air Pollution, lockdown, stubble burn.

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FUNGAL MEDIATED CONVERSION OF FOOD WASTE TO COMPOST

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Abstract

Food wastage is one of the wastes released from diverse sources such as households, food processing industries, institutions, hospital, catering services and other sectors while manufacturing, managing, and processing or on consumption steps. Recent studies show that composting is an effective technique for bioconversion of waste. Composting can transform food waste into hygienic, humus rich, products which conditions soil and enhances plant growth. Organic components of food wastes consist of vegetables, fruits, cooked food wastes and many others. This study focuses on the management of food waste and converting the waste into compost. Fruit and vegetable waste were collected from the canteen in VIT University, Vellore. The cleaned vegetables and fruits were blended together and fungal strain isolated was screened for the production of different enzymes such as amylase, protease, lipase and cellulose. These enzymes can break down complex compounds present in the fruit and vegetable waste thus accelerating the degradation process. Morphological identification was performed and fungus was confirmed as *Aspergillus niger*. Degradation ability of food waste crude extract was analyzed using HPLC. The potent fungus showed 95% of degradation rate. The waste was inoculated with the isolated fungi and converted to compost within 3 months duration.This compost showed good shoot and root length for *Vigna radiata* as confirmed in pot study. A significant reduction of food waste was achieved using biological methods to combat the increasing food waste crisis. These food wastes are converted to compost which can be used as a developing pathogen free soil amendment.

Keywords: food waste, lipase, protease, degradation, *Vigna radiata*, compost.

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ISOLATION AND CHARACTERIZATION OF BIOFILM PRODUCING BACTERIA FROM WATER TREATMENT TANK

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Abstract

Biofilm is a community of bacteria and other microorganisms, which provides various advantages like nutrition, protection from host defenses. However, biofilm is the main cause of the increase in antibiotic resistant microorganisms. Development of biofilms occurring on the inner surface of storage vessels offers a suitable medium for the growth of microorganisms and consequently contributes to the deterioration of treated drinking water quality. Biofilm formers secrete enzymes into the extracellular space to hydrolyze macromolecules into constituents that can be imported for microbial nutrition. The present study aims at the screening, isolation and characterization of biofilm producing bacteria from water treatment tanks using tube test, plate assay and ELISA technique. The 12 predominant isolated bacterial colonies were further studied for the presence of extracellular enzymes which are responsible for their growth and biofilm formation. Differential plate assay techniques were used for the qualitative detection of exoenzymes. Siderophore production was also analyzed to confirm the secretion of chelating agents. Reduced biofilm formation therefore represents a pleiotropic cost of defection from siderophore production. Seven out of twelve bacterial isolates showed positive results for biofilm formation in tube assay and ELISA plate assy. The potential strains were identified using the standard morphological and biochemical tests. These strains tested positive for lower production of siderophore. From the obtained results it can be concluded that the exoenzyme activity is not solely mediated by community composition, but possibly influenced by bacterial communication, which is known to regulate such pathways in many bacteria.

Keyword: Biofilm, exoenzyme activity, ELISA technique, water treatment tank, siderophore, bacteria.

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RECENT ADVANCEMENT IN PRODUCTION OF BIODIESEL USING OLEAGINOUS YEAST

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Abstract

Environmental conditions such as depletion of sustainable and renewable resources that triggers the high energy demand and energy independence, have led scientists to consider the production of biodiesel in future use. Biodiesel is a kind of biodegradable, non-toxic and ecofriendly biofuel that is typically produced by Transesterification of triacylglycerol (TAGs) and having similar composition same as of pre-existing diesel fuel but discharges fewer pollutants. In general, biodiesel has been produced from edible and non-edible oils, but the competition with food and limited resources, a large amount of research focuses on the single cell oil (SCOs) production . The SCOs accumulation in oleaginous yeast have been considered alternative products for biodiesel. These oily yeast are *Rhodotorula minuta*, *Rhodotorula glutinis*, *Rhodosporidium toruloides*, etc,. These oleaginous yeast are considered to accumulate 70% or more of their cellular weight in the form of microbial oil. Although the commercialization and increased demands in economical industries, have led towards high production cost of feedstock that lower the yield of lipid. Therefore to reduce the cost, lignocellulosic biomass such as wheat and rice straw, sugarcane molasses, cheese whey can be the promising approach to obtain commercial viability. In recent studies, low cost substrate in production of microbial lipids could be more beneficial by lowering the cost of downstream processing and fermentation strategies and accumulate higher lipid yield. New separation techniques such as saponification of yeast cells have been used. Several fermentation techniques have also been modified. Inhibitors are also playing a major role in production of microbial lipids.

Keyword: Biodiesel, Oleaginous yeast, lignocellulosic biomass, Fermentation.

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STRATOSPHERIC CALCITE AEROSOL VS STRATOSPHERIC SULPHUR AEROSOL FOR CLIMATE GEOENGINEERING

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Abstract

The globalization had brought with it, severe impact on the environment such as global warming. In order to eliminate the adverse effects of global warming, climate geoengineering is the conscious, large-scale interventions in the natural climate system of Earth. The two most prominent ideas of climate geoengineering are solar radiation management and carbon di-oxide removal. Studies have shown the importance of stratospheric aerosols spray in lower stratosphere (at a height of 10 km to 15 km) to create a global dimming effect, in solar radiation management climate geoengineering projects. This study taken under consideration was focused on contrasting the feasibility of use of sulphate and calcite aerosols in solar geoengineering.

The studies on the injection of sulphate aerosols into the stratosphere suggests that sulphate aerosols can potentially counteract the globally averaged temperature increase by reflecting and absorbing a certain fraction of sunlight back into the space. But, this approach towards solar geoengineering would entail new risks. The use of sulphate aerosols will result in increased ozone depletion. Therefore, an increased amount of solar ultraviolet-B energy will be reaching the surface, which might have a detrimental impact on health and biological populations on the surface of our planet. Also, the presence of an increased amount of Sulphur derivatives in the stratosphere will be a contributor to acid rain.

The studies on injecting calcite aerosols into the stratosphere suggests that the method could be a viable alternative of sulphate aerosols. The calcite aerosols will convert hydrogen halides and nitric and sulfuric acids into stable salts. This can be achieved while avoiding accelerated ozone depletion, increased penetration of UV rays through the atmosphere and acid rain, through the use of calcite aerosols.Moreover, the radiative heating of the lower stratosphere would be roughly 10 times less than that produced using sulphate aerosol. The studies underway will paved the way for a clean green approach in climate geoengineering.

Keywords: Climate geoengineering, Solar radiation management, Sulphate Aerosol, Calcite Aerosol, Global average temperature.

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A REVIEW OF MULTIPLE APPLICATION OF TANNASE AND DEVELOPING ZERO WASTE TECHNOLOGY

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Abstract

In India, 40-60% of solid waste generated annually is from food and agricultural sources. The disposal of organic waste leads to social, environmental, and economical issues. However, such residual plant biomass otherwise considered as wastes can potentially be converted into different value-added products including biofuels, bioproducts including enzymes, biomass for energy generation, bio-supplements for animal husbandry and agriculture. Tannase and its byproduct, gallic acid have many potential applications in food, feed, pharmaceutical and chemical industries. The present study focuses on utilization of organic wastes like peel of pomegranate, spent tea powder, Indian blueberry seeds, Indian gooseberry seeds, tamarind seed powder, taro and elephant foot yam as a natural source of tannin. These substrates are used for production of tannase and gallic acid through microbial fermentation. Post-fermentation the residual is used as a source of bioformulation that will aid in plant growth promotion. Through these we are going to produce a zero-waste technology, an improved and efficient waste management technique. Promising laboratory isolates of genus *Bacillus* and *Aspergillus* were used for tannase and gallic acid production. Maximum activity and gallic acid content at optimized condition for fungus *F1* and bacteria *B2.2* and *B2.7* were 4.44 U/ml/min, 0.54mg/ml, 4.82 U/ml/min, 0.55 mg/ml and 4.34 U/ml/min, 0.54 mg/ml, respectively. The study reveals that tannase and gallic acid production using food and agricultural wastes through microbial fermentation is more advantageous to commercially available synthetic tannic acid. These enzymes and phytochemicals can be utilized in different industries including food industry for the development of functional foods, improving animal feed quality, health industry for medicines and pharmaceuticals, and the beverage industry for clarification of fruit juices, among others. The use of waste and its residue to produce various bioactive components is an important step towards sustainable development.

Keywords: Organic wastes, tannase, gallic acid, phytochemicals, bioformulation.

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IMPACT OF PESTICIDES AND BIOPESTICIDES IN THE PRESENCE OF SALT STRESS ON *Cicer arietinum* AND *Phaseolus vulgaris* PLANTS

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Abstract

Plants grow in the environment and the environment is continuously changed, which is often unfavorable or challenging for plant growth and development. In terms of agriculture, various types of chemicals used to increase agricultural production for the growing population, are the possible reason behind this changing environment. Due to changes in the environment, several types of stresses are increases that adversely affect growth, development or productivity of plants. There are two types of environmental stresses; abiotic and biotic. Abiotic stresses such as drought, heat, light, salt, soil pH, heavy metals, ultraviolet radiation etc. Salt stress is a major abiotic stress which restricts the spread of plants in its natural habitats. Salt stress impacts the plant growth by affecting water balance, generating plant nutrition's imbalance, and influencing plant physiological and biochemical processes. Biotic stress includes different types of pests such as insects, herbs, fungi, weeds, nematodes, etc. These pests negatively affect agriculture by destroying around 35% of all potential food crops before harvest worldwide. For the control of the pests, various types of pesticides such as insecticide, herbicide, fungicide, weedicide and nematicide etc. are used. However, the excessive use of pesticides affects the plant growth, germination, biomass and plant yield. In this study, we observed the effect of pesticides (phorate and malathion) and biopesticide in the presence of salt stress on plants (*Cicer arietinum* and *Phaseolus vulgaris*). Pesticides negatively affected the plant growth but in the presence of salt stress, negative effects were more observed.

Keywords: Pesticides, biopesticide, environment, agriculture and salt stress.

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ENVIRONMENTAL IMPACT, MONITORING, TOXICITY AND BIODEGRADATION OF ORGANOPHOSPHATE WEEDICIDE ANILFOS: A CRITICAL REVIEW

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Abstract

Weeds are unwanted plants that grow in the agricultural field beside the planted crops and they compete for soil nutrients, water, and space. Crop protection cost increases due to weeds as they serve as an alternate host to multiple pathogens, insects, nematodes, etc. Weeds account for around 50% of the total annual crop losses of agricultural production in India, yield losses may reach up to 100 % if left uncontrolled. Weedicides are an integral component of modern agriculture to eradicate weeds efficiently. The application of weedicides helps farmers to increase crop yield and crop quality. However, weedicides contaminate soil, water and have negative side effects on soil microorganisms, plants, and other non-target organisms. Anilfos is an organophosphate weedicide used to control the pre/post-emergence monocot and dicot weeds, especially in paddy crops. The annual consumption of anilofos in India for the year 2019-20 is 138 MT.

Studies show that anilofos causes an inhibitory effect on *chlorophyll a* and *carotenoids* in *Synechocystis sp* even at 20 ppm. A daily administration of anilofos at 4.7-9.4 ppm for 3 months caused genotoxic and cytotoxic effects on the somatic and germ cells of Swiss albino mice. The synergistic impact of anilofos with other pesticides and heavy metals like arsenic are very harmful to various aquatic and terrestrial animals. To date, only one micro-organism, *Rhodanobacter xiangquanii* isolated from a wastewater treating system is reported to have anilofos biodegradation potential. Thus there is an urgent need to make microbial formulation for bioremediation of anilofos. This review critically analyses the environmental impact, toxicity, and the research gaps for bioremediation of organophosphate weedicide anilofos.

Keywords: Organophosphateweedicide, Anilfos, Yield loss, Biodegradation, Genotoxic, cytotoxic.

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MITOCHONDRIA AS AN IMPORTANT TARGET IN HEAVY METAL TOXICITY

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Abstract

Heavy metals are those metals which are having relatively higher density and are poisonous even at low concentrations. Once ingested, heavy metals get accumulated in the body. Few metals like aluminium may get excreted while others get accumulated in various organs of the body for a long time. These metals interfere with the normal structure and functioning of the cells. These divalent metals cause oxidative stress inside the cell and leads to excessive production of Reactive Oxygen Species (ROS) and due to high affinity of ROS towards thiol and selenol groups, ROS binds with antioxidants and makes them incapable of defiance against growing concentration of free radicals. The toxicity of metals is associated with their oxidative state and their reactivity to other compounds. However, in recent years, many studies have been published which demonstrated that mitochondria being a site of cellular oxygen consumption and energy production, can be a target for metals toxicity. Several toxic effects of heavy metals on mitochondria include disturbance in calcium homeostasis and mitochondrial membrane potential, uncoupling of oxidative phosphorylation, alteration in the activities of ETC complexes, mitochondrial proteins, lipids and DNA damage, and so on. Many studies have suggested that dysfunctional mitochondria can lead to many serious diseases including cardiovascular, pulmonary, organ damage, diabetes and many more. Using antioxidants such as chelators, vitamin E and C, herbal medicine, and by increasing the amount of antioxidants, oxidative injuries caused by metals may be restored. However, further experiments are yet to be carried out to explain certain aspects of the mechanism of metal toxicity.

Keywords: Mitochondria, Heavy Metal, Toxicity, Reactive Oxygen Species, Diseases.

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POTENTIAL EFFECTS OF INSECTICIDE ON NON TARGET ORGANISMS: A STUDY USING DROSOPHILA MODEL

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Abstract

Environmental safety and food security are the primary priorities of the infrequently increasing human population in the planet. As a result, vast quantities of insecticide chemicals are released into the atmosphere on a regular basis which has contributed significantly to improved crop yields and also in the management of insect-borne diseases (malaria, dengue etc.) to improve human health and wellbeing. However, excessive and indiscriminate application of insecticides does not only destroy targeted pests; it also impacts non-target species and the environment. Insecticides are commonly used to combat weeds and insect infestation in crop fields and disease vectors in households and workplaces. Some insecticides interrupt the nervous system, while others may by some other means i.e., damage their exoskeletons, repel them or control them. About 2 million tonnes of insecticides are used annually globally. Based on the chemical structure, major insecticides are grouped into: Organochlorines, Organophosphates, Carbamates, Pyrethroids and Triazines. Research on this issue has been significantly facilitated by the use of efficient genetic modelling insects such as *Drosophila melanogaster* as it has short, simple reproduction cycle; their genome is 60% homologous to that of humans, 75% of the genes responsible for human disorders are homologous to flies and whole genome is freely available in public domain which makes possible to study the molecular aspect of insecticidal research. Although each insecticide may affect at a different degree of danger to non-target species, it is very crucial to understand their cyto and genotoxicity effects on the non-targets.

Keywords: Insecticide, Non-target species, Genotoxicity, *Drosophila melanogaster*.

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TECHNIQUES OF NITRATE REMOVAL FROM GROUNDWATER- A REVIEW

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Abstract

Nitrate pollution of groundwater is a major concern across the world, as nitrate cause methemoglobinemia and cancer in Humans. Several techniques have been developed to reduce nitrate from water which vary in degree of efficiency, cost of operation and its merits and demerits. This paper reviews various techniques of nitrate removal that has been carried out including Reverse Osmosis, Ion exchange, Electrodialysis, Catalytic denitrification, Membrane bioreactor, Nanofiltration and Biological denitrification. According to literature, Physicochemical techniques are effective in nitrate reduction but cost of operation is very high.

Hence, biological denitrification is a more effective and acceptable technique for denitrifying groundwater and industrial wastewater.

Keywords: Nitrate, Methemoglobinemia, Cancer, Denitrification, Groundwater.

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ROLE OF TRAVEL COST METHOD AS A NON-MARKET VALUATION METHOD IN DETERMINING ECONOMIC COST OF THE RECREATIONAL SITES IN INDIA: A BIOECONOMIC PERSPECTIVE

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Abstract

Bioeconomic studies have provided a robust approach for the valuation of non-market valued products using two different approaches viz. revealed preference and stated preference methods, which includes various approaches for estimating the cost of products that cannot be directly valued using conventional cost analysis methods. With scarce studies, primarily from India, one of the commonly used Non-market valuation methods to determine the cost of sites within India is the Travel cost method (TCM). The travel cost method is mostly used to estimate the cost of recreational activities. It is considered as one of the oldest and simplest methods used till now. It is mostly used for calculating consumer surplus and economic worth of the recreational area. This approach however involves more data analysis and somewhat more complex analysis, however, produces more reliable results. Non-Market Value methods are used to estimate indirectly the cost of habitat or site based on the spending pattern and number of visits which an individual's travel spend to visit a specific site. Largely the data also depends on the income, demography, spending, attributes of the habitat, or place. There are further two types of travel cost methods viz. Zonal travel cost methods and individual travel cost methods primarily categorized the respondent based on the zone of origin (country or state) and individual primary response. The primary data help in the analysis of willingness-to-pay, a parametric analysis used for cost estimation.

Keyword: Travel cost method, Non-market valuation method, Biological resources, Cost, Willingness-to-pay.

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PRESENCE AND REMEDIATION OF AMOXICILLIN AND TETRACYCLINE BY *Ocimum basilicum*: A SUSTAINABLE APPROACH

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Abstract

Presence and fate of antibiotics in the environment and related risk for plants and human health is a serious concern. The present review is elaborated upon an overview of antibiotics presence in the soil and water in the environment. Further, this review also highlights the fate of these antibiotics in soil, water and their uptake by plants. Antibiotics are released in the environment and may cause significant impact on different environmental channels. This review briefly discusses the research undertaken so far and benefits of using *Ocimum basilicum* for remediation of antibiotics. A sustainable approach to mitigate antibiotics contamination of the environment is the need of the hour. *Ocimum basilicum* seems most suitable for phytoremediation of heavy metal contamination. Therefore, we can say *Ocimum basilicum* isemerging as an ideal plant for phytoremediation.

Keyword: Amoxycilin, Tetracyclin, *Ocimum basilicum,* Phytoremediation.

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