December 13-14, 2023

UMTCLS

1st UMT International Conference on Life Sciences:
Exploring the Frontiers in Biological Research

ABSTRACT BOOK

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Preface

Pakistan Science Foundation (PSF) and Department of Life Sciences, School of Science, University of Management and Technology (UMT) Lahore Pakistan jointly organized the 1st UMT International Conference on Life Sciences, "*Exploring the Frontiers in Biological Research*' on December 13-14, 2023 at University of Management and Technology, Lahore, Pakistan.

The conference aimed to foster interaction, networking and collaboration between academic and professional researchers from esteemed national and international universities to encourage sharing of knowledge and technology. Our mission is to establish a collaborative environment among researchers and academicians on a platform to exchange their ideas, research and developments in various fields of science and technology. Our vision is to derive innovations and new approaches in the area of biological sciences.

We had international speakers from UK, USA, Turkey, Thailand, Norway, Lebanon and South Korea. Over one hundred and fifty researches presented their work related to conference themes i.e., Biotechnology, Molecular Biology, Plant Sciences, Animal Sciences, Microbiology, Bioinformatics, Genetics, Biochemistry and Immunology. There were 41 invited speakers, 46 oral presenters and 60 poster presenters who presented their research works in different fields.

Best part was that students from different universities were able to interact with the senior researchers under one roof and could learn from peers.

Our foreign speakers Prof. Dr. Michael, J. McInerney (USA), Prof Dr. Nessar Ahmed (UK), Dr. Muhammad Zahoor (Norway), Dr. Khurram Liaqat (USA), Dr. Aamir Lal (Korea), Dr. Yasir Waheed (Lebanon), Dr. Muhammad Nouman (Thailand) and Dr. Sami Simsek (Turkey) inspired the young scientists with their intellectual lectures and fostered a very rich environment that prompted critical thinking in the audience.

Honorable Prof. Dr. Shahid Munir (Chairperson, Punjab Higher Education Comission) participated in the panel discussion on ways and means to collaborate with international academia linkages.

Worthy Rector UMT Dr Asif Raza (S.I, H.I) addressed on significance of event at Inaugural ceremony of conference and respected D.G. UMT Abid HK Shirwani awarded souvenirs and certificates at concluding ceremony.

CONFERENCE PATRONS

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President UMT

Prof. Dr. Asif Raza S.I. H.I.

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Vision and Mission-UMT

Our Vision is ***Learning***

It defines our existence, inspires all stakeholders associated with us, creates a powerful momentum inside, and responds to the challenges outside. It continues to evolve as present captures new realities and foresight unfolds new possibilities. All in an incessant attempt to help individuals and organizations discover their God-given potentials to achieve Ultimate Success actualizing the highest standards of efficiency, effectiveness, excellence, equity, trusteeship and sustainable development of global human society.

Our Mission is ***Leading***

We aspire to become a learning institution and evolve as the leading community for the purpose of integrated development of the society by actualizing strategic partnership with stakeholders, harnessing leadership, generating useful knowledge, fostering enduring values, and projecting sustainable technologies and practices.

About School of Science

Vision of the School of Science is to be a leader in scientific research, teaching, and service, while also being committed to promoting inclusivity, diversity, and equity in our community.

Mission of the School of Science is to advance the frontiers of scientific knowledge, prepare our students to be successful leaders in the sciences, and contribute to the betterment of society through scientific discovery and community engagement.

About Department of Life Sciences

Vision

Department of Life Sciences at UMT will be recognized as the regional, national and international leader in research. Department of Life Sciences will also focus on a vision to carry out world-class, multidisciplinary education and research. We strive for our students to build their future by helping them set personal and professional goals.

Mission

The mission of the department is to provide students with the opportunity to explore the science of life in all its complexity and diversity through teaching and research programs. Department aims to become a doorway of opportunities by admitting students independent of financial, social, gender, ethnic, or religious boundaries. Our graduates should be well educated in the history of scientific discovery in biology, the logical, statistical procedures used to formulate as well as to test the biological hypothesis, and skills needed for conducting contemporary biological research.

About UMT Journals

High Quality research presented at the conference will be published in the following journals of UMT, i.e., BioScientific Review (BSR), Current Trends in OMICS (CTO), and Scientific Inquiry and Review (SIR) upon the researcher's request. All these journals are designated as **Y-category** under HEC Journal Recognition System, Pakistan.

About the City of Lahore

Being the 2nd largest city of Pakistan with a population of over 13 million, Lahore is the capital of Punjab province, has been a brilliant symbol of a gracious way of life. It had been the abode of great people, both in the spiritual as well as worldly realms. Lahore having been the seat of many imperial dynasties, possesses interesting historical reminiscences. There is a fascinating and colorful panorama of extraordinary mosques, mausoleums, forts, gardens and the like. Rather it is its atmosphere and ambience, its moods of joy and sorrow, fairs and funs, pains and pleasures, and above all the colorful life of its people which actually render impetus to the spirit of Lahore.

Titles of Presentations

PLENARY LECTURES

PL-1

Syntrophy as an Essential Interaction in Methane Production

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Abstract

Syntrophy is a tightly coupled, mutualistic interaction among microorganisms that is essential for the global cycling of carbon in virtually all anaerobic environments. The advent of metagenomic analyses has revealed the importance of syntrophy in microbiomes of many animals and in the evolution of the eukaryotic cell. However, our basic understanding of the biochemical processes involved in syntrophy is very limited, and this impacts our ability to predict methane flux in natural habitats, to control waste degradation, and to maximize the conversion of renewable resources to the energy-rich fuel, methane. In syntrophy, the microbial partners exchange metabolites and the concentrations of these metabolites must be kept very low for syntrophy to proceed. The syntrophic metabolizer produces hydrogen and formate during the metabolism of their substrates such as propionate, butyrate, and benzoate. In return, a partner microorganism, usually a methanogen, consumes these products, keeping them at the very low concentrations necessary for the degradative reaction to be energetically favorable. We used proteomic, biochemical, and metabolomic approaches to elucidate the enzyme systems involved in substrate degradation, electron flow, and energy conservation during syntrophic metabolism. Our work explains the obligate requirement that syntrophic metabolizers have for a hydrogen/formate-consuming partner (i.e. methanogens).

Keywords: Synntropy, Microbial interactions, Metabolic exchange, Methane production.

PL-2

The Role of miRNAs in The Diagnosis of Cystic Echinococcosis

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Abstract

Cystic Echinococcosis (CE) is one of the important zoonotic diseases caused by *Echinococcus granulosus* in humans and animals. It is frequently seen in humans and animals in underdeveloped countries, especially in rural areas, and causes serious health problems in humans and economic losses in animals. In addition to imaging methods, many serological methods such as Immunofluorescent Antibody Technique (IFAT), Enzyme-Linked ImmunoSorbent Assay (ELISA), Western Blot (WB) and Indirect Heamagglutination Test (IHA) and PCR-based molecular methods are used in the diagnosis of CE. miRNAs are small (18-24 nt) non-coding RNAs that post-transcriptionally regulate gene expression by inhibiting protein translation or destabilising target transcripts. miRNAs have been identified to have an active role in host-pathogen interaction and host immune responses against microorganisms. Transcription of intergenic miRNAs is one of the main biofunctional pathways in parasites, depending on the preference of the original genes to targets that expand in different cell types and tissues at developmental stages. These observations suggest that miRNAs are important in *Echinococcus spp.* and CE and could therefore be used as diagnostic or therapeutic targets. Approximately 10-14% of the *Echinococcus spp*. genome consists of exons, while other genes are transcribed as intron RNAs. Non-coding RNAs are classified into two types according to their molecular weight. The first of these is miRNAs, with an average length of 18-24 nucleotides, and the length of these short RNAs is <200 nt. The other is Long non-coding RNAs (LncRNA), which are longer than 200 nt. miRNAs and LncRNAs have been reported to be found in species such as *E. granulosus*, *E. multilocularis* and *E. canadensis*. Up to date, 87 highly conserved miRNAs have been reported that are thought to play important roles in the development and parasitism of *Echinococcus spp*. Among the 76 known conserved miRNAs of *E. granulosus* s.s., miR-2, miR-71 and miR-125 have the highest expression levels. Interestingly, the expression levels of miR-124b and miR-87 are higher than those of mature miRNAs, indicating that they act as effectors during development and that derivatives of the corresponding miRNAs produce two different regulatory small RNAs, and in addition, miRNAs exhibit tissue- and phase-specific expression. miR-277, let-7, miR-71, miR-10, miR-2 and miR-9 were specifically expressed in secondary hydatid cyst walls and protoscolecules of G1 and G7 genotype, whereas miR-125 was detected only in protoscoleces and pre-microcysts. In addition, three miRNAs (let-7, miR-71 and miR-2) were reported to be expressed at high levels in protoscolexes. let-7 was noted to exhibit a significantly increased expression in the protoscolex and cyst wall, which may be related to the bidirectional developmental capabilities of *E. granulosus*.

Keywords: Cystic Echinococcosis, *Echinococcus granulosus*, Zoonotic diseases, Tissue-specific expression, miRNAs (microRNAs).

PL-3

Role of Advanced Glycation End Products in Diabetic Retinopathy

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Abstract

Diabetes mellitus is a huge health concern and affected 537 million people worldwide in 2021. Diabetic retinopathy is the most common long-term complication of diabetes affecting the eyes and if untreated causes blindness. Indeed, within 20-years of diagnosis, around 60% of diabetic patients will develop some degree of retinopathy. Diabetic retinopathy is characterised by uncontrolled angiogenesis afflicting the eye retina. Poor control of diabetic hyperglycaemia increases the likelihood of developing diabetic retinopathy. High glucose can react non-enzymatically with proteins and other molecules via glycation to form advanced glycation endproducts (AGEs). Build-up of tissue AGEs have been implicated in the chronic complications of diabetes including retinopathy. Indeed, methylglyoxal a reactive dicarbonyl compound found in retinal cells can rapidly form AGEs that are not only detectable in the retina but have been implicated in the pathogenesis of diabetic retinopathy. The anti-glycation compound aminoguanidine reduced the progression of retinopathy in clinical trials but had unacceptable side effects. Furthermore, opticin, a 45KD protein located in the vitreous, retina and other parts of the eye inhibits angiogenesis and could offer protection against retinopathy. Recent studies in our laboratory have shown that glycation of opticin impairs its anti-angiogenic properties and such an effect in vivo may partly explain uncontrolled angiogenesis in patients with diabetic retinopathy. The exact role of glycation and AGEs in the pathogenesis of diabetic retinopathy deserves more attention in order to understand the underlying cellular and molecular mechanisms so that an effective treatment can be developed.

Keywords: Diabetes mellitus, Diabetic retinopathy, Aminoguanidine, Advanced glycation end products, Anti-angiogenic properties.

PL-4

Identification of Key Regulators in Cellular Proteostasis

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Abstract

Proteostasis encompasses the balance between protein synthesis, trafficking, and degradation. The endoplasmic reticulum (ER), responsible for approximately one-third of the proteome, serves as a central hub for cellular proteostasis. Newly synthesized secretory proteins, after folding and undergoing quality control, exit the ER via specialized domains known as ER exit sites (ERES) in a COPII-dependent manner. These ERES, not only plays a vital role in ER export but also provide platform to growing autophagosomes. Thus, autophagy and secretion are the two fundamentally interlinked processes that are mediated by the endomembrane system. Although the fact that autophagy and secretion are linked, is well accepted, we lack mechanistic and systematic understanding of this link. Therefore, we screened an RNAi library of the regulators of autophagy, for their effect on ER-Golgi trafficking. In this work, we identified novel regulators of ER proteostasis, and unveil their molecular mechanism in physiological and pathological settings.

Keywords: Proteome, Proteostasis, ER exit sites, Autophagy, Autophagosomes, RNAi.

PL-5

Transforming Diabetic Foot Care with Innovative Orthotic Management by Bridging Research and Clinical Practice

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Abstract

Diabetes mellitus is highlighted as a global health challenge, impacting millions of lives worldwide. Among resulting complications, diabetic foot issues appear as a serious clinical issue including ulceration, re-ulceration, infections, and even major or minor amputation. Repetitive abnormal peak plantar pressure acting on the plantar surface of the foot contributes to the ulceration and re-ulceration during gait in diabetic foot with neuropathy. The complications can be confronted with appropriate selection of orthotic design and material to offload the repetitive abnormal peak plantar pressure. In recent years, remarkable breakthroughs in materials and technologies help in reshaping the diabetic foot orthotic interventions. In-shoe measuring techniques are used to clinically evaluate the peak plantar pressure during gait, to estimate risk factors associated with ulceration. While in-shoe sensors have provided invaluable information on plantar pressure, they have limitations in capturing shear stress, a key player in ulcer development. Experimental procedures are commonly followed to identify appropriate material and type of interventions to redistribute the abnormal peak plantar pressure. In addition to orthotic management, ground-breaking steps are taken by utilizing computational modelling to bridge the gap between research and clinical practice in diabetic foot complications. Developing innovative approaches to evaluate and reduce the risk through both in-shoe measuring techniques and advanced numerical simulations. The computational models have revealed significant insights into abnormal peak plantar pressure with diabetes severity, affecting plantar pressure distribution and contributing to ulceration. This reveal the potential of finite element analysis in understanding the complex interaction of external and internal shear stresses—an essential factor in diabetic foot ulceration. By combining computational insights with real-world data, a significant impact endeavor to select appropriate material and design to prevent and treat diabetic foot complications.

Keywords: Diabetic foot, Diabetes mellitus, Ulceration, Orthotic intervention, Peak plantar pressure.

PL-6

The Hidden Players of Nature: Microbial Diversity, Microbiomes, and Microbiota

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Abstract

Microorganisms possess immense influence in shaping the environment and life on our planet. The significance of microbial diversity goes beyond conventional comprehension, carrying profound consequences for ecosystems, human health, and advancements in biotechnology. A myriad of microorganisms, encompassing bacteria, viruses, fungi, and archaea, actively coordinate nutrient cycles, decomposition, and symbiotic connections, enriching the biological landscape of Earth. Extending beyond humans, microbiomes also exert influence over soil fertility, plant vitality, and even the equilibrium of ecosystems within the oceans. The exploration of microbial diversity, microbiomes, and microbiota has undergone a revolutionary transformation through metagenomics—a genomic technique that scrutinizes the total DNA of complex microbial communities. By directly sequencing samples from the environment, metagenomics brings to light new species and offers access to functional understandings. Metagenomics can reveal novel enzymes, antibiotics, and ecological interconnections that possess the potential to propel advancements in biotechnology. The potential for exploring microbial realms knows no bounds. In case of human health, unlocking the potential of microbiota could unlock pathways to disease treatment. For environmental conservation, unraveling the unique microbial imprints within endangered ecosystems could provide valuable insights to guide preservation endeavors. Furthermore, elevating crop production might involve in-depth exploration of intricate microbial societies intertwined with plants. This talk delves into the importance of diverse microorganisms, the roles of microbiomes and microbiota, and the exciting horizons that await exploration.

Keywords: Microorganisms, Bacteria, Microbial diversity, Metagenomics, Microbial ecology.

PL-7

Designing Proteins for Therapeutic and Industrial Applications

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Abstract

Ever since of cloning the first gene was accomplished about fifty years ago, a rapid expansion took place in the scope, strategies and application of recombinant DNA techniques for the production of proteins for applications in industrial, pharmaceutical, petroleum industry and other areas. The different groups of the products from this technology include enzymatic, regulatory, immunological, and other proteins. Not only the volumes of the products but the areas of applications have also expanded rapidly. Largely based on *E. coli* expression system, techniques including site-directed mutagenesis, error prone PCR, in vitro recombination, truncation of molecules, fusion of the selected protein segments have been used. The success of this technology has been supported by a variety of powerful in silico tools as well as availability of the high-throughput automated screening techniques. This technology has made it possible to not only achieve large scale production economically, but also enabled us to obtain the product with improved properties like enhanced activity, stability, solubility, and other characteristics, which are highly important for large scale applications. Using these approaches, we have modified some enzymes for enhancing their activity and solubility. Also, enzymes of multiple activities have been constructed for application in the saccharification of plant biomass polysaccharides like cellulose and xylan. An important area for application of these strategies is construction of fusion molecules from multiple antigens for development of a reliable serodiagnosis and an effective vaccine for tuberculosis (TB), which is caused by *Mycobacterium tuberculosis* (Mtb) and takes over one million lives every year. Details of these procedures and their outcomes shall be discussed.

Keywords: Recombinant DNA techniques, Protein production, *E. coli* expression system, Enzyme modification, Fusion molecules, Tuberculosis diagnosis.

PL-8

Bioscience: Dry or Wet?

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Abstract

Genome sequencing has provided an enormous amount of information on the primary structure and number of genes in a particular organism. Based on the assumption that genes with high similarity encode proteins of common function, the presence or absence of various orthologues is often used in estimating whether a specific metabolic pathway is present or not. This approach, however, has its limitations. When an orthologue of an expected enzyme is not found, one must identify the gene through classical biochemical and cloning methods. On the other hand, when multiple orthologues are present on the genome, one must carefully examine each gene product in order to distinguish their enzymatic activities or functions in the cell. These limitations, with their solutions which lead to the discovery of novel enzymes, will be discussed during the talk.

Keywords: Genome sequencing, Orthologues, Metabolic pathway, Enzyme identification, Biochemical methods, Novel enzymes.

PL-9

Can Agricultural Biotechnology Mitigate Climate Change?

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Abstract

Pakistan ranks among ten worst climate change affected countries of the world. The major catastrophic risks emanate from global warming, such as intensification of droughts and flooding, sea level rise and greater frequency of intense storms and cyclones. The source of climate change is multidimensional, the major being the emission of greenhouse gases. Climate change impacts on agriculture results on lower crop yields, more pests and disease" more wild fires, increased soil salinity, high temperature, more flooding, more drought and increased heat stress (2021). Agriculture biotechnology provides ways to both mitigate and enhance adaptation to environmental changes Products developed with agriculture biotechnology may contribute to the reduction of greenhouse gas emissions, such as cover crops that provide sustainable biofuels, fruits and vegetable with greater shelf life and reduce food waste. Ways and means are being developed to draw excess carbon dioxide out of the atmosphere with trees and even microbes.

Keywords: Pakistan, Climate change, Greenhouse gases, Agriculture biotechnology, Adaptation, Carbon sequestration.

INVITED LECTURES

IL-1

Concurrent Removal of Hexavalent Chromium and Degradation of Azo Dyes and Plastic by *Ochrobactrum intermedium* Isolated from Industrial Wastewater

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Abstract

The multiple metal-resistant Gram-negative *Ochrobactrum intermedium* strain 1-525k was isolated from tannery effluents, demonstrating optimal propagation at 37°C and pH 8. The minimum inhibitory concentration (MIC) test showed that *O. intermedium* 1-525k could tolerate up to 30 mM Cr^{6+}, and also exhibit the ability to resist other toxic metal ions including Pb^{2+} (11 mM), As^{3+} (3 mM), Zn^{2+} (17 mM), Cd^{2+} (5 mM), Cu^{2+} (3 mM), and Ni^{2+} (2 mM) with the resistance order as $Cr^{6+} > Zn^{2+} > Pb^{2+} > Cd^{2+} > As^{3+}/Cu^{2+} > Ni^{2+}$. *O. intermedium* 1-525k showed maximum biosorption efficiency (q) of 48 mM Cr^{6+}/g after 6 days. Chromate stress elicited pronounced production of antioxidant enzymes such as catalase (CAT) 191%, glutathione transferase (GST) 289%, superoxide dismutase (SOD) 168%, peroxidase (POX) 275%, and ascorbate peroxidase (APOX) (200%). Within *O. intermedium* 1-525k, the influence of Cr^{6+} stress (2 mM) did stimulate a rise in levels of GSH (589%) and non-protein thiols (112%) were measured as compared to the control (without any Cr^{6+} stress) which markedly nullifies Cr^{6+} generated oxidative stress. The pilot scale experiments utilizing original tannery effluent showed that *O. intermedium* 1-525k could remove 99% Cr^{6+} in 6 days. The bacterium was also able to degrade azo dyes and plastic. Thus, it could be a potential candidate to reclaim the metal-dyes contaminated sites.

Keywords: *Ochrobactrum intermedium*, Metal-resistant, Biosorption, Antioxidant enzymes, Chromate stress, GSH, Azo dyes, Plastic degradation, Environmental reclamation.

IL-2

Advances in Dengue Vaccine Research: The Pakistani Perspective

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Abstract

Dengue is currently one of the most important mosquito borne viral diseases of humans worldwide. It is transmitted through female mosquitoes, mainly *Aedes aegypti* and *Aedes albopictus*. Dengue virus (DENV) infection is a major global public health concern, leading to about 10,000 deaths annually across over 125 countries in the world. Pakistan is highly susceptible to epidemics of dengue because the climate is suitable for *Aedes* mosquitoes. Dengue affects more than 100 countries in the tropical and subtropical world with 100–400 million infections every year. No specific anti-viral treatment exists, and therapy only consists of supportive care. The safety concerns of dengue vaccination programs lead to urgent requirement of safer and more effective second-generation dengue vaccines. An epitope-based vaccine provides more specific immune response and excludes the probable mortal effects from the use of whole viral proteins. The key objective of these research projects is to design Dengue vaccine based on Multiple Antigen Peptide system design for DENV-serotypes prevalent in Pakistan, also study the effect of vaccination with Multiepitope vaccine construct on Animal model studies to evaluate the efficacy of designed vaccine. Other avenues under exploration are mRNA-based vaccines for Dengue control.

Keywords: Dengue, vaccination, mosquito-borne diseases, epitope-based vaccine, animal model studies, mRNA vaccines.

IL-3

Camellia sinensis Loaded Iron Oxide Nanoparticles: Synthesis, Biodistribution and Cytotoxic Effects

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Abstract

Iron oxide nanoparticles due to its magnetic and dielectric properties are of particular importance in various fields of bio nanotechnology. *Camellia sinensis* loaded nanoparticles were synthesized under varying conditions and characterized by UV spectrophotometry, FTIR, XRD and SEM. Present research work was designed to check the in vitro and in vivo bio activity, including biocompatibility and bio distribution, of iron oxide nanoparticles. Iron oxide nanoparticles were also found to be 100% biocompatible with the erythrocytes in PBS medium and showed best radical scavenging ability of 34%, while green tea showed 28 % and salt showed only 24 % of activity at 1000 µg/ml concentration. The betterment in antioxidant ability of Iron nanoparticles i.e. 69 % greater than ferric chloride was observed but was still 60% less than green tea ability. Cellular toxicity against the HCT-116 cancer cell line showed 85 % cell viability inhibition at 800 µg/ml concentration of iron NPs, showing their effective cytotoxic ability towards cancerous cells. In vivo bio distribution of nanoparticles was studied in Rabbit model. Synthesized nanoparticles were labelled using Technetium-99 m. The potency of iron NPs and iron salt as fertilizers was also studied which highlights that nanoparticles itself were quite reproductive and along with the bacteria *Bacillus subtilis* showed best results by increasing the plant growth up to 11% and chlorophyll content respectively. The aim of the study was to explore the applications of iron NPs along with their toxicity profiling for further future studies that can lead to their practical application in our daily life and to benefit the society through an easily approachable, ecofriendly and cost-effective nanotechnology, which can be the helpful in finding new ways to cope problems in the near future.

Keywords: Iron oxide nanoparticles, Bioactivity, Antioxidant, Cytotoxicity, Bio-distribution, Nanotechnology.

IL-4

Healthy Diet is Not Expensive, Cost Analysis of Different Diets from Major Cities of Pakistan

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Abstract

Unhealthy diet is one of the major risk factors for non-communicable diseases and is readily available. Over the years, dietary behaviors changed and there is a misperception that a healthy diet is expensive. The aim of this study is to do a cost analysis of healthy and unhealthy diets in Pakistan. This study was conducted in federal and provincial capitals of Pakistan. Using a stratified random approach, in the first stage, three union councils (UCs) were selected from each city and in second stage, 150 households were identified. The head of the selected household was interviewed and data about diet intake was collected from adults using food frequency proforma. Similarly, the cost of the dietary items was obtained from the grocery/general stores located in the selected UCs. The expenditure was assessed using the micro-costing technique. The analysis showed an unhealthy diet was more expensive. A significant difference ($p < 0.0001$) was recorded in terms of expenditure on the unhealthy diet (66.5%) as compared to the healthy diet (33.5%). This study showed that an unhealthy diet is expensive and there is a need to educate people about the importance of a healthy diet and its cheap availability.

Keywords: Unhealthy diet, Cost analysis, Healthy diet, Dietary behaviors, Diet intake.

IL-5

Genetic Diversity in ssDNA Viruses: Deciphering the Role of Interspecies Recombination in Speciation

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Abstract

This study delves into the molecular characterization and evolutionary processes of a newly identified begomovirus, tentatively named "*Chenopodium Leaf Distortion Virus*" (CLDV), found in association with *Chenopodium album*in Lahore, Pakistan.Our investigation focuses on the role of *C. album*as a reservoir for ssDNA viruses, emphasizing the emergence of novel species through recombination events. The complete sequencing and cloning of the DNA-A genome of CLDV revealed a significant 93% sequence similarity to both rose leaf curl virus and duranta leaf curl virus. Notably, the virus exhibited a unique genomic composition, incorporating genetic material from diverse sources. Employing advanced phylogenetic networks and recombination detection methods, our analysis unveiled extensive recombination events within the viral sequences. Koch's postulates were rigorously fulfilled through the successful infection of both *C.album* and *Nicotiana benthamiana*by the infectious clone of CLDV, confirming its pathogenic potential. In light of these findings, we propose the name "*Chenopodium Leaf Distortion Virus*" (CLDV) for this distinct ssDNA plant virus, highlighting its speciation dynamics driven by recombination. Our research contributes to a deeper understanding of the broader trend of recombination among ssDNA viruses, with potential implications for their evolutionary trajectories. We believe that presenting these findings at the conference will foster valuable discussions and insights into the molecular evolution of plant viruses and their impact on diverse host plants.

Keywords: CRESS DNA virus, Begomovirus, Recombination, Evolution.

IL-6

The New Hepatitis Elimination Strategy and Repurposing of COVID-19 Infrastructure for Hepatitis Elimination

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Abstract

During the last seven years, some progress is made in the fight against hepatitis. The key driver was the World Health Organization’s hepatitis control strategy 2016-2021. However, funding commitments remain inadequate to meet the elimination targets. Recently, the progress on hepatitis elimination targets was evaluated and the new strategy 2022-2030 for the control of hepatitis is formulated. The strategy comprised five core areas including Hepatitis B virus (HBV) vaccination, prevention of mother-to-child transmission of HBV, injection and blood safety, harm reduction, and test and treatment of Hepatitis B Virus (HBV) and Hepatitis C virus (HCV). From 2015-2020, the coverage of the third dose of HBV vaccine among children has increased from 82% to 90%, and the birth dose of HBV vaccination has increased from 38% to 50%, with a target of 90% coverage by 2030. The proportion of blood units screened for bloodborne diseases has increased from 89% to 95%, with a target of 100% by 2030. The number of safe needles distributed per person who injects drugs has also increased. The number of deaths from viral hepatitis has decreased from 1.4 million to 1.1 million per year, with a target of 0.5 million annual deaths by 2030. HBV and HCV drug prices are reduced in 20% of the countries, and the target is to reduce drug pricing in 60% of the countries so that the maximum number of people can obtain drugs. Approximately 30% of people living with HBV and HCV are diagnosed and treated, and the target is to diagnose 90% of cases and treat 80% of cases by 2030. It was estimated in 2021, that hepatitis elimination requires an investment of US $6 billion per year till 2030. Many countries with well-developed hepatitis control programs lack the financial resources to achieve their targets. The facilities and infrastructure developed during COVID-19 pandemic can be utilize to control hepatitis pandemic. PCR based diagnostic facility

established for COVID-19 detection can be used for hepatitis diagnosis. COVID-19 pandemic resulted in establishment of excellent vaccination infrastructure linked with NADRA database, which can be utilization to increase HBV birth dose and HBV adult vaccination. COVID-19 pandemic did a behavior change towards the attitude and perception of self-testing, which can be utilize to promote hepatitis self-testing. Telemedicine infrastructure developed during COVID-19 can utilize to follow hepatitis patients on their diagnosis and treatment.

Keywords: Hepatitis, Elimination strategy, Vaccination, Blood safety, Treatment access, COVID-19 impact.

IL-7

The Undiagnosed Rare Disease Clinic (URDC): Ending the Diagnostic Odyssey of Patients with Rare Genetic Diseases

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Abstract

The Undiagnosed Rare Disease Clinic (URDC) established in January 2020, is a multidisciplinary collaborative research clinic that focuses on providing genetic diagnosis for patients and families who are dealing with uncertainty of an undiagnosed rare disease and diagnostic odyssey. Recently (September 2023), URDC has been designated as Indiana University Diagnostic Center of Excellence as the clinical site of the Undiagnosed Disease Network (UDN). To identify rare disease-causing variants underlying the genetic condition in our URDC cohort, the URDC team has developed a multi-modal pipeline including in-house sequencing of genome and transcriptome by Indiana University's Center for Medical Genomics (CMG), AI-based variants prioritization via a customized version of Emedgene and transcriptomics and Human Phenotype Ontology terms-based gene prioritization algorithm. Case 1: *MBTPS1* (NM_003791.4) encodes Site-1 protease (S1P) is a serine protease that functions sequentially with Site-2 protease (S2P) regulating cholesterol homeostasis and endoplasmic reticulum stress response. *MBTPS1* variants are associated with Spondyloepiphyseal dysplasia, Kondo-Fu type (MIM: 618392, cataract, alopecia, oral mucosal disorder, and psoriasis-like (CAOP) syndrome, and Silver–Russell-like syndrome (SRS). In this report, we describe a 14-year-old female with a complex medical history including early-onset cataracts, laryngomalacia, feeding dysfunction, white matter volume loss, inguinal hernia, joint hypermobility, retrognathia, speech delay and dysmorphic features. Additionally, features of ectodermal dysplasia including decreased sweating, heat intolerance, dysplastic nails, chronically dry skin, and hair growth issues were also observed. Previous testing including *MECP2* sequencing, SRS and Angelman and Prader-Willi testing, metabolic screening, CMA karyotype analysis were all negative. Exome sequencing analysis identified compound heterozygous variants in the *MBTPS1* gene. The 3D modeling predicts a slight local perturbation of the loop region in the mutant protein due to difference in interaction pattern in wild and mutant structure of S1P. The RNA-seq analysis of splice variant showed skipping of exon 21, predicted to result in frameshifting p. (Ser901fs28*) leading to non-sense mediated decay (NMD). To our knowledge only eight studies

have been published that described the *MBPTS1*-related disorders. Interestingly, we observed the ectodermal dysplasia in the patient that further expands the phenotypic spectrum of *MBTPS1* gene related disorders. Of note, we have begun the treatment with Vit.B12 and our patient's hair has begun to grow back. This case expands our current knowledge of this rare syndromic condition and expand the genetic and phenotypic spectrum of the *MBTPS1*- related disorders. Case 2: A 15-year-old male was referred to URDC with a history of migraine, dilatation of the cerebral artery, cerebral infarct, stroke, dysphagia, elevated hemoglobin A1c, recurrent pancreatitis and elevated sweat chloride. The whole exome sequencing (WES) and whole genome sequencing (WGS) data was analyzed manually and by utilizing Emedgene, an artificial intelligence (AI) based platform for genomic analysis. We found a hemizygous, non-canonical splice site variant c.906+5G>A in *COL4A6* (NM_001847.4) gene. Our human genetic data, coupled with in silico data supports that *COL4A6* is the most likely candidate gene for stroke, dilatation of the cerebral artery and Cerebral infarct in the patient. We found one additional patient through gene matcher having partial phenotypic match with our patient. The *COL4A6* gene is involved in causing hearing loss and Alport syndrome but the role of *COL4A6* in causing stroke, cerebral infarct and dilatation of the cerebral artery is not well understood. To date, only study published that explained the role of *COLA46* in causing cerebral infarction and stroke. This study will expand the genetic and phenotypic spectrum of *COL4A6* gene.

Keywords: Undiagnosed Disease Network, Rare diseases, Genetic diagnosis, Genetic variants, Genetic disorders, Genomic analysis, Phenotypic spectrum, Clinical research.

IL-8

Livestock Species Under Productive and Adaptability Pressure Under Changing Climate of Pakistan with Focus on Yak and Camel from North to South

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Abstract

The Global Climate Change (GCC) has become high risk concern these days as it has pushed Pakistan among top ten badly affected countries. We have seen rapid weather changes resulting in severe rains, floods in the country. The Livestock sector is the main contributor of agriculture sector in Pakistan however our local livestock species are under increasing stress of productivity, adaptability and heat tolerance under GCC. The genomic studies, however, provide us opportunities to contest with the issues being faced by our animals and genitic identification of the better productive and adaptive animals having better genetics. Under this context we started studies on genomics of our local animals from northern cold, moderate and southern hot regions of Pakistan. In this context we sampled the animals from cold regions Yak (*Bos grunniens*) and moderate to hot regions Buffalo (*Bubalus bubalis*), Cattle (*Bos indicus*) and hot regions Camel (*Camelus dromedarius*) of Pakistan. The mRNA expression pattern of Heat Shock Proteins (HSPs) and immunity-related protein genes were studied through qRT-PCR in the PBMCs of selected breeds sampled from different regions in the Molecular Biology and Genomics Lab of the Virtual University of Pakistan. Differential gene expression patterns were detected in different breeds during the study period. These studies provided an insight into the expression pattern in various genes that may be potentially associated to improve the heat tolerance, adaptability and production under continuously changing climates of Pakistan. There are number of opportunities for scientific communities to explore genetics of local animal species by using modern NGS based technologies.

Keywords*:* Global Climate change, Heat tolerance, Production, Adaptability, Livestock, Heat shock proteins, Immunity-related genes, qPCR, Gene expression, Pakistan.

IL-9

Early Diagnosis and Prognosis of Lung Cancer Through Liquid Biopsy Using Cell Free Circulating Biomarkers

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Abstract

Lung cancer is the leading cause of cancer deaths worldwide, and the high mortality rate is predominantly related to late diagnosis. Therefore, non-invasive early detection of lung cancer could reduce the number of patients diagnosed with advanced disease, which is associated with a poor prognosis. A key to early detection is to identify changes at the DNA level that predispose to carcinogenesis. But unfortunately, no blood-based DNA biomarker for lung cancer detection has been validated for clinical use. The recently discovered free circulating DNA (fcDNA) derived from tumor cells in plasma has attracted the attention of scientific community as a promising, non-invasive tumor 'liquid biopsy' with both quantitative and qualitative significance. It offers a valuable and pragmatic substitute for surgical resection. In recent years, raised levels of tumor-associated genetic and epigenetic changes in fcDNA have been found in lung cancer patients. Therefore, quantification of circulating plasma DNA and the molecular characterization of specific genetic and epigenetic changes can be a valuable tool in the screening and managing lung cancer. But research in this context is in its very early phase and thus lacks standardized and robust procedures necessary for routine fcDNA biomarker assessment in clinical practice. This study proposes to investigate the diagnostic accuracy of a panel of fcDNA markers in detecting lung cancer using a highly proficient real time PCR and combined novel reference gene selection strategy with our study collaborators. We are using different combinations of biomarkers to devise a superlative multi-marker panel with an increased sensitivity and specificity. Our ultimate objective for this study is to establish a blood-based screening test for lung cancer for routine clinical application in high risk individuals which would help greatly to increase the survival rate of lung cancer patients.

Keywords: Lung cancer, Early detection, Circulating DNA, Liquid biopsy, Biomarker panel, Real-time PCR.

IL-10

Protein Engineering Approaches for Efficient Hydrolysis of Plant Polysaccharides

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Abstract

Starch is the most abundant polysaccharide, which has a significant contribution as a rich source of energy to human nutrition. The enzymatic hydrolysis of starch requires a highly thermostable, soluble, and efficient catalytic nature of alpha-amylase. The enzyme production through recombinant DNA technology faces challenges related to their soluble expression, purification, thermostability and catalytic activities. Enzyme modification through protein engineering technologies: site-directed mutagenesis, truncation and fusion with affinity/solubility tags or carbohydrate-binding modules are the only suitable approaches to overcome the problems associated with recombinant DNA technology. In this study, the α-amylases from two hyperthermophilic sources *Methanocaldococcus jannaschii* and *Pyrococcus abyssi* were selected for efficient hydrolysis of plant polysaccharides. Structural and functional insights on α-amylase from *M. jannaschii* and *P. abyssi* were computationally explored to evaluate a catalytic domain and its fusion with a small ubiquitin-like modifier (SUMO). The recombinant proteins' production, characterization, ligand binding studies, and structural analysis of the cloned amylase native full gene, catalytic domains and fusion enzymes were thoroughly analysed in this comparative study. The truncated and fusion showed 2-fold and 2.5-fold higher specific activities (µmol min-1 mg -1) than native amylase at 95°C at pH 6.0. Molecular modelling and MD simulation results showed that the removal of the extra loop (178 residues) at the C-terminal of the catalytic domain exposed the binding and catalytic residues near its active site, which was buried in the native enzyme. The effect of the SUMO solubility tag has been primarily observed in the catalytic domain of *P. abyssi* in terms of their soluble and stable expression. The temperature ramping and secondary structure analysis through CD spectrometry showed no notable alterations in the secondary structures but verified the correct folding of these amylase thermostable amylase variants. The chimeric fusion of amylases with thermostable α-glucosidases makes it a potential candidate for the starch degrading processes.

Keywords: α-Amylase, Starch, İndustrıal Enzyme, Extremophilic, *Methanocaldococcus jannaschii*, *Pyrococcus abyssi.*

IL-11

21st Century Expedition: Exploring Indigenous Microbial Resources for Novel Antibiotics and Anticancer Drugs

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Abstract

The antibiotics resistance especially the emerging multidrug resistant (MDR) and most recently extensively drug resistant (XDR) bacterial pathogens necessitates the further screening and discovery of new antibiotics. Microbial natural products especially the secondary metabolites produced by many bacteria and fungi have served as the major source of most of the commercially available antibiotics and chemotherapeutics. The interesting fact is most of these natural reservoirs are still less explored with reference to the screening for new drugs. The *Actinobacteria* are gram positive filamentous bacteria having high GC content in their genome and are the leading producers of most of the antibiotics and chemotherapeutics. In our search for novel antibiotics, we have isolated a large number of *actinobacteria* strains from different ecological niches in Pakistan and abroad. The isolated strains were identified by microbiological, biochemical and genomics approaches such as 16S rRNA gene sequencing, whole genome sequencing (WGS) etc. The laboratory scale fermentation of the strains and subsequent solvent extraction, chromatographic purification and structure elucidation of the active molecules by mass spectrometry (MS) and NMR spectroscopy, yielded a significant number of clinically useful antibiotics and chemotherapeutic agents. The compounds belonging to different structural classes (e.g. aminoglycosides, macrolides, puromycins B-E, nocardamine, ferrioxamine E, aranciamycin, actinomycins, SM-173-B, pactamycate, taurocholic acid, oxachelin C, mitomycin, benzoformamides and several new compounds were identified. Further the indirect screening approach using whole genome sequence data, genome mining and investigations through AntiSmash platform indicated the immense potential of the isolated strains for the production of medicinally useful secondary metabolites. Overall the study revealed that the microbial natural products still are the major reservoirs for the discovery of novel bioactive molecules, and should continuously be explored to discover novel drugs.

Keywords: Microbial natural products, Antibiotic resistance, *Actinobacteria*, Novel antibiotics, Chemotherapeutics.

IL-12

Resilient Crop Production: Pyramiding RNAi with Cry Toxins in Cotton Enhanced Control of Pink Bollworm

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Abstract

Cotton, *Gossypium spp*, is an important cash crop that significantly contribute to the country's GDP with most common cultivated species around the world are *Gossypium hirsutum* and *Gossypium barbadense*. Insect pests cause 20-40% yield loss in Pakistan annually. Genetically modified Bt cotton was developed in the 1990s to control the insect pest attack. But with time, insects developed resistance against the Bt toxins. This study aimed to pyramid RNAi with Bt cotton to prolong the resistance against pink bollworm. Pink bollworm is a notorious insect that causes the loss of millions of cotton bales annually. We hypothesize that pyramiding RNAi with Bt synergistically enhances the plant's resistance against insects by lowering the survival rates. We exploited Cadherin and V-ATPase genes in PBW as potential RNAi targets and revealed their efficacy in plant-mediated insect bioassays. It was evident from this study that the RNAi strategies and Bt genes can control the insect effectively rather than Bt genes alone.

Keywords: Cotton, Bt cotton, Resistance, RNAi, Pink bollworm, Cadherin gene, V-ATPase gene, Insect bioassays, Synergistic effect.

IL-13

Engineered Lytic Proteins and Engineered Bacteriophages

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Abstract

Antimicrobial resistance is a serious threat to public health resulting in high morbidity and mortality. The incidence of drug resistance in bacteria increases day by day; consequently, MDR, XDR and PDR are evolving at a high rate. To address the impacts of antimicrobial resistance, research groups throughout the world are focused on developing new antibiotics, analogues of current antibiotics, and compounds that could be used as alternatives antibiotics. Some promising alternatives include new antimicrobial peptides, liposomal mediated targeted delivery of the antimicrobials, CRISPR-Cas-mediated disruption of antibiotic resistance genes in the bacteria, bacteriophage therapy, or treatment with bacteriophage lytic proteins. Bacteriophages, which are viruses specifically targeting bacteria, have gained attention for their ability to effectively combat bacterial infections. This is achieved through lytic phages and their associated gene products including phage enzymes and lytic proteins such as endolysins, holins, and spanins, which serve as bio-agents in the fight against bacterial infections. Once bacteriophages identify, attach to, and lyse bacterial hosts resulting in reduction in bacterial populations. Bacteriophages present an alternative therapeutic approach to antibiotics due to their unique advantages. These advantages include a narrow spectrum of action, ensuring the preservation of normal flora, as well as the ability to replicate at the site of infection. Additionally, bacteriophages exhibit qualities such as non-toxicity and cost-effective production. Extensive research confirms their effectiveness against multidrug-resistant pathogenic bacteria in human subjects. Notably, phages possess a high degree of specificity, targeting only specific bacterial strains, a trait that is largely species-specific in reported cases. Bacteriophage derived lytic proteins are also used as therapeutics in some instances. Some researchers use phages and antibiotics synergistically whereas others use different phages in combinations as cocktail. After many animal model trials, bacteriophages are making their way for the class I/II clinical trials. In some cases, phages are being deployed for the treating life-threatening infections due to MDR, XDR and PDR pathogens.

Keywords: Antimicrobial resistance, Antibiotics, Bacteriophage therapy, Drug-resistant bacteria, CRISPR-Cas, Clinical trials.

IL-14

Multi-Parametric Detection of Non-Cell-Autonomous and Cell-Autonomous Deaths in Cancer Cells

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Abstract

Epithelial cells require attachment to extracellular matrix to suppress an apoptotic cell death. It is described as a nonapoptotic cell death program in matrix-detached cells that is initiated by a previously unrecognized and unusual process involving the invasion of one cell into another. This phenomena of cell in cell structures called entosis (non-cell autonomous cell death). Live internalized cells are either degraded by lysosomal enzymes or released and this mechanism is commonly observed as “cell-in-cell” cytological feature in human cancers. Cell death modalities induced by anticancer-therapies have been extensively studied but entosis induced by anticancer treatments has never been investigated. We have analysed the lethal fates of cancer cell by multispectral imaging flow-cytometry based technology in which we have treated the cells with different anticancer drugs and are co-cultured with untreated cells observing that anticancer agents can simultaneously trigger cell-autonomous and non-cell-autonomous death. After ionizing radiation, oxaliplatin or cisplatin treatment, fractions of treated cancer cell populations were eliminated through cell-autonomous death mechanisms, while other fractions of the treated cancer cells engulfed and killed neighboring cells through non-cell-autonomous processes including cellular cannibalism. These results reveal that chemotherapy and radiotherapy can induce both non-cell-autonomous and cell-autonomous death of cancer cells, highlighting the heterogeneity of cell death responses to anticancer treatments and the unsuspected potential contribution of non-cell-autonomous death to the global effects of anticancer treatment.

Keywords: Cancer treatments, Apoptotic cell death, Entosis, Anticancer drugs, Heterogeneity, Non-cell-autonomous death.

IL-15

Phenotypic and Genotypic Characteristics of a Live-Attenuated Genotype I Vaccine of Japanese Encephalitis Virus

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Abstract

The phenotypic and genotypic characteristics of a live-attenuated genotype I (GI) strain (SD12-F120) of Japanese encephalitis virus (JEV) were compared with its virulent parental SD12 strain to gain an insight into the genetic changes acquired during the attenuation process. SD12-F120 formed smaller plaque on BHK-21 cells and showed reduced replication in mouse brains compared with SD12. Mice inoculated with SD12-F120 via either intraperitoneal or intracerebral route showed no clinical symptoms, indicating a highly attenuated phenotype in terms of both neuro invasiveness and neurovirulence. SD12-F120 harbored 29 nucleotide variations compared with SD12, of which 20 were considered silent nucleotide mutations, while nine resulted in eight amino acid substitutions. Comparison of the amino acid variations of SD12-F120 vs. SD12 pair with those from other four isogenic pairs of the attenuated and their virulent parental strains revealed that the variations at E138 and E176 positions of E protein were identified in four and three pairs, respectively, while the remaining amino acid variations were almost unique to their respective strain pairs. These observations suggest that the genetic changes acquired during the attenuation process were likely to be strain-specific and that the mechanisms associated with JEV attenuation/virulence are complicated.

Keywords: Japanese encephalitis virus, Genotype I, Live-attenuated strain, Phenotype, Genotype, Attenuation process.

IL-16

MetGenoX: A Metagenomics Support Package

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Abstract

Metagenomics is a data intensive interpretation field aiming to study an entire microbial ecosystem (metagenome) collectively. Hence, metagenomics work flow is extensive and bioinformaticians have developed software for each component of the pipeline separately. Consequently, Metagenomics requires researchers to be comfortable in downloading, installing and scripting software that lack basic GUIs. As researchers struggle with these skills, there is a dire need to develop software packages that can speed-up the learning curve by automating the installation process while allowing the users to choose between different tools. Therefore, this paper presents MetGenoX, a GUI-based software package that eases the installation of 133 tools belonging to the metagenomics pipeline via resolving all necessary dependencies while providing the user complete control over the choice of software needed for their particular need.

Keywords: Metagenomics, Metagenome, Software package, GUI-based, Installation automation, Bioinformatics tools.

IL-17

Tailoring Molecular Recognition in Predesigned Multifunctional Enzyme Mimicking Porphyrin Imprinted Interface for High Affinity and Differential Selectivity; Sensing Etoposide in Lung Cancer Patients

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Abstract

Nanozymes are cost-effective and robust but they lack specificity and selectivity, limiting their potential practical applications. Herein, molecularly imprinted polymers (MIPs) were grown in combination with multifunctional 5,10,15,20-tetrakis(4-hydroxyphenyl)-21H,23H-porphyrin (THPP) oxidase-like nanozyme to engineer THPP@MIP interface with high affinities and differential selectivity for structurally related target analytes. THPP nanozyme displayed a high level of predefined binding affinity for etoposide (ETO), and served as a predesigned functional monomer to rationally tailor the selectivity of THPP@MIP surface in the presence of different guest molecules. THPP nanozyme in combination with conventional monomers was imprinted on a portable and disposable cellulose paper matrix under UV light to create a UV-cured imprinted interface for optical detection of ETO. The THPP@MIP enzyme mimicking interface, having ETO specific and selective target recognition pockets, catalyzed the oxidation of colorless 3,3′,5,5′-tetramethylbenzidine (TMB) to generate visible blue oxidized TMB (oxTMB) without exogenous hydrogen peroxide (H O). The ETO binding on the THPP@MIP surface blocked the channels for TMB access to THPP cavities. The THPP@MIP sensor permitted to detect ETO in the linear range of 0.005–10 μg mL, with a limit of detection (LoD) of 0.002 μg mL, and showed a remarkable specificity and selectivity against other drug molecules. Furthermore, the THPP@MIP sensor successfully differentiated the serum samples of lung cancer patients and healthy volunteers. The obtained results were validated with standard High performance liquid chromatography-mass spectrometry (HPLC/MS) analysis of the serum samples. Additionally, ETO injection/infusion solutions and ETO-free serum samples were used to perform the matrix effect and recovery studies. This work demonstrates that molecular imprinting with predesigned, enzyme mimicking, high-affinity functional monomer can serve as a highly selective and specific universal interface for broad spectrum sensing applications in various analytical domains.

Keywords: Nanozymes, molecularly imprinted polymers, THPP@MIP interface, Selective detection, Optical sensing, ETO detection.

IL-18

Navigating Ethical Challenges in AI Deployment for Biomedicine Therapeutics, Research, and Diagnostics

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Abstract

Artificial Intelligence (AI) focuses on creating systems and algorithms capable of performing tasks that typically require human intelligence. In biomedicine, AI has made significant strides, revolutionizing research, treatment, and diagnostics. This presentation delves deep into the ethical challenges that come with deploying AI in the field of biomedicine. Covering research, treatment, and diagnostics, it explores the delicate balance between accessing patient data and ensuring privacy. The talk dives into the complexities of AI-driven diagnostics, touching on issues of bias, fairness, explainability, transparency, and accountability. Moving beyond individual concerns, the discussion broadens to the societal impact, focusing on how AI might inadvertently worsen healthcare disparities. Key areas of emphasis include the necessity of diverse training data, ensuring fair access, and ongoing evaluations to prevent biases. The presentation is geared towards guiding stakeholders in the biomedical field towards responsible AI deployment, aiming for transparency, fairness, and equitable progress in the dynamic intersection of AI and biomedicine.

Keywords: Artificial intelligence, Biomedicine, Ethical challenges.

IL-19

Navigating the Nanoscale Frontier to Leverage Nano-Informatics for Precision Nano-Medicine with Engineered Silver Nanoparticles

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Abstract

Nanomedicine, a groundbreaking fusion of nanotechnology and healthcare, holds immense potential for revolutionizing medical diagnostics, treatments, and drug delivery. At the core of this transformation is nanoinformatics, a crucial technology that addresses the intricate challenges and opportunities in applying nanoscale materials and technologies to healthcare. Nanoinformatics in nanomedicine is the linchpin for navigating the unique challenges and opportunities inherent in applying nanoscale materials and technologies to healthcare. This encompasses intricate tasks, including designing nanoparticles, understanding their interactions with biological systems, and ensuring precise and safe drug delivery. This study underscores nanoinformatics as a powerful solution, highlighting its ability to efficiently manage, analyze, and interpret data the computational analysis of designed silver nanoparticles targeting virulent and antibiotic resistance genes, including spa, LukD, fmhA, and hld from *Staphylococcus aureus*. The binding affinities of AgNP with spa, LukD, fmhA, and hld were -7.16, -6.5, -6.45, and -3.3 kJ/mol, respectively, which infers a good docking score except of hld which is -3.3 kJ/mol due to its small size. These insights point to the effectiveness of engineered silver nanoparticles in combating multidrug-resistant *Staphylococcus* species, promising a brighter future in healthcare. Nanoinformatics emerges as an indispensable tool, propelling nanomedicine into a new era of personalized healthcare. Its significance is evident in its capacity to streamline the complexities of nanoscale healthcare applications, enabling personalized medicine while guaranteeing safety and efficacy. As nanomedicine continues to redefine healthcare, nanoinformatics stands as the cornerstone of this revolutionary transformation.

Keywords: Nanoinformatics, Nanomedicines, Silver nanoparticles, Personalized medicine, Healthcare.

IL-20

Osmotin Inhibits Hypoadiponectinemia-Induced NLRP3 Inflammasome Activation to Improve Dementia

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Abstract

Hypoadiponectinemic conditions with either decreased production or a deficiency in circulating adiponectin levels exert detrimental effects on different organs, particularly the brain. Similarly, the functional NLRP3 inflammasome (a multiprotein complex) contributes to several inflammatory and neurodegenerative diseases, including Alzheimer's disease (AD). The link between hypoadiponectinemia-induced energy deprivation and NLRP3 inflammasome activation in the brain remains elusive. Here, we report for the first time that osmotin (a structural homologue of adiponectin) potentially inhibits NLRP3 inflammasome activation in the brains of young adiponectin knockout (AKO), aged AKO and APP/PS1 mice via the AdipoR1/AMPK pathway. Osmotin prevented NLRP3 inflammasome-mediated amyloidogenic amyloid beta (Aβ) production and aggregation and memory impairments and suppressed long term potentiation (LTP). Moreover, both in vitro and in in vivo osmotin treatments ablated NLRP3 inflammasome activation and the associated AD pathology. Based on our current findings, both osmotin and adiponectin (used as a gold standard) potentially inactivate hypoadiponectinemia-induced NLRP3 inflammasome function and associated dementia.

Keywords: Inflammasome, Osmotin, Adiponectin, Amyloid Beta, Hypoadiponectinemia.

IL-21

Comparison & Activity Analysis of Lipase and Cellulase Embedded MOF Synthesized Using De-Novo and Hydrothermal Method.

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Abstract

Enzymes such as cellulase and lipase play pivotal roles in various industrial applications, yet their susceptibility to denaturation under different pH and temperature conditions poses challenges in terms of stability, usability, and activity. This research explores the use of Metal-Organic Frameworks (MOFs) as a promising strategy for enzyme immobilization to enhance their performance. Specifically, cellulase was immobilized on a MOF, Zn-benzene 1-4 di-carboxylic acid (BDC), through hydrothermal and de novo approaches. Comparative analyses revealed that Zn-cellulase-BDC synthesized through the de novo method exhibited superior activity, stability, catalytic performance, and lifespan compared to the hydrothermal method and the free enzyme. Similarly, the study investigates the enhancement of lipase performance and stability through MOF encapsulation. Despite the acknowledged benefits of MOFs, there remains a need to identify the most efficient method. This paper employs two distinct synthesis methods to produce Enzyme-MOF complexes, aiming to determine the approach that holds greater potential for improving enzyme efficiency in various industrial applications.

Keywords: Enzyme immobilization, Metal-Organic Frameworks (MOFs), Cellulase, Lipase, Industrial applications, Synthesis methods.

IL-22

Effect of *Pseudomonas aeruginosa* Strain ZK Biofilm on The Mechanical and Corrosion Behavior of 316L Stainless Steel and α-brass

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Abstract

This research work aims to investigate the effect of the aerobic bacterium, *Pseudomonas aeruginosa* on the mechanical and electrochemical properties of the 316L stainless steel and α-brass. These properties of both the alloys were determined after 7 days of exposure to the controlled and inoculated media at 37℃. The microstructural and electrochemical test results revealed the deleterious effects of *Pseudomonas aeruginosa*. After exposure to the inoculated medium, the scanning electron microscopy (SEM) results showed the larger pitting and formation of relatively dense biofilm on α-brass compared to 316L stainless steel. The tensile strength and hardness of 316L stainless steel were slightly affected after exposure to the controlled and inoculated media. After exposure to the controlled medium and inoculated media, the tensile strength of the α-brass was least affected but a significant decrease in the hardness (from 165 HV to 124 HV) was observed due to the severe attack induced by the *Pseudomonas aeruginosa*. Similarly, the open-circuit potential of the 316L stainless steel in the inoculated medium was measured to be less active (-410 mV vs Ag/AgCl) than α-brass (-550 mV vs Ag/AgCl). In the inoculated medium, potentiodynamic polarization curves confirmed the severe attack of *Pseudomonas aeruginosa* on α-brass (7.15 × 10–2 mm/year) compared to 316L stainless steel which registered a corrosion rate of 5.14 × 10–4 mm/year.

Keywords: *Pseudomonas aeruginosa,* Potentiodynamic polarization, Passive film, Scanning electron microscope.

IL-23

Vaccine Production: Molecular Level

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Abstract

The constant demand of new and improved vaccines needs to explore new strategies. The development of molecular techniques paved the way for development of new and improved vaccines. The potential antigenic properties are determined by using these techniques followed by improved strategies for the expression and delivery of desired gene. These techniques led to the development of third generation vaccines. Third generation vaccines are still in the experimental phase. The most recent addition in vaccinology is DNA vaccine in which either 'Naked DNA' is used directly or packaged in a recombinant virus or bacteria. The vaccines are developed by recombinant DNA technology or genetic engineering. Molecular biology enables the biologist to isolate gene of desired antigen of microbe and insertion into the vector. Strategies are; Using engineered vector which express desired antigen as vaccine. The engineered vector is grown and made to express antigen followed by purification and injection of antigen as subunit vaccine. Deletion of portion of DNA thus making the attenuated virus unable to revert into wild form. Reassortment of genomes of virulent and avirulent strains. Broadly vaccines produced by molecular techniques are fall into three categories, Recombinant antigen vaccines, Live vector vaccines and DNA vaccines.

Keywords: Vaccine development, Third generation vaccines, DNA vaccines, Subunit vaccines, Attenuated virus, Virulent strains, Recombinant antigen vaccines, Live vector vaccines.

IL-24

Highly Synergistic Antibacterial Activity of Copper (II)-Based Nano Metal-Organic Framework

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Abstract

Copper (II)-based metal-organic framework in bulk crystals and nano-fibers particles were synthesized via hydrothermal method. X-ray study indicated that Cu-MOF possesses 1D structural network and the Cu(II) centrs are surrounded by different types of coordination environments. The width of the as-synthesized nanofibers was nearly 120±20 nm, while the size of Cu-MOF was about 200 μm. The antibacterial potency of the nanofibers and Cu-MOF particles against *Escherichia coli* (*E. coli*) and *Bacillus subtilis* (*B. subtilis*) was checked through, colony count method

andminimal inhibitory concentration. The MIC of Nanofibers are in the range of 150-200 µg/ml, while for Cu-MOF are in range of and 200-2500 µg/ml against both *E. coli* and *B. subtilis*, respectively. According to Nanofibers antibacterial results, the greater antibacterial potency of nanofibers as compared with Cu-MOF and ligand alone. The synergistic antibacterial mechanism was also proposed on the basis of the generation of reactive oxygen species (ROS) and slow the release of copper (II) ions.

Keywords: Cu-MOF, Nanofibers, Antibacterial activity, Antibacterial mechanism, ROS.

IL-25

Identification of Isobenzofuranone Derivatives as Promising Antidiabetic Agents: Assessment of Enzyme Inhibition Studies and Computational Docking Analysis

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Abstract

Diabetes mellitus, one of the major health challenges of the 21st century, is associated with numerous biomedical complications including retinopathy, neuropathy, nephropathy, kidney diseases, cardiovascular diseases and liver disorders. To control the chronic hyperglycemic condition, the development of potential inhibitors of drug targets such as α-glucosidase and α-amylase remains a promising strategy and focus of continuous efforts. Therefore, in the present work, a concise library of isobenzofuranone derivatives (3a–q) was designed and synthesized using Suzuki-Miyaura Cross-coupling approach. The biological potential of these heterocyclic compounds against carbohydrate-hydrolyzing enzymes; α-glucosidase and α-amylase, was examined. In vitro inhibitory results demonstrated that the tested isobenzofuranones were considerably more effective and potent inhibitors than the standard drug, acarbose. Different compounds emerged as the lead candidate against several enzymes even better than standard drugs used during assay. In silico molecular docking and dynamics simulations validated the in vitro data for these compounds whereas pharmacokinetics and toxicity profile revealed the drug-likeness properties of potent inhibitors.

Keywords: Heterocyclic drugs, Diabetes, Suzuki-Miyaura cross-coupling, α-glucosidase, α-amylase, Molecular dynamics simulations, In-vivo activity.

IL-26

Antimicrobial Effect of Silver Nanoparticle Based Whey Emulsions and Edible Films to Prolong Shelf Life of Fruits and Vegetables

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Abstract

The objective of this study is to develop and assess the antimicrobial properties of whey-based emulsions and edible films incorporated with silver nanoparticles (AgNPs), aiming to extend the shelf life of fruits and vegetables. For this, isolation and characterization of bacterial and fungal strains were carried out from food samples, with identification accomplished using 16S and 18S rDNA ribotyping techniques. The AgNPs-infused emulsions and films were applied to fruits and vegetables, demonstrating an extension of their shelf life for up to 15 days. The treated samples underwent analysis to determine both their antimicrobial and antioxidant properties. The results of the study exhibited that the utilization of AgNPs significantly boosted the effectiveness of the coated samples. The SEM analysis revealed the presence of distinct AgNP sizes – 21 nm, 22 nm, 28 nm, and 62 nm. Inhibition zones were measured against specific bacterial strains including *Staphylococcus aureus* SR1, *Escherichia coli* SR2, *Salmonella enterica* SR3, as well as fungal strains like *Aspergillus flavus* SF1, *Aspergillus tamari* SF2, and *Aspergillus niger* SF3. The total viable count, represented as log CFU/ml, was remarkably reduced to a range of 0 to 3.301, contrasting with the control sample which exhibited a count of 6.423. Antioxidant levels for different fruits and vegetables, including strawberry, taro root, guava, peas, green chili, and carrot, were determined as 56.12%, 23.36%, 26.10%, 7.6%, 36.04%, and 33.81% respectively ($p < 0.05$). In conclusion, the AgNPs-infused whey protein emulsions displayed the most robust antimicrobial activity, thereby positioning them as a viable approach for extending the shelf life of various fruits and vegetables. This research sheds light on the potential of AgNPs as a means to enhance food preservation and safety.

Keywords: Whey protein isolates, Whey emulsions, Whey edible films, Silver nanoparticles (AgNPs), Shelf life.

IL-27

A PCR-Based Hemagglutinin Subtyping Tool to Aid in the Surveillance of Avian Influenza Viruses in Migratory Wild Birds

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Abstract

Avian influenza virus (AIV) is a negative sense, RNA virus. Migratory wild birds (MWBs) are the natural reservoir and the source of the spread of AIVs to all species. All recent outbreaks of AIV in poultry can be traced back to MWBs.

Most recent human pandemics occurred due to influenza viruses of avian origin. Early detection of AIVs using appropriate surveillance tools can play a pivotal role in curtailing AIV outbreaks by detecting the emergence of highly pathogenic AIV that can infect domestic poultry and mammals, new subtypes, and antigenic/genetic variants. Novel tools are needed to early detect and subtype AIVs. A SYBR® Green-based real-time reverse transcription-polymerase chain reaction (rtRT-PCR) panel was developed for direct hemagglutinin (HA) subtyping of AIVs in oropharyngeal-cloacal (OPC) swabs from MWBs. Under optimal conditions, the PCR panel detected AIVs of all 16 different HA subtypes with an average limit of detection of 102.6 copies/reaction (2 µl of extract). In testing 90 OPC swabs from 13 MWB species, the PCR provided a significantly faster turnaround of results and demonstrated the presence of more subtypes and concurrent infection among MWBs compared to what the current surveillance testing algorithm showed. In conclusion, the newly developed SYBR® Green rtRT-PCR panel can be a useful tool for monitoring MWBs for AIVs. This tool can be adapted for the detection of human influenza or similar viruses.

Keywords: Avian influenza, Migratory wild birds, Outbreak detection, Surveillance tools, Real-time PCR, Hemagglutinin subtyping, Novel diagnostic tools.

IL-28

Effect of Colchicine on Cellular and Humoral Immune Responses in Mice

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Abstract

The present research was planned to investigate the effect of colchicine on cellular and humoral immune responses in mice. Cellular immune responses were evaluated in nitric oxide (NO) production assay, delayed type hypersensitivity (DTH) assay, macrophage engulfment assay and cyclophosphamide induced neutropenic test. While, Humoral immune responses were assessed by carrying out Jerne hemolytic plaque formation, mice lethality test and haemagglutination assay. Colchicine was given to mice at doses of 40µg/kg, 80µg/kg and 160µg/kg intraperitoneally. Data were statistically investigated by ANOVA and chi square test. NO formation variance was significantly ($P<0.0001$) decreased in lipopolysaccharide (LPS) activated macrophages and macrophages alone in colchicine administered groups. Delayed type hypersensitivity (DTH) exposed significant ($P<0.0001$) reduction in skin thickness of colchicine administered groups. In macrophage engulfment assay, significant ($P<0.0001$) decline in engulfment of sheep red blood cells (SRBCs) was detected by macrophages in colchicine administered groups. Colchicine administered groups revealed significant ($P<0.0001$) decline of TLC and neutrophil count. There was dose dependent reduction in plaque formation significantly ($P<0.0001$) at all doses of Colchicine. There was significant ($P <0.0001$) decrease in HA titer of colchicine treated groups. The HA titer response was dose dependent. Colchicine boosted the mortality after injection of bovine *Pasteurella multocida* culture. Therefore, it is concluded that colchicine suppresses the cellular and humoral immune responses in mice.

Keywords: Colchicine, Cellular immune responses, Humoral immune responses, Nitric oxide, Delayed type hypersensitivity assay, Macrophages.

IL-29

Genetic Diversity in Bats from Bajaur Agency, FATA, Pakistan, Analyzed by 16S rRNA

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Abstract

Bats play a vital role in maintaining ecological balance and are essential contributors to biodiversity. This study focuses on unraveling the genetic diversity of bat populations in Bajaur Agency, Federally Administered Tribal Areas (FATA), Pakistan, utilizing the 16S rRNA gene as a molecular marker. The research involved the collection of bat specimens representing diverse species across the region. Genomic DNA was extracted, and the 16S rRNA gene was amplified using polymerase chain reaction (PCR). Subsequent sequencing and bioinformatics analyses were conducted to decipher the genetic diversity present within these bat populations. Preliminary findings indicate a rich diversity of mitochondrial DNA sequences, highlighting the unique genetic signatures of various bat species in Bajaur Agency. Phylogenetic analysis allowed for the identification of evolutionary relationships and potential cryptic species within the studied populations. This research not only contributes valuable insights into the genetic diversity of bats in the region but also provides a foundation for future conservation efforts and biodiversity management. Understanding the genetic makeup of bat populations is critical for preserving these ecologically significant mammals and the ecosystems they inhabit. The utilization of the 16S rRNA gene in this study offers a robust and informative approach, shedding light on the intricate genetic patterns within bat communities. The findings from this research contribute to the broader understanding of bat genetics, aiding in the formulation of effective conservation strategies and the sustainable management of bat populations in Bajaur Agency and similar regions.

Keywords: Genetic diversity, Bats, Bajaur agency, FATA, Pakistan, 16S rRNA, Mitochondrial DNA, Population structure, Conservation, Ecological resilience, Molecular marker.

IL-30

Molecular Modelling of Cyclopeptides Targeting Non-Structural NS5A Protein of Hepatitis C Virus

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Abstract

Viruses are the commonly known pathogenic enemies causing variety of infections, the majority of which are harmful. Out of which some are lethal, while others are only harmful, HCV is among one of the most lethal viral infections. Many people died as a result of HCV due to a lack of awareness and commonly available effective treatments. HCV replication is carried out by *NS5A* and *NS5B* protein-coding genes that help HCV to interact with the host for further replication and pathogenicity. Cyclotides from various plants have antimicrobial properties and can help design peptide-based therapeutic drugs for treating and inhibiting HCV. In-silico research was performed to identify the best cyclotides capable of inhibiting HCV replication. The current study focuses on the potential of cyclopeptides for HCV-NS5a silencing, which would likely inhibit the expression of the *NS5a* gene. PEP-FOLD3 online software was used to retrieve cyclotide and NS5A protein sequences, and CHEMIRA software was used for visualization. Docking was performed with (MOE), and the results showed that screened cyclotides are highly efficient against NS5A protein. The binding affinities of these peptides were found as Vico B -19.1503, Hylf E -19.5936, Cycloviolacin O9 -18.7225, Varv peptide D -17.0158 and Hylf L -16.4553. The binding energies shows that these peptides could be potential drug candidates.

Keywords: Antiviral peptides, HCV, *NS5A*, Cyclotides, In-silico docking, Potential drug candidates.

IL-31

Bacteriophages: Older but a Ray of Hope in the Era of Antibiotic Resistance

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Abstract

The hospital acquired infections are becoming a major challenge for patient care. The bacteria causing noso-comial infections usually show marked resistance against commonly used antibiotics. The current antibiotic research will not be able to combat all the emerging antibiotic resistant microorganisms. The lytic phages and their gene products can be used as therapeutic agents against bacteria. The bacteriophages are host specific, show no side-effects, which make them an attractive option for treating the bacterial infections. However, the activation of immune system can clear the bacteriophages, narrow host range of bacteriophages, and contamination of host bacteria or their cell components are some problems which are hindering their use as therapeutic agent and needs further research. Currently, we are following the one-health approach and investigating the potential of bacteriophages for controlling the bacterial infections in both animals and human. The isolated bacteriophages are phenotypically and genetically characterized. The expression of bacteriophage-based proteins for their potential antibacterial/antibiofilm activity is also under question. The bacteriophages characterized in our lab have successfully rescued the bacteremic mice infected with *Pseudomonas aeruginosa*. Recently, out bacteriophage cocktail reduced the mortality level up to 50% in broiler chickens compared with non-treated controlled challenged with *Salmonella gallinarum*. Currently we are working to tackle the hurdles faced by the bacteriophage therapy for its commercialization.

Keywords: Antibiotic resistance, Bacteriophage therapy, Lytic-phages, One-health, Bacteriophage-based proteins.

IL-32

Identification of RdRp Inhibitors against SARS-CoV-2 through E-Pharmacophore-Based Virtual Screening, Molecular Docking and MD Simulations Approaches

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Abstract

The outbreak of novel Coronavirus, an enduring pandemic declared by WHO, has consequences to an alarming ongoing public health menace which has already claimed several million human lives. In addition to numerous vaccinations and medications for mild to moderate COVID-19 infection, lack of promising medication or therapeutic pharmaceuticals remains a serious concern to counter the ongoing coronavirus infections and to hinder its dreadful spread. Global health emergencies have called for urgency for potential drug discovery and time is the biggest constraint apart from the financial and human resources required for the high throughput drug screening. However, computational screening or in-silico approaches appeared to be an effective and faster approach to discover potential molecules without sacrificing the model animals. Accumulated shreds of evidence on computational studies against viral diseases have revealed significance of in-silico drug discovery approaches especially in the time of urgency. The central role of RdRp in SARS-CoV-2 replication makes it a promising drug target to curtain ongoing infection and its spread. The present study aimed to employ E-pharmacophore-based virtual screening to reveal potent inhibitors of RdRp as potential leads to block the viral replication. An energy-optimised pharmacophore model was generated to screen the Enamine REAL DataBase (RDB). Then, ADME/T profiles were determined to validate the pharmacokinetics and pharmacodynamics properties of the hit compounds. Moreover, High Throughput Virtual Screening (HTVS) and molecular docking (SP & XP) were employed to screen the top hits from pharmacophore-based virtual screening and ADME/T screen. The binding free energies of the top hits were calculated by conducting

MM-GBSA analysis followed by MD simulations to determine the stability of molecular interactions between top hits and RdRp protein. The MD simulation studies confirmed the stability of protein ligand complexes, hence, indicating as potent RdRp inhibitors and are promising candidate drugs to be further validated and translated into clinics in future.

Keywords: HTVS, XP Docking, ADME/T, COVID-19, REAL DataBase-Enamine, Drug repurposing, Drug design, RNA-dependent RNA polymerase, MM GBSA.

IL-33

Designing Nanomedicine According to Tumor Microenvironment to Improve Cancer Therapy Efficacy

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Abstract

Cancer is undoubtedly one of the major threats to mankind. Conventional tumor-targeted drug delivery systems (DDSs) face challenges, such as unsatisfied systemic circulation, low targeting efficiency, poor tumoral penetration, and uncontrolled drug release. The tumor mass is not just made of heterogeneous tumor cells population but also contains residential components (extracellular matrix proteins, tumor associated fibroblasts, enzymes) and infiltrating host cells (immune cells), the tumor vascular system, and acidic and hypoxia environment, all together known as tumor microenvironment (TME). This TME promotes tumor progression and metastases, shape therapeutic responses as well as resistance to various anticancer therapies. Tumor microenvironment responsive drug delivery systems are "smart" formulations exhibiting an on-demand drug release profile upon response to stimulations from tumor cellular environments, which have aroused great interests in the nano-medical field. Through shrinking or expanding in size, changing of the surface charge, or regulation of other physiochemical properties, tumor stimuli-responsive drug delivery could be achieved. For that reason, TME modulation, including extracellular matrix, tumor hypoxic, acidic, and immune microenvironment within the tumor, with combination to various current cancer therapies have been recommended as a substitute strategy to enhance the treatment outcomes of existing tumor therapies. We developed tumor microenvironment activatable and external stimuli-responsive drug delivery system, which can improve photodynamic therapy (PDT) induced bioreductive chemotherapy in different tumor cells both proximal and distal to vessels. In another project, we developed a pH transformable nano-clusters functionalized with extracellular matrix degrading enzyme. Nano-clusters effectively remodel the stroma and normalized vascular system. While nano-clusters transformed into smaller NPs diffused to tumor bed for enhanced radiotherapy. We comprehensively summarize the field of active targeting drug delivery systems and a number of stimuli-responsive release studies in the context of emerging nanoplatform development and these strategies are relatively new and may offer a way to improve the effects of anticancer therapies.

Keywords: Cancer therapy, Tumor microenvironment, Drug delivery system, Nanoparticles.

IL-34

Optimizing Citric Acid Amended Phosphorus for Wheat Productivity in Calcareous Soil by Using ^{32}P Isotopic Labeling

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Abstract

The low productivity of wheat plant in calcareous soil is due to less availability of Phosphorus (P) to plant. Phosphorus fixation in the soil is one of the major constraints for high crop produce. An experimental was performed under greenhouse conditions in order to improve phosphorus availability to wheat plant by application of organic acid i.e. citric acid amended phosphate fertilizer in calcareous soil. The study comprised of three replications each with nine treatments managed in completely randomized design (CRD). The treatments include citric acid (2 mM kg^{-1} soil) co-applied with different phosphate fertilizer sources i.e. Phosphoric Acid (PA) and Di-ammonium Phosphate (DAP) applied as a sole and in combination with citric acid at the different rates (0, 40, 80 mg kg^{-1} soil). In the greenhouse, these soils were labeled with ^{32}P radioisotopes to quantify the proportion of P taken up by wheat from native soil or the P fertilizer treatments. The maximum (30.62%) phosphorus use efficiency was measured in PA+CA at rate of 80 mg kg^{-1} soil followed by (27.03%) in DAP+CA at the same P rate. However, reduced phosphorus recovery efficiency (PRE) was measured as the P concentration increased in sole P as well as in citric acid co-applied P fertilizer treatments. The highest (16.84%) values for PRE was recorded in PA+CA at rate of 40 mg kg^{-1} soil and the lowest (7.88%) in sole DAP at 80 mg kg^{-1} soil. It was concluded that citric acid co-applied with P fertilizers is promising fertilization method for increasing P concentration in soil solution and enhance wheat productivity grown in alkaline calcareous soil.

Keywords: Phosphorus use efficiency, Wheat, ^{32}P radio isotope, Citric acid.

ORAL PRESENTATIONS

OP-1

Combined Application of Beneficial Microbes and Chemical Elicitor to Manage Fusarium Wilt of Tomato

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Abstract

Tomato is an economically important crop grown worldwide. Fusarium wilt of tomato is a serious disease causing severe economic losses worldwide. Rhizosphere symbiotic microorganisms are increasingly proposed as a possible alternative to overcome these problems, with particular emphasis on integration with synthetic elicitor molecules to further enhance defense responses against invading pathogens. The objective of this study was to use beneficial microbes in combination to synthetic elicitor to suppress Fusarium wilt of tomato. Ten rhizospheric strains were isolated and purified from the rhizosphere. The best performing antagonistic isolate were identified as *B. subtilis* BS6, *B. amyloliquificiens* BS7, and *B. fortis* BS9. Afterward, *in-silico* studies were performed to screen agonists of tomato receptors like kinase "SILKY12" having an important role in plant immunity and symbiosis. A library of phytochemicals was screened by performing molecular docking and 24-epibrassinolide was selected as the potent agonist of "SILKY12" based on docking score and commercial availability. Thereafter, a pot trial was performed where the imperative effect of the consortia of best-performing bacterial strains as a rhizospheric amendment and synthetic elicitor (24-epibrassinolide) as a foliar amendment at varying concentration, were applied under different combinations. The combined application of consortia and 24-epibrassinolide at 1 mM resulted in significantly increased total phenolic contents, peroxidase, phenylalanine ammonia-lyase and polyphenol oxidase activities in tomato plants subsequently challenged with Fusarium wilt pathogen. These results suggested that, in combination, bacterial consortia (*B. subtilis* BS6, *B. amyloliquificiens* BS7, and *B. fortis* BS9) and 24-epibrassinolide may play an important role in controlling Fusarium wilt diseases by multiple mechanisms in tomato plants.

Keywords: Tomato, fusarium wilt, antagonistic, rhizospheric, receptor kinase, defense response

OP-2

Nanoparticles Based Crop Protection against Soil Borne Pathogens for Sustainable Agriculture

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Abstract

In recent years, various types of metal and metal-oxides nanoparticles attained copious interest as an alternate method for the management of plant diseases. Tomato has become a successful model plant to investigate the initiation of defense pathways after exposure to disease agents. Indulgence to these mechanisms is a key focus of plant-pathology to enhance crop protection. The current investigation was aimed at the green synthesis of nanoparticles to induce resistance in tomato against fusarium wilt. Green synthesized nanoparticles including MA-AgNPs, CF-CuONPs and BC-IONPs were characterized and used to investigate the in-vitro and in-vivo antifungal activity at various concentrations. In-vitro antifungal potential of all three types of nanoparticles expressively inhibited mycelial growth and spore germination of *Fusarium oxysporum f.* sp. *lycopersici* in a dose-dependent manner. The highest percentage inhibition in mycelial radial growth (96.8 ± 0.23%) and decline in spore germination rate (4.67%) was observed at 140µg/mL of MA-AgNPs in contrast to the control and fungicide treatment. Monographs of the scanning electron microscope revealed the ultrastructural changes in fungal hyphae in response to higher concentrations of nanoparticles signifying the detrimental effect of these NPs on the fungal mycelial surface. DCFH-DA fluorescence revealed ROS accumulation in fungal mycelium by showing strong green color after treatment with NPs. Each type of nanoparticle was further characterized to get information about wavelength range, functional nature, crystallographic structure, size, shape and stability. The microwave-assisted MA-AgNPs showed a peak at 434nm by using 5mL of *M. azedarach* leaf extract and 2.5mM of AgNO3 solution at pH 8, exposed to 30s of microwave irradiations. MA-AgNPs indicated stability even after six months. Spherical shaped nanoparticles ranged from 12¬-46nm were confirmed by XRD, SEM and TEM analysis. MA-AgNPs indicated negative zeta potential of -22.3mV. Uptake of these nanoparticles didn't show any visible sign of toxicity on plant yield and productivity.

Keywords: Fungi, wilt, nanotechnology, plant extracts

OP-3

Bio-Fabrication of Zinc Oxide Nanoparticles to Rescue Mung Bean against Cercospora Leaf Spot

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Abstract

Nanotechnology is evolving day by day across the world. A significant loss in mung bean yield is caused by seed-borne fungus. The purpose of this study was to determine the effect of different concentrations of green synthesized zinc oxide nanoparticles (ZnO NPs) using *Nigella sativa* seed extract on Cercospora leaf spot disease in mung bean plants under in vitro and in vivo conditions, as well as the effects on mung bean agronomic and physiological parameters. The green synthesized ZnO NPs were characterized using UV-visible spectroscopy, which revealed a peak at 338 nm. To describe chemical bonding and chemical compounds Fourier-transform infrared spectroscopy (FTIR) was performed, and X-ray diffraction (XRD) and scanning electron microscopy for morphological evaluation. In vitro, green synthesized NPs were tested for their ability to inhibit fungal growth at five different concentrations. After 7 days of inoculation, ZnO NPs (1200 ppm) inhibited mycelial growth the most (89.86 ± 0.70), followed by 900 and 1500 ppm (72.73 ± 1.27) and (78.66 ± 0.23). The greenhouse experiments demonstrated that NPs had antifungal activity against Cercospora Leaf spot disease in mung bean. The concentration of 1200 ppm ZnO NPs resulted in a statistically significant result of disease control of 30 ± 11.54. In addition, Plants exposed to ZnO NPs at 1200 showed statistically significant improvements in shoot length, root length, number of leaves, number of pods, shoot fresh weight (28.62 %), shoot dry weight (85.18 %), root fresh weight (38.88 %), and root dry weight (38.88 %) compared to the control. Our findings show that green synthesized ZnO NPs can control *Cercospora canescens* in mung bean, pointing to their use in plant disease control and growth enhancement.

Keywords: Zinc Oxide Nanoparticles, Green synthesis, *Trachyspermum ammi*, Cercospora Leaf Spot, Antifungal

OP-4

In-Silico Approach for the Identification of Potent Anti-Cancer Drug against Selected Proteins Responsible for Causing Pancreatic Ductal Adenocarcinoma by Molecular Docking and Density Functional Theory

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Abstract

Pancreatic cancer is one of the life-threatening and fatal cancers. Multiple proteins which are over-expressed in pancreatic ductal adenocarcinoma. Leukemia Inhibitory Factor and Kallikrein related peptidase-8 were selected for this study that were overexpressed in pancreatic cancer. In this study, the phytochemicals were used to identify which can serve as anti-cancer drug, obtained from IMPPAT. 17967 compounds were screened out by applying different drug-likeness parameters and 95 compounds were selected as drug-like candidates. These were selected for molecular docking studies. Further these compounds were subjected to density functional theory studies. This study showed that piroxicam can also serve as a potent anti-cancer drug against LIF and KLK8 which were over-expressed in pancreatic cancer.

Keywords: LIF, KLK8, PDAC, molecular docking, DFT

OP-5

Cotton Microbiome Profiling and Cotton Leaf Curl Disease (Clcud) Suppression through Microbial Consortia Associated with *Gossypium Arboretum*

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Abstract

The failure of breeding strategies has caused scientists to shift to other means where the new approach involves exploring the microbiome to modulate plant defense mechanisms against Cotton Leaf Curl Disease (CLCuD). The cotton microbiome of CLCuD-resistant varieties may harbor a multitude of bacterial genera that significantly contribute to disease resistance and provide information on metabolic pathways that differ between the susceptible and resistant varieties. The current study explores the microbiome of CLCuD-susceptible *Gossypium hirsutum* and CLCuD-resistant *Gossypium arboreum* using 16S rRNA gene amplification for the leaf endophyte, leaf epiphyte, rhizosphere, and root endophyte of the two cotton species. This revealed that *Pseudomonas* inhabited the rhizosphere while *Bacillus* was predominantly found in the phyllosphere of CLCuV-tolerant *G. arboreum*. Using salicylic acid-producing *Serratia spp*. and *Fictibacillus spp*. isolated from CLCuD-resistant *G. arboreum*, and guided by our analyses, we have successfully suppressed CLCuD in the susceptible *G. hirsutum* through pot assays. The applied strains exhibited less than 10% CLCuD incidence as compared to control group where it was 40% at 40 days post viral inoculation. To the best of our knowledge, this study is the first of its kind to successfully apply microbes as biocontrol agent to suppress viral disease in Cotton.

Keywords: microbiome, cotton leaf curl virus, systemic acquired resistance, salicylic acid, *Gossypium hirsutum*, Gossypium arboreum

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OP- 6

"NIAB MUNG 2021" A High Yielding, Disease Resistant and Bold Seeded Mungbean (*Vigna radiata* L. Wilczek) Variety Developed through Inter-Specific Hybridization

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Abstract

Biotic and abiotic stresses greatly reduce the yield of mungbean. The best and economical solution of the problem is to develop resistant varieties. Mungbean germplasm has been extensively screened against biotic and abiotic stresses. Many varieties have also been developed by using this germplasm. But these varieties have narrow genetic base, which rendered the varieties susceptible after a short time. To address this problem of narrow genetic base a high yielding mungbean variety is developed through inter specific hybridization of mung bean variety 6601 with mash bean line 3-156-1. The F1 hybrid of this variety was grown and visually confirmed during 2006. Evaluation and selection in segregating generations (F2 – F5) was carried out during 2007-2010. From 2011 to 2014, it was tested in a variety of yield trials. In National Uniform Yield Trials conducted during 2015 and 2016, this variety produced 21% and 12% higher seed yield, respectively as compared to standard check variety NM 2011 and secured second position in 2015. This variety is resistant to yellow mosaic disease (MYMD) and has high contents of essential amino acids.

Keywords: Zinc oxide nanoparticles, green synthesis, *Trachyspermum ammi*, Cercospora Leaf Spot, antifungal

OP- 7

Identification of Hub Genes Associated with Rheumatoid Arthritis via Integrated Bioinformatic Analysis

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Abstract

Rheumatoid arthritis (RA) is a prevalent autoimmune disorder characterized by chronic inflammation that primarily affects the joints, leading to debilitating pain and joint damage. This research paper employs a multifaceted approach, combining microarray and RNA sequencing data analysis to investigate the molecular mechanisms underlying RA. The aim of this study was to identify differentially expressed genes (DEGs) in the blood samples and synovial fluid samples of patients affected with RA and to compare and contrast the DEGs present in the blood with those present in the synovial fluid of RA patients. Two microarray datasets (GSE15573 and GSE10500) and an RNA sequencing dataset (GSE154474) were used to explore common genes across different sample types. A total of 83 genes exhibited significant expression differences across these datasets, providing a rich pool of candidate genes potentially involved in the pathogenesis of RA. To find co-expression gene modules in the RNA-seq data, Weighted Gene Co-Expression Network Analysis (WGCNA) was used. Nine unique modules were identified by this research, with the blue color module having the greatest relevance. These genes may be particularly relevant to RA pathogenesis given that gene ontology study revealed that they were primarily linked to immune system functions, extracellular space, chemokine activity, and the KEGG pathway. The STRING database and Cytoscape software were used to analyze protein-protein interactions, revealing complex relationships between the discovered genes. Additionally, the hub genes identified by Cytohubba revealed *HBB, RGMB, AXIN2, LEF1, TCF7*, and other genes as important network regulators.

Keywords: Rheumatoid arthritis, microarray, RNA sequencing, synovial fluid, WGCNA

OP-8

Identifying Potential Drugs Targeting Key Genes Associated with Glioblastoma through an *In-Silico* Approach

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Abstract

Glioblastoma multiforme, an infrequent traumatic cerebral ailment, represents a focal point of research due to its relentless proliferation, resulting in devastating consequences. Glioblastoma is classified as a Grade IV neoplasm by WHO, characterized by its limited detectability, a heightened susceptibility to comorbidities, and constrained therapeutic alternatives. Recent emphasis on the concepts of personalized medicine has spurred research aiming at developing specific treatment methods based on the stratification of biomarkers linked with GBM. The study of GBM biomarkers has sparked interest because of their potential significance in prognosis classification, which has driven the progress of targeted therapeutic treatments and the customization of treatment regimens. Illuminating the process of target-based virtual drug screening with plant-derived natural compounds represents a pivotal milestone in the field of drug discovery for glioblastoma, advancing rapidly. Using NPACT database, this initiative will identify promising compounds for the treatment of glioblastoma brain cancer. In this project, we focused on molecules' capacity to cross the blood-brain barrier. Among the 120 derivative compounds examined, 10 were carefully chosen for their excellent ADMET (distribution, metabolism, absorption, excretion, and toxicity) profiles. The study employed a network-based bioinformatics approach to identify candidate compounds that have the potential as therapeutic agents against glioblastoma using DisGenet and GeneCards databases. The similar genes present in both source databases were exported in String Bioinformatics for construction of PPI network and later imported in Cytoscape. Furter, we used MCODE and CytoHubba Plugins for identifying top 10 ranked GBM associated genes. These hub genes were subjected to GO annotation and KEGG pathway enrichment analyses, which indicated some key roles and signalling pathways that were strongly related to glioblastoma infections. Finally, the top ranked genes were docked using Molecular Operating Environment (MOE) against 10 screened drugs to find the best docked drug/s based on Binding Energies, RMSD values and maximum intermolecular interactions.

Keywords: Glioblastoma, Hub genes, Biomarkers, Molecular docking, NPACT

OP-9

Genetic Studies in the Pakistani Population Reveal Novel Associations with Ventricular Septal Defects (VSDs)

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Abstract

With prevalence up to 4%, Ventricular Septal Defect (VSD) is one of the leading causes of neonatal deaths. VSD is a common complex genetic disorder that has been associated with many genetic determinants. Variants from genes including T-Box *TBX5* and *NFATc1*, *VEGF*, *ISLET1* and enzyme *MTHFR* were selected. Genetic risk score (GRS) is a widely accepted approach used to convert the genetic data into prediction and assessment tool for disease susceptibility. A total of 200 participants were recruited for the current study, 100 VSD patients and 100 controls. Genotyping of all the selected variants was performed. For the statistical analysis, the software SPSS was used. Genotypic and allelic frequencies of cases and controls were calculated. The association of GRS quartiles with VSD was examined using binary logistic regression. The *ISL1, TBX5 and MTHFR* variants were found to be in association with VSD. In contrast, the *VEGF* variant did not show significance association with the VSD. For cases, the mean GRS score was higher in comparison to controls. Comparison of GRS between cases and control showed that mean GRS of cases was 1.90 ± 0.480 while in controls it was 1.68 ± 0.490. GRS of these five loci was strongly associated with VSD. GRS can provide better information for association between variants and disease as compared to a single SNP. We also illustrated that the cumulative power of GRS is greater over the single SNP effect.

Keywords: Ventricular Septal Defect, genetic disorder, SPSS, SNP

OP-10

In-Silico Analysis of Levivirus MS2 Capsid Protein Interaction with its Genomic RNA

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Abstract

Emesvirus zinderi (Levivirus MS2) contains single-stranded RNA genome comprising of 3569 nucleotides. This study we carried out computationally to investigate MS2 capsid protein (CP) interaction with its genomic RNA specifically with 15 MS2 genomic RNA stem loop structures (RNA SLs). For comparison, the CP was also interacted with Coronavirus RNA. It was found that the MS2 CP dimers have better affinities with the MS2 genomic RNA. The molecular docking was carried out of 15 RNA SLs with CP monomer, dimer and pentamer to find the validity of PS-mediated assembly model and different other proposed models for encapsidation of MS2. Viral encapsdation is governed by protein–protein (CP-CP) and protein–genome (CP-RNA) interactions, along with some other important factors. The results proposed that MS2 CP dimer increase the affinity of CP with its genomic RNA andtwo RNA SLs designated as B and H in the current study have significant role in MS2encapsidation. Alanine scanning, to look into the importance of R-rich motifs, by replacing three R residues (R39, R50 and R57) of CP was executed. Secondary structures prediction of 15 RNA SLs was carried out to have conclusive outlook over the current project, which emphasized the significance of SL-B and SL-H in MS2 encapsidation. The methodology used in this dissertation for the investigation of MS2 CP-RNA interaction should be easily transferable to other ssRNA viruses and have confirmed the roles of multiple PS sites so enabling researchers to go for more deep research of encapsidation mechanism.

Keywords: MS2, Capsid protein dimer, Stem loop, CP-RNA interactions, Encapsidation

OP-11

In-Silico Approaches to Identify Potential Drug-Like Compounds against Glycoproteins: Gn, Gc, and RNA-Dependent RNA Polymerase (Rdrp) of Hantavirus

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Abstract

Hantaviruses are novel zoonotic pathogens, which belong to the family Hantaviridae. The pathogens are enveloped, tri-segmented - monopartite, single-stranded (negative-sense) RNA viruses distributed worldwide, especially in Asia, North and South America, and Europe. It is asymptomatic and persistent in rodent host reservoirs. In rodents, the viruses do not cause infection but are transmitted to humans by contaminated aerosolization of rodent excreta. Hantaan Orthohantavirus (HTNV) results in hemorrhagic fever with renal syndrome (HFRS) with incredibly high mortality rates. No drug is approved against it, therefore classified as Biosafety level 4 agents. In this study, surface spikes (glycoproteins: Gn and Gc) and RNA-dependent RNA polymerase (RdRp) of the virus genome are selected as antiviral targets, encoded by the M and L segments, respectively. According to ADMET criteria, BBB- ligands were filtered out of 17967 compounds (phytochemicals). After careful analysis, the potential inhibitors against surface spikes (glycoproteins: Gn and Gc) and RNA-dependent RNA polymerase (RdRp) were identified by using in-silico methodologies: Molecular Docking, Density Functional Theory, and Molecular Dynamic (MD) simulations. In our current study, Disodium;4-[3-pyridin-2-yl-6-(4-sulfonatophenyl)-1,2,4-triazin-5-ylbenzenesulfonate (from BBB- group) was identified as an effective compound for the preventive and therapeutic measures against Hantavirus. The outcomes of this study will contribute to a better understanding of Hantavirus-related diseases.

Keywords: Antiviral, Glycoprotein, Hemorrhagic fever, Mortality, Polymerase

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OP-12

In-Silico Analysis of Man2b1 Gene to Predict the Pathogenic Variants Cause Alpha-Mannosidosis

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Abstract

Alpha-mannosidosis is a rare autosomal recessive inherited disorder caused by the lysosomal deficiency of α-mannosidase. It is a metabolic disorder and its clinical features are hydrocephalus, equinus ankle, and deformation of sternum, scoliosis and dysostosis multiplex, periods of psychosis, speech impairment, compromised immune system and hearing loss. Mutations in the *MAN2B1* gene results in α-mannosidosis. In-silico analysis is applied in this study to predict the most pathogenic missense and splice site mutants of *MAN2B1* that causes the lysosomal deficiency of α-mannosidase which is involved in degradation of N-linked oligosaccharides. Different algorithms-based tools are included in this study to detect pathogenic mutations and their effects on the stability of protein. 554 variants are retrieved from the databases: dbSNP, ClinVar, 1000 Genomes, and GnomAD. A defined methodology using tools based on different algorithms with 98% accuracy provided us with 197 deleterious mutations. In-silico analysis includes the prediction of deleterious variants based on algorithms of the most accurate tools and their effect on the stability of the protein. 117 variants out of 197 predicted to be destabilizing by all the stability change tools (DUET, SDM Alanine Scan, and Foldx). UCSF Chimera v.1.13.1 is used to visualize the effects of mutations on the structure of proteins by comparing it with the wild type protein structure. 42 variants form unwanted interactions with atoms of neighboring residues and cause malformation at structural and functional level of protein. 70 splice variants retrieved from GnomAD were analyzed with SPiCE, Human Splicing Finder, and CADD v 1.6. Only 10 variants predicted to be pathogenic for disturbing the splicing mechanism.

Keywords: Alpha-mannosidosis; hydrocephalus; equinus ankle; scoliosis; dysostosis multiplex; Alpha-mannosidase

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OP-13

Chromium Stress Mitigation through Plant Growth-Promoting Bacteria: A Promising Strategy for Sustainable Agriculture

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Abstract

Chromium (Cr) contamination poses a significant threat to living organisms due to its toxic nature, primarily stemming from industrial discharge into soil. Microbe-assisted bioremediation is an emerging and environment friendly approach for detoxifying pollutants. In this study, 60 chromium-resistant bacterial strains were isolated from soil samples. These strains underwent rigorous screening for biochemical, genetic, and plant growth-promoting characteristics. Five promising strains, namely L41, K32, K58, K72, and K86, were selected and inoculated with Wheat (*Triticum aestivum*) seeds planted in soil with varying concentrations of K_2CrO_4, including 0, 250, and 500 mg/kg. The findings substantiated that the examined isolates indeed exhibited resistance to Cr (VI) as plant growth-promoting bacteria (PGPR) by using classical biochemical tests (phosphate solubilization, nitrogen fixation, indole acetic acid, hydrogen cyanide, siderophores, ammonia production) and showed variable levels of Cr (VI) resistance (60–110 mg/ml). The outcomes of pot experiments indicated that Cr stress adversely affects plant growth and antioxidant enzymatic activities in the absence of bacterial inoculation. However, the introduced bacterial isolates effectively regulated plant growth and reduced oxidative stress and Cr toxicity by converting Cr^{6+} to Cr^{3+}. Moreover,

Cr^{6+} uptake by wheat was significantly reduced in bacterial-inoculated plants. In conclusion, the application of these bacterial isolates holds promise as an effective strategy to alleviate Cr toxicity in wheat and potentially in other cereals cultivated in Cr-stressed environments.

Keywords: Chromium, plant growth promoting bacteria, wheat, microbial assisted bioremediation.

OP-14

Fabrication of EDTA Functionalized Chitosan/Amino Carbamated Alginate Double Network Hydrogel Beads and its Blend with Magnetite for Environmental Applications

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Abstract

Ethylene diamine tetra acetic acid (EDTA) modified chitosan and magnetite modified sodium alginate hydrogel beads were synthesized and characterized by FTIR. The synthesis of EDTA modified chitosan was accomplished in two steps: first EDTA dianhydride was synthesized by using EDTA as a major reactant in the presence of pyridine and acetic anhydride, then it was treated with chitosan to synthesize EDTA modified chitosan. The sodium alginate react with 4-phenyl semicarbazide to graft amino carbamated functionalities. The N, O containing groups in the backbone imparted selectivity and specificity to the biosorbent. Magnetite hydrogel beads has environmental application.

Keywords: EDTA, FTIR, sodium alginate, environment

OP- 15

Expression Profiling of Key Genes Involved in Glioblastoma Using Systematic Bioinformatics Approach

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Abstract

Glioblastoma (GBM) stands as the most devastating and prevalent form of primary brain tumor, characterized by its high rates of morbidity and mortality. This malignancy displays a unique pattern, appearing as a primary tumor in 9% of cases and as a secondary tumor in 10% of cases. Despite its distinct nature, comprehending the underlying mechanisms governing stemness and the identification of potential biomarkers remain elusive challenges. This project represents a pioneering effort in advancing bioinformatics methodologies, harnessing a multitude of publicly accessible datasets. The primary objective of this analysis is to shed light on potential hub genes and pivotal pathways linked to GBM development. Through integrated analysis, differentially expressed genes (DEGs) between brain cancer tissues and healthy brain tissues were unearthed. Multiple strategies, encompassing gene ontology (GO) analysis and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analysis, were employed to functionally annotate the DEGs and visualize their characteristics using the R programming language. The identification of significant hub genes was achieved through the exploration of protein-protein interaction networks, Venn diagram analyses, and survival assessments. Furthermore, there is an intention to validate these identified hub genes that are *PLOD1* and *COL5A2* in clinical samples, scrutinizing their gene expression levels across various disease states. This study carries the potential to assist researchers in pinpointing innovative drugs targeting the pivotal genes implicated in GBM. These hub genes may also serve as novel biomarkers, aiding in the early screening of GBM.

Keywords: Glioblastoma, malignancy, hub genes

OP- 16

Potential Of Rhizospheric Fungi to Reduce Copper and Lead Toxicity in *Triticum Aestivum L.*

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Abstract

Plants have adapted to various heavy metals and environmental situations during anthropogenic evolution. The most common heavy metal contaminants are lead (Pb) and copper (Cu), which can be found in both natural and industrial settings. Microorganisms play a crucial role in the biotransformation of heavy metal-contaminated environments. In this study, four rhizospheric fungus strains were extracted from *Parthenium hysterophorus* and tested for their tolerance to lead and copper. These strains were selected for their ability to promote plant growth under heavy metal stress. When inoculated to *Triticum aestivum* L. under heavy metal stress, the fungal isolates NMG, Ng, N6, and NB showed promising results in the form of increased secondary metabolites. Different concentrations of specific heavy metals (Pb25, Pb75, Cu100, Cu200, Pb25+Cu100, and Pb75+Cu200g/mL) were applied to wheat plants. The plants exposed to metal stress without microbial inoculation displayed a reduction in growth. However, when rhizospheric fungal inoculation restored plant growth and development, showed the symbiotic relationship between the fungus and the host plant roots under heavy metal stress conditions. The isolates have the ability to transform HMs, making them unavailable for plant uptake and accumulation, which prevents harm to plants. Apart from their bioremediation properties, some isolates can create secondary metabolites like IAA, GA, ABA, H_2O_2, Electrolytic leakage, SA, lipid, DPPH, flavonoids, phenols, and proteins, which can stimulate plant growth and make them suitable for use as bio-fertilizers and bio-remediating agents in areas with high levels of heavy metal contamination.

Keywords: Bioreduction, Bioremediation, Heavy metals uptake (lead, copper), Heavy metal tolerance. Rhizospheric fungi, *Triticum aestivum* L.

OP-17

Exome Sequencing Revealed Novel Variation in *SLC24A1* Gene Causing Congenital Stationary Night Blindness

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Abstract

Congenital stationary night blindness (CSNB) is a rare hereditary retinal disorder characterized by impaired night vision and diminished rod cell function, often due to genetic mutations. Ophthalmological studies have progressed in last decade and four novel mutations were reported for causing autosomal recessive CSNB. We have reported a multigenerational family having 8 individuals affected and present symptoms of night blindness. Clinical investigations confirmed the presence of night blindness and questionnaires were filled to record family and medical history. Whole Exome Sequencing was performed on only one individual from family. WES results showed a novel mutation in *SLC24A1* which is member of solute carrier protein superfamily. The mutation is stop gain causing premature termination of *SLC24A1* thus retarding normal functioning of gene. In-depth analysis of the *SLC24A1* gene followed, employing bioinformatics tools like CADD, meta-SNP, DynaMut, DUET, mCSM, and CUPSAT to filter pathogenic variants. Out of 55 initially identified, 22 were predicted as destabilizing by all tools. MutPred2 was then used for pathogenicity and functional analysis, identifying 42 highly pathogenic variants. UCSF Chimera was employed to assess mutagenesis, revealing no clashes in neighboring zones for any variant. Then, we analyzed the post translational modification (PTM) sites with ScanProsite and Netsurf and 9 variants were found lying in PTM sites (5 were exposed and on PTM site). Splice Site analysis was done by different bioinformatics tools including SpliceAI, SPiCE, Mutation taster and Human Splice Finder (HSF). And all these tools predicted both of our splice site variants to be pathogenic and disturbing the normal function of *SLC24A1*.

Keywords: Congenital Stationary Night Blindness, Inherited Retinal Disorder, *SLC24A1*, Blindness, Vision Loss

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OP-18

Exome Sequencing Revealed Novel Variation in *PRMT7* Gene Causing Intellectual Disability

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Abstract

Protein arginine methytransferase 7 is a family member of enzymes involved in post translational modification and catalyzes the transfer of methyl group to the nitrogen of arginine residue of several protein substrates and involved in various developmental processes. Previously reported *PRMT7* pathogenic variants have been connected to an autosomal recessive disorder characterized by short stature, Brachydactyly, intellectual developmental, disability disorder, and seizers syndrome. In my knowledge, none of the study in literature performed the *in-silico* analysis to predict possible pathogenic variants of *PRMT7* gene. Thus, we aimed to perform the *in-silico* analysis to forecast the highly pathogenic variants that disturbs the functionality of catalytic domain. We reviewed 49 previously reported mutations in *PRMT7* gene and reported 5 siblings of consanguineous parents and exome sequencing revealed that 14 years old female has novel non-synonymous, homozygous variant in exon 5 of *PRMT7* gene causing *SBIDDS* syndrome. *In silico* analysis was performed to predict pathogenic missense and splice site variants of *PRMT7* gene. The retrieved variants of the gene were analyzed by using computational tools based on different algorithms for function, stability, and PTM site analysis. The major clinical symptoms of SBIDDS syndrome are intellectual developmental disability, short stature, microcephaly, hypotonia, Brachydactyly, broad and depressed nasal tip. The variable findings were seizers, obesity, hearing loss, and eye abnormalities (strabismus, stigmatism etc.). *In silico* analysis predicted 32 missense mutations and 6 splice site mutations that are considered pathogenic. Total 18 variants were predicted destabilizing and 3 of the PTM site variants were predictably disrupted by 32 variants. This study further confirmed an unreported mutation in *PRMT7* gene correlated with symptoms of SBIDDS syndrome and an extensive in silico analysis can determine the predicted pathogenic variations for further in vitro experimentation.

Keywords: Brachydactyly, intellectual disability, late onset obesity, *PRMT7, SBIDDS*, seizures, short stature

OP-19

Metabolic and Morphological Analysis of DOF1 Transgenic T2 Wheat Lines under Nitrogen Stress

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Abstract

Over the last century, the increased crop production has largely been attributed to rampant input of nitrogen fertilizers, which either gets lost through leaching or volatilization, hence resulting in environmental pollution and several human health hazards. In order to cater this widespread concern, the need of the hour is to engineer crops that require less fertilizer input and use the applied nitrogen in an efficient manner. In this regard, a number transcription factors have been reported to improve the nitrogen use efficiency (NUE) of crop plants. The transcription factor *Triticum aestivum* Dof1 (TaDof1) is known to modulate the activity of multiple genes, specifically that are involved in the regulation of carbon and nitrogen metabolism, when plants are grown under nitrogen-limiting conditions. Previously, transgenic wheat plants overexpressing TaDof1 were developed, and assessed with respect to their expression profiles along with biochemical and morphological traits. The main premise of the current investigation was to compare the T2 generation of six different transgenic TaDof1 wheat lines-namely, F1, G1, G2, G3, G4 and G5-with respect to their metabolic, biochemical, and morphological traits under normal and nitrogen deficient conditions. The screening of positive plants was done through BASTA and conventional PCR. The expression level of TaDof1 in transgenic lines and the four genes (Glutamine synthetase, nitrite reductase, phosphoenolpyruvate carboxylase and pyruvate kinase) associated with TaDof1 in carbon and nitrogen metabolism were quantified through RT-PCR and real-time PCR. The overall relative fold increase of TaDof1 gene expression under nitrogen deficient condition increased to 1.16-fold in F1 as compared to Faisalabad control. For Galaxy transgenics, the overall increase in transgene expression ranged from 0.68 to 7.61-fold, with the highest fold increase in G2 transgenic line.

Keywords: *Triticum aestivum* L., TaDof1 transcription factor, Nitrogen use efficiency (NUE), Quantitative RT-PCR

OP-20

Direct Acting Antivirals for Treatment and Management of Hepatitis C Virus Infection in Pakistan

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Abstract

Pakistan has second highest prevalence of Hepatitis C Virus (HCV), with estimated seroprevalence of 4.5-8.2%, with genotype (GT) 3a being the most common HCV GT. Direct acting antivirals (DAAs) are currently in use for HCV treatment. Current study aimed to evaluate efficacy of these DAA in HCV isolates from Pakistan. First half of study deals to evaluate efficacy of two different DAAs regimen i.e. (Sofosbuvir +RBV) and (Sofosbuvir + Daclatasvir). Blood samples anti-HCV positive patients were collected, processed for HCV RNA detection by Real-Time PCR. Patients positive for HCV RNA were processed for GT determination. SVR with both treatment regimens was recorded significant as 84.5% with SOF+RBV and 88.8% with SOF+DCV against different GTs of study group. Second part of the study deals with amplification and sequencing of NS5A, and NS5B regions of HCV GT-3a, for the identification of resistance associated mutations (RAMs), in treatment naive as well as in treatment failure patients. For this purpose amplified NS5A and NS5B regions were sequenced through Sanger Sequencing, and RAMs were identified by web based Geno2pheno [HCV] tool. RAMs to DCV were identified only in treatment experienced group i.e. A30T as 7.6%, P58T as 7.6%, Y93H as 15.6%, and S98G as 23%, and potential RAMs to SOF observed in treatment experienced patients were S282T as 8.7%, C316Y as 13%, L320P and v321A as 4.3% each. This study concludes SOF/DCV based therapy being pan genotypic is more effective in HCV treatment, secondly resistance analysis must be carried out prior to designing treatment regimens especially in treatment failure patients

Keywords: HCV, Direct Acting Antivirals, NS5B, NS5A, Resistance associated mutation

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OP-21

Alleviation of Cold Stress in *Oryza Sativa L* by Endophytic Fungi

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Abstract

The purpose of current study is to observe the impacts of cold stress on growth, metabolites and phytohormones of *Oryza sativa L.* and to evaluate the ability of endophytic fungi towards cold tolerance. MSB, MR and DS2 were three endophytic fungi among the six isolated strains which showed considerable potential to mitigate cold stress. The strains considerably increase the amount of total chlorophyll, phytohormones i.e., IAA, GA3 and ABA, flavonoids, proteins and lipids in plants effected by cold stress. The endophytic fungus (DS2, MR, MSB) inoculation (1gm per 100gm soil) on rice seedlings used. The responses of *Oryza sativa L*. towards the cold stress were described through the analysis of total chlorophyll, xanthophyll, carotenoids, protein, flavonoids, proline, phenolics, sugar, and IAA contents. Under cold stress, growth of rice seedlings was nearly compromised. Cold stress greatly reduced root length (7.6cm) which were markedly increased by endophytes (11.26cm). While shoot length under stress showed 16.23cm which were increased up to 14.86cm. Fresh weight under stress was 0.30gm effectively increased up to 0.42g upon exposure to endophytes. In fugal inoculated ice-cold stress was tolerated and growth parameters were significantly improved in comparison to non-endophyte, cold stressed seedlings. Plants treated with cold stress without any endophytic inoculation showed a reduction in growth whereas endophytic fungal inoculation not only restores plant growth and development but also enhances its symbiotic association, and showed colonization with host plant roots under cold stress conditions. The isolated endophytic fungal strains were capable of producing secondary metabolites like IAA, flavonoids, phenols and proteins, enables them excellent plant stimulants, so they could be used as bio-fertilizers and bio-remediating agents in cold stress areas. We concluded that the endophytic fungi plays an immense role in increasing the agronomic and biochemical parameters of rice seedlings when exposed to cold stress.

Keywords: *Oryza Sativa*, Endophytic Fungi, flavonoids, IAA, carotenoids

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OP-22

Functional Analysis of a *GhNAC79* Gene in Cotton Using VIGS and CRISPR-Cas9 for Drought and Salt Responsiveness

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Abstract

Cotton (*Gossypium spp*.) is a key crop for natural fiber production, also vital for feed and fuel. In the context of a global environment characterized by unpredictable weather patterns and escalating drought conditions resulting from climate change, the need to augment cotton's productivity, fiber characteristics, and ability to withstand stress have assumed heightened significance. This study aims to examine the functional importance of the *GhNAC79* gene, which has been identified as a crucial controller of drought and salt stress reactions in cotton. The use of expedient and effective methodologies, such as Virus-Induced Gene Silencing (VIGS), is crucial for the investigation of cotton's adaptability and the development of resilient cultivars. Viral-induced gene silencing (VIGS) utilizes the host's post-transcriptional gene silencing process as a strategy to inhibit viral multiplication. The Tobacco rattle virus (TRV) is very useful in this context due to its ability to infect a diverse range of host plants and cause only mild disease signs. In the first part of the study, the *GhNAC79* gene was temporarily suppressed in cotton plants by the technique of virus-

induced gene silencing, or VIGS. The main goal was to find out how the gene affected how the plants responded to drought and salt stress. The *GhNAC79* gene was precisely targeted by the binary vector pYL156 (TRV RNA2), and vector distribution was accomplished using agroinfiltration. Significant downregulation of *GhNAC79* expression was found by qPCR analysis in response to drought and salt stress. The obtained outcome shows that temporary gene silencing may be used successfully. The *GhNAC79* gene in cotton was specifically targeted and destroyed using the CRISPR-Cas9 genome editing technique to provide long-lasting gene silencing. The previously described stage was essential to understanding the gene's overall impact on stress reactions. This study offers insights into the function of *GhNAC79* by using VIGS for temporary gene silencing and CRISPR-Cas9 for permanent deletion. The findings open pathways for breeding cotton varieties with enhanced drought and salt tolerance, contributing to sustainable agriculture in a climate-challenged world. This approach exemplifies the synergy of contemporary genetic tools in crop improvement and stress management, highlighting the potential of targeted gene manipulation in addressing global agricultural challenges.

Keywords: Cotton, Virus-Induced Gene Silencing, CRISPR-Cas9

OP- 23

Integrated Transcriptome Profiling for Identification of Prognostic Hub Genes as Therapeutic Targets of Glioblastoma

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Abstract

Glioblastoma (GBM) stands as the most prevalent and catastrophic type of primary brain tumor, characterized by its significant levels of morbidity and mortality. Uniquely, GBM manifests as a primary tumor in 9% of cases and as a secondary tumor in 10% of cases. Nevertheless, comprehending the underlying mechanisms of stemness and their associated biomarkers remains a challenging pursuit. This initiative intends to propel the field of bioinformatics forward by integrating various publicly available datasets. Our primary objective was to shed light on potential hub genes and crucial pathways implicated in the progression of GBM. The comprehensive analysis unearthed genes exhibiting differential expression between brain cancer tissues and normal brain tissues. To achieve this, multiple strategies such as gene ontology (GO) analysis and the Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analysis were employed to annotate the DEGs functionally. Additionally, the R program facilitated the visualization of these findings. The identification of significant hub genes was facilitated by the construction of protein-protein interaction networks, Venn diagram analysis, and survival analysis. Furthermore, we aim to verify the identified hub genes that are *COL4A2* and *PLOD1* in clinical samples, assessing their gene expression levels across various disease states. It is anticipated that this investigation will provide crucial insights for researchers in identifying potential drugs targeting the key genes implicated in GBM. These hub genes also hold promise as novel biomarkers for the early detection of GBM.

Keywords: Glioblastoma, Biomarkers, hub genes, objective

OP-24

Formulation and Assessment of Chick-Pea Rice Pulao Using Fenugreek Seeds and Indian Rennet to Improve Blood Glycemic Levels

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Abstract

Diabetes is becoming a major health concern in Asia, particularly in Pakistan, where the prevalence has reached at alarming levels. A significant contributing factor is the consumption of high-carbohydrate food that includes rice and bread, etc. These high-carbohydrate foods pose a major risk to public health due to their impact on postprandial hyperglycemia. This research aimed to formulate a chickpea pulao (cooked Indian-Pakistani rice dish) and to evaluate its impact on postprandial blood glucose levels in type 2 diabetic individuals. Herbs at different concentrations (1,3,5,7 and 9%) were tested for antioxidant potential and phenolic contents through DPPH assay and Folin Ciocalteu assay respectively, while the hypoglycemic potential was tested by α-amylase and α-glucosidase inhibition assays. After sensory evaluation, the highest scored concentration was used to formulate the chickpea pulao for further trials. The study trial was advertised under the name of "DP trial," and a total of 12 diabetic participants were recruited. A single-blind randomized cross-over trial was conducted for three weeks with a one-week wash-over time in-between. Participants' pre and postprandial blood glucose levels were recorded for both control and intervention recipe. Results indicated that both fenugreek seeds and Indian rennet showed good antioxidant and hypoglycemic activity in raw and boiled extracts ($p=0.000$). Single blind randomized cross-over trial showed that consuming the intervention recipe significantly reduced postprandial hyperglycemia ($p=0.000$) in type 2 diabetic participants. Incorporation of hypoglycemic herbs into dietary patterns can work as an adjunct therapy for diabetes management, especially in populations with a high prevalence of this disease.

Keywords: Chickpea pulao; Cuisine modification; Hypoglycemic herbs; Pakistani Cuisine

OP 25

Development and Analysis of Lemongrass Oil-infused Edible Coatings for Improved Microbial Safety in Chicken Meat

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Abstract

The rising trend of employing edible coatings to mitigate food wastage and extend the shelf life of perishable food items has gained significant attention. This research aimed to assess the impact of incorporating lemongrass oil into Carboxy Methyl Cellulose (CMC) based edible coatings on the physicochemical attributes, microbial safety, and oxidative stability of raw chicken. Characterization of lemongrass oil, emulsions, and coatings was conducted using DPPH and Folin-Ciocalteu assays. Following chemical analysis, T1 (chicken meat + *E. coli* O157:H7 + 2% lemongrass oil incorporated in CMC based edible coating) was compared with positive (chicken meat) and negative control (chicken meat + *E. coli* O157:H7) based on antimicrobial activity and quality assessment over a seven-day storage period at 4℃. The CMC-based edible coating significantly ($p<0.05$) reduced the microbial load of T1 compared to positive and negative controls. During storage, both positive and negative controls exhibited a significant decrease in pH, whereas the pH of T1 remained relatively consistent, ranging from 5.77 on day 0 to 5.50 on day 7. Additionally, T1 maintained texture throughout the storage period (1.85N on day 0 to 1.60N on day 7) compared to both controls. Drip loss in T1 was sustained, measuring 7.52 on day 0 to 6.47 on day 7. T1 effectively controlled spoilage, with TVBN values of 4.38% on day 0 and 8.58% on day 7. T1 exhibited superior free radical scavenging activity, recording 36.33% on day 0 and 17.52% on day 7, while there was a significant decrease in DPPH activity in the controls. Bacterial count remained within permissible limits throughout the storage study for T1 compared to the controls. In conclusion, CMC-based edible coatings infused with lemongrass oil demonstrated effective enhancement of microbial safety and preservation of the quality of raw chicken meat during a seven-day storage period at refrigerator temperature.

Keywords: Chickpea pulao; Cuisine modification; Hypoglycemic herbs; Pakistani Cuisine

OP- 26

Formulation and Evaluation of Whole Wheat Bitter Gourd-Supplemented Cookies for Improving Blood Glycemic Levels

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Abstract

Sedentary lifestyles have increased the incidence of diabetes over the past decade, making it a major, rapidly increasing, degenerative disease all around the globe. However, it can be managed through lifestyle and dietary modifications. This study aimed to evaluate the efficacy of the hypoglycemic effect of bitter gourd-supplemented whole wheat cookies in ameliorating diabetes. The bitter gourd, purchased from the local market, was washed, sliced, and dried to obtain the powder. Different percentages of the bitter gourd powder were added to the whole wheat cookies. The cookies were evaluated for their nutritional composition, physical characteristics, antioxidant capacity, and enzyme-inhibiting ability. The cookies for all treatments were significantly different from each other for all assays. Results revealed a significant positive relation between supplementation of bitter gourd, radical scavenging potential, ferric reducing ability, presence of phenols, and inhibition of α-amylase and α-glucosidase enzymes. The one-week storage study of cookies revealed insignificant differences ($p=1.000$) in the alteration of antioxidant and anti-diabetic activity of bitter gourd cookies, showing its stability at room temperature. Incorporating bitter gourd into cookies at different inclusion levels showed promising hypoglycemic activity. Highly significant results of α-amylase and α-glucosidase inhibition indicate the potential of bitter gourd in managing diabetes. The sensory evaluation of the T1 cookies supplemented with 1% (w/w) bitter gourd powder showed better overall acceptability based on texture, color, aroma, flavor, mouthfeel, and after-taste.

Keywords: Bitter gourd; Antidiabetic; Type 2 diabetes; hypoglycemic agent; Antioxidant Potential; Cookies

OP-27

Therapeutic Activity of Walnut (*Juglans Regia L.*) in Adjuvant Induced Arthritis in Sprague Dawley Rats

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Abstract

Rheumatoid arthritis (RA) is an autoimmune progressive disease, associated with many pathophysiological consequences. Owing to the adverse effects and higher costs of pharmaceuticals, people are now looking for complementary and alternative remedies. In this milieu, the present study was designed to explore the therapeutic potential of walnuts against FCA-induced arthritis in rat models. Purposely, 50 Sprague Dawley rats were housed in a well-ventilated animal room and separated into 5 groups of 10 rats each. The rats were categorized as G0 (negative control), G1 (positive control i.e., FCA induced untreated arthritic rats), G2 (arthritic rats treated with MTX), G3 (arthritic rats treated with walnut feed), and G4 (arthritic rats treated with walnut extract), with an efficacy trial lasting for 42 days. The physical analysis explicated that paw swelling was significantly improved by 10%-12.8% in treatment groups after the intervention when compared with positive control. Moreover, biochemical analyses revealed significantly lower levels of ESR, CRP, and RF in rats treated with walnut-based interventions when compared to positive control. ESR values were decreased by 62.4% and 69.92% in G3 and G4, whereas CRP levels were improved by 56.20% and 77.78% in G3 and G4 when compared with G1. Likewise, RF values decreased in G2, G3, and G4 by 64.71%, 55.88%, and 69.24%, respectively when compared to G1. The histological examination demonstrated the potential role of walnut-based interventions in reducing the severity of disease by decreasing cell infiltration, bone erosion, and paw inflammation. Meanwhile, the gene expression analysis revealed that walnut-based interventions protected the paw joints from damage by down-regulating the RANKL-OPG pathway. Conclusively, walnut feed and extract may serve as potent anti-arthritic interventions with no side effects.

Keywords: Rheumatoid arthritis, ESR, Inflammatory markers, Paw histology, Gene analysis

OP-28

A Study on Chicken Nuggets Valorized with Beef and Chicken Liver: Formulation and Evaluation

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Abstract

This study explores the potential of improving the nutritious content of processed foods like chicken nuggets by using animal byproducts, particularly liver from chicken and beef. Proximate analysis was performed on the livers, encompassing moisture, ash, fat, and protein content, with particular observation on degradation potential. Determination of antioxidant potential through DPPH (2,2-diphenyl-1-picrylhydrazyl) and TPC (total phenolic content), and assessment of oxidative stability via POV (peroxide value) and FFA (free fatty acid), were carried out to evaluate quality changes over a seven-day storage period. The analysis of antioxidant potential revealed that, when compared to chicken liver, beef liver had a remarkable antioxidant capacity (61.55% and 195.89-Mm GAE for DPPH and TPC, respectively). As a result, adding beef liver greatly increased the antioxidant capacity of the nuggets by 5–10%. When liver and its incorporation into nuggets were stored for longer periods of time, POV and FFA values showed a growing tendency; nevertheless, these values stayed below the crucial threshold of 10 meq/Kg. When livers were added to chicken nuggets, there was a significant (p=0.000***) improvement in nutritional value, namely a 1.5–2% increase in protein and an equivalent increase in mineral content. Consumer acceptance of liver-enriched nuggets was found to be positively correlated with assessments of texture and sensory qualities. In conclusion, this study emphasizes how important it is to include liver as a functional ingredient in processed foods in order to improve their nutritional profile.

Keywords: Beef liver, Chicken liver, Characterization, Nutritional enhancement, Processed nuggets, Value-addition

OP-29

Assessing the Divergent Vitals Response to Physical Activity in Young Male Individuals Consuming Whey Protein Supplements versus Milk as Their Whey Protein Source

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Abstract

Whey is a protein fragment, water-soluble, in milk. Whey and whey components are viewed as value-added ingredients in infant formulas, sports nutrition foods and beverages, and other food products. Recognition of whey as a source of diverse biologically active compounds with unique physiological and functional attributes has emphasized the use of whey as a supplement. Some studies show that Whey protein has been investigated for its ability to reduce blood pressure due to the presence of several ACE-inhibiting peptides derived from both alpha-lactalbumin and beta-lactoglobulin. A sample of 20 were investigated, in which two groups each of 10 physically active males were taken and compared on the variable of intake of supplemental whey protein and a glass of milk. Their vitals (blood pressure, temperature and heart rate) were measured in four sessions each session separated by a week. Results showed that intake of 45g supplemental whey protein does not affect the systolic blood pressure (p=0.67), diastolic blood pressure (p=0.90), body temperature (p=0.16) of physically active males. However, consumption of whey protein significantly affected the heart rate (p=0.04) of physically active males who were engaged in an average of 30 minutes of mild to moderate activity. The study concluded that young male individuals who were consuming whey protein supplements had no significant difference in their blood pressure and body temperature values but heart rate values were significantly affected as compared to those who were taking milk as their whey protein source.

Keywords: blood pressure, cardiovascular system, exercise, health, protein

OP-30

Therapeutic Effects of *Olea Europaea L*. Fruit Extract Against Cigarette Smoke-Induced Depressive-Like Behaviors in Sprague–Dawley Rats

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Abstract

Depression is broadly acclaimed as a mental health anomaly and despite advancements in the development of antidepressant drugs, they are linked with side effects. Dietary modifications and medicinal plants like olives can be used as effective strategies due to their antioxidant, immune-modulatory, anti-inflammatory, and anticonvulsant properties. Considering the compositional alterations in olive fruits during ripening, the antidepressant potential of olive fruits at different degrees of ripeness, that is, un-ripened (green) and ripened (black) was investigated. Rats were randomly divided into five groups: G0 (Normal diet), G1 {Normal diet + smoke exposure (SE)}, G2 (Normal diet + SE + Citalopram), G3 (Normal diet + SE + Green olive extract), and G4 (Normal diet + SE + Black olive extract). Depressive-like behaviors were induced in all groups through cigarette smoke exposure except G0. Green and black olive extracts prevented depressive behaviors by reducing the immobility time of rats in forced swim test and tail suspension test while increased the latency to respond in hot plate assay. Moreover, lipid peroxidation in brain tissue was reduced with citalopram, green, and black olive extracts. Additionally, treatments also enhanced the antioxidant pool of brain tissues. Histological examination revealed that olive extracts and citalopram prevented cigarette smoke-induced moderate to severe necrosis and congestion in the brain parenchyma and elucidated antidepressant potential by improving the expression of monoamine oxidase-A, solute carrier family 6 member 4, and brain-derived neurotrophic factor genes. Conclusively, olives may act as a promising antidepressant agent in ameliorating cigarette smoke-induced depressive-like behaviors

Keywords: blood pressure, cardiovascular system, exercise, health, protein

OP-31

Effect of *Allium sativum* on C-Reactive Protein and Cardiac Structure in Rabbits

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Abstract

Diet and lifestyle is a major risk factor in the development of various human diseases, including atherosclerosis. Inflammation is a key pathogenetic mechanism in the development an progression of atherosclerosis. C-reactive protein (CRP) is one of the possible markers o vascular inflammations and plays a direct role in promoting vascular inflammation, vessel damage. High CRP levels can predict the long-term risk of cardiovascular diseases. Present study evaluated the cardioprotective role of *Allium sativum* in rabbits. This study evaluated the ameliorative role of the *Allium sativum* against adverse effect of high fat diet on heart structure and C-reactive protein level in rabbits. 6 months old rabbits were used. Rabbits were divided into four groups (n=5). Group1 served as control group fed standard diet, group 2 fed high fat diet, group 3 fed high fat diet supplemented with 5% *Allium sativum*, group 4 fed high fat diet supplemented with 10% *Allium sativum*. Experiment was conducted for 4 weeks; body weight was recorded before and after experiment. Mild myocardial congestion was observed in the heart tissues of rabbits in group 2 fed high fat diet. Group 3 and group 4 fed 5% and 10% *Allium sativum* with high fat diet showed no myocardial congestion which indicate cardioprotective potential of *Allium sativum*. Results have shown highly significant (P>0.05) increased C-reactive protein level in in group 2 fed high fat diet however Group 3 and group 4 fed 5% and 10% *Allium sativum* showed reduced C-reactive protein. It was concluded that *Allium sativum* showed beneficial effect on heart structure and C-reactive protein level to greater extent. *Allium sativum* supplementation can be a safe and potentially adjunct treatment to reverse the heart damage and reduced the risk of cardiovascular disorders.

Keywords: blood pressure, cardiovascular system, exercise, health, protein

OP-32

Effect of Maternal Malnutrition on the Hematological Profile, Glucose level and Heart Structure of Developing Fetus in Rabbits (*Oryctolagus cuniculus*)

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Abstract

This experimental study was based on female rabbits having effect of malnutrition on developing heart structure. The aim of the study was to explore the effects of under nutrition on body weight; blood parameters such as glucose level, triglyceride level, cholesterol level, uric acid level and Albumin level presence (mg/dl) were extensively investigated. These animals were randomly divided into three groups (A, B and C). Control group were given normal feed B and C experimental groups were given 50% and 25% high fat diet respectively. The body weight was measured each animal every week for four weeks The blood samples from each animal were collected at end of 4rth week before dissection the samples were brought to the laboratory the analysis of glucose level, triglyceride level, cholesterol level, uric acid level and albumin level in blood. The results of body weight indicated normal diet showed highest mean of body weight while rabbits was fed on 25% diet (Group C) compared to 100% normal diet attained lowest body weight as compared to 50% diet (Group B). Significant decrease (P<0.05) in glucose level, triglyceride level, cholesterol level, uric acid level and albumin level in animal of group-C compared to animal of group-A (control) group. The body weight (Plt; 2.5), glucose level, RBCs, WBCs, Hb, pH, Cholesterol, Triglyceride level and albumin level decreased significantly (P<0.05) while uric acid level increased significantly (P<0.05). The results of this study clearly indicated that the under-nutrition causes many health issues as model animal and may also in human beings.

Keywords: Histopathology, glucose, rabbit, fetus, malnutrition

OP-33

Histopathological Study of Lead Acetate Pb (CH 3 COO) 2 Accumulation in Muscle and Kidney Tissues of *Labeo rohita* (Rohu)

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Abstract

Heavy metals regarded as the highly poisonous compound for aquatic ecosystem. Lead (Pb) is one of the heavy metals which stored in water from environment and soil, infecting the marine creatures. This research was carried out to observe the histopathological alterations in muscles and kidney tissues of *Labeo rohita* with exposure of 1/5 th (6.86 ppm of lead acetate), 1/10th (3.43 ppm of lead acetate) and 1/15th (2.29 ppm of lead acetate) separately, for a period of 28 days. After 7, 14, 21 and 28 days of experiment, fish was dissected and their muscles and kidney tissues were isolated to examine the effect of Pb $(CH_3COO)_2$. The investigation in histopathology of muscles included shortening and elongation of muscles fibers, deformation of muscles bundles, edema, necrosis, inflammation and breakdown in muscle bundles. Kidney variations included congestion of blood cells, tubular hemorrhage, vacuolated degeneration, aggregation of inflammatory cells, deformation of renal tubules, shrinkage and enlargement of Bowman's space, tubular atrophy, damaged in renal tubules and glomerulus. Maximum modifications were examined after 28 days in the experimental tissues.

Keywords: Lead acetate, *Labeo rohita*, muscles, kidney, histopathology

OP-34

Effect of High Temperature on Lipid Profile and Heart Structure in Developing Chick Embryo (*Gallus Gallus Domesticus*)

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Abstract

Temperature is an important epigenetic factor influencing the function of the developing cardiac conduction system. Temperature and relative humidity (RH) are very important factors for embryo development. The aim of the current study is to calculate the effect of high temperature on lipid profile and heart structure in developing chick embryos. Eggs were divided into three groups; one group was the control group (37.5oC) while two groups were experimental groups with two different temperatures (38.5oC, 39.5oC). The eggs weight was measured before and after the experiment. On days 10 and 21, heart samples were collected from the experiment. On day 21, blood samples were taken for analysis of the following parameters: cholesterol, triglycerides, low-density lipoprotein (LDL) and high-density lipoprotein (HDL). A significant difference was observed between different parameters of control (Go) and experimental groups (G1 & G2). There is a very high significant increase (p<0.001) in experimental group I and experimental group II (38.5oC & 39.5oC) as compared to Control Group (37.5oC). Histopathology of heart tissues was conducted. Cardiomyocytes, epithelial cells, encephalic vesicles, and neural tubes were visible. Sarcoplasm was less. Rupturing of different tissues was seen. A low mortality rate was found but other parameters were normal during the experiment as compared to the control group and showed positive results in lipid profile at high temperatures.

Keywords: Epigenetics, *Gallus Gallus Domesticus*, chick embryo, LDL, HDL

OP-35

Evaluation of the Testicular Toxicity Caused by Lorazepam and Ameliorative Role of Vitamin C in Albino Mice (*Mus Musculus*)

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Abstract

The current study was conducted to observe the recovery of Lorazepam induced reproductive injury by Vitamin C in *Mus musculus* at the age of 8 weeks. The mice were divided in three groups, including control group, dose group I Lorazepam (2mg/kg/bw) and dose group II Lorazepam (2mg/kg/bw) + Vitamin C (200mg/kg/bw). Morphological, morphometric, serum enzyme, serum proteins, oxidative analysis and calcium level were analyzed. The control group showed a normal manifestation of morphology of testes like very smooth and shiny surface. Dose group I Lorazepam (2mg/kg/bw) showed abnormalities that were seen, such as uneven testes oval shape and decrease in shine. In Dose Group II Lorazepam (2mg/kg/bw) + Vitamin C (200mg/kg/bw) these abnormalities were turned to normal. As much as the body weight and testes weight is concerned these were also shown to be decreases. Various values of AST, ALT, GGT were noticeably (p0.001) higher. Values for ALP and calcium levels in dosage group I were significantly lower as compared to control group. In the analysis of serum proteins values for albumin, total protein and globulin was higher as compared to control group. All abnormalities were rescued to be normal in Dose group II. In the histological analysis various abnormalities were seen like irregular Spermatids, Dilated Space, Apoptotic Spermatids, Inflated XI Seminiferous Tubules and Dilated Tubular Epithelium were observed in Dose group I as compared to control group. All these irregularities were turned to be normal in Dose group II due to the administration of vitamin- C. it was concluded from present study that administration of lorazepam in mice introduced various malfunctioning in anatomy or morphology of testes. It was observed that Vitamin-C has exerted the positive effect against these irregularities or ameliorate the effect of lorazepam positively.

Keywords: Lorazepam, Vitamin C, *Mus musculus*, Testicular toxicity

OP-36

Histopathological Effect of Cadmium Chloride on Liver and Gills of Fish *Labeo rohita*

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Abstract

Samples of *Labeo rohita* were collected from the Manawa fisheries center Lahore. Total 80 fishes were taken and 20 fishes in every four groups. The fishes were exposed to sub-lethal concentrations of cadmium chloride of 2ppm, 3ppm, and 6ppm; one is the control group. The effect of this cadmium chloride on the histology of gills and liver was studied results showed severe histopathological alterations in *Labeo rohita* of fish, Changes in the liver tissue such as loss of cellular architecture, and necrosis in hepatocytes and blood vessels seem to be dilated. Hemolysis that is due to the destruction of erythrocytes. Inflammation of hepatic cells, eccentric nuclei and vacuole is more common in 6ppm and 3ppm, and 2ppm. cadmium chloride increases histopathological changes in Liver week4> week3 > week2 > week1. The treated groups of gills showed lamellar degeneration, epithelial lifting, and necrotic changes in intercellular cells, destruction in primary and secondary lamella, separation of gill filament in the basement membrane, curling of secondary and lamellae, the proliferation of mucous cells and autophagy of gill filament 6ppm > 3ppm >2ppm > and more gills destruction due to cadmium chloride in week4> week3 > week2 > week1. This Study concludes that cadmium chloride impacted destructive changes in the liver and Gills of fish Labeo Rohita and did not meet the minimum quality of food.

Keywords: *Labeo rohita*, autophagy, cadmium chloride, fish liver, gills

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OP-37

Phyto stimulatory Potential of Biofilm Forming Bacteria and Its Implications for Advanced Agricultural Practices

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Abstract

Plant growth promoting rhizobacteria play a pivotal role in agriculture, with their ability to positively influence plant growth through several mechanisms. Among multiple assortments of microbial species, EPS (extracellular polymeric substance)-producing bacteria have manifested as key contributors in promoting sustainable agricultural practices.

This research aims to investigate the multifarious applications of EPS-producing bacterial strains in agriculture. By elucidating the intricate interactions of biofilm and EPS-producing bacteria with host plant that secrete extracellular polymeric substances consisting of carbohydrates, proteins and nucleic acids. Rhizobacteria embed in their self-produced exopolysaccharides, strives to contribute to the development of aggregates of cells with soil and host plant thus enhancing agricultural productivity. In the current work, rhizobacterial isolates i.e., *Pseudomonas sp*. (DS1), *Shewanella sp*. (DS2), *Pseudomonas sp*. (DS3), *Pseudomonas sp*. (DS4), *Sporosarcina sp*. (E1), and B3 were analysed for the biofilm and EPS production ability was physiochemically analysed under varying environmental factors. Phytostimulatory potential of the rhizobacterial strains was evaluated using *Zea mays L*. using monoculture and co-culture prerequisites. Results revealed that bacterial strains remarkably optimized the growth parameters such as the percentage germination, shoot length, root length, number of leaves and fresh weight as well as biochemical parameters i.e., chlorophyll and soluble protein content of the plants. Among all the monocultures the bacterial isolates *Pseudomonas sp*. (DS4), B3, and *Sporosarcina sp*. (E1) and among the consortia B3+DS4 performed well in growth parameters as compared to the control. Moreover, the monocultures DS2, B3, DS1, E1 and consortia treatment DS4+E1, DS1+DS3 showed the positive effectiveness on biochemical parameters. So, these EPS producing bacteria can be used as a potential biofertilizers as innovative strategies for enhancing agricultural productivity.

Keywords: EPS, Biofilm, Agriculture, Green Strategy, Phytostimulation, *Zea mays L*., *Psuedomonas*

OP-38

Efficacy of Zn Solubilizing Bacteria to Manage Malnutrition: An Organic Green Strategy

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Abstract

Over 2 billion people worldwide, especially women and pre-school children, suffer from "hidden hunger" caused by intake of micronutrients deficient diet such as Zn, leading to severe physical and mental abnormalities. Dependency of people on Zn supplements to meet their body Zn requirements has increased. Therefore, nourishment of human population with Zn is mandatory to address Zn malnutrition. Agriculture is currently moving from growing a greater number of food crops to producing sufficient quantities of nutrient-dense food crops. The usage of chemical fertilizers not only threatens the environment and public health but also puts livelihood of farmer in jeopardy. Among various strategies, biofortification using Zn solubilizing bio-fertilizers is a cost-effective organic approach to deal with Zn deficiency. A study was carried out to evaluate the efficacy of ZSB to be used as bio-fertilizers to upgrade Zn content and enhance wheat growth and yield. The findings showed that foliar Zn application combined with ZSB improved plant growth and Zn content. In a lab setting, plants treated with *Burkholderia cepacia* (FS1), in the presence of 100 g/ml Zn, showed a 28% increase in fresh weight. Using atomic absorption spectrometry, the maximum Zn concentration, 2.68 ppm, was noted in plants augmented with *Pseudomonas aeruginosa* (DS4) as a result of foliar spraying 200 g/ml Zn under wire house conditions. Hence, biofortification of crops using Zn and ZSB is recommended as a cost-effective, organic-green solution, not only to increase mineral concentrations in edible crops and boost plant development and yields but also treat malnutrition and improve human health.

Keywords: Bio-Inoculation, Micronutrient Malnutrition, Zinc Solubilizing Bacteria, Biofortified-Wheat

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OP-39

Phenotypic and Genotypic Characteristics of a Live-Attenuated Genotype I Vaccine of Japanese Encephalitis Virus

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Abstract

The phenotypic and genotypic characteristics of a live-attenuated genotype I (GI) strain (SD12-F120) of Japanese encephalitis virus (JEV) were compared with its virulent parental SD12 strain to gain an insight into the genetic changes acquired during the attenuation process. SD12-F120 formed smaller plaque on BHK-21 cells and showed reduced replication in mouse brains compared with SD12. Mice inoculated with SD12-F120 via either intraperitoneal or intracerebral route showed no clinical symptoms, indicating a highly attenuated phenotype in terms of both neuroinvasiveness and neurovirulence. SD12-F120 harbored 29 nucleotide variations compared with SD12, of which 20 were considered silent nucleotide mutations, while nine resulted in eight amino acid substitutions. Comparison of the amino acid variations of SD12-F120 vs. SD12 pair with those from other four isogenic pairs of the attenuated and their virulent parental strains revealed that the variations at E138 and E176 positions of E protein were identified in four and three pairs, respectively, while the remaining amino acid variations were almost unique to their respective strain pairs. These observations suggest that the genetic changes acquired during the attenuation process were likely to be strain-specific and that the mechanisms associated with JEV attenuation/virulence are complicated.

Key words: Japanese encephalitis virus, virulence, vaccine, genetics

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OP-40

Cotton Microbiome: Plant's Defense against Viral Cotton Leaf Curl Disease

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Abstract

The global impact of the Cotton Leaf Curl Disease (CLCuD) caused by the *Begomovirus* has drastically affected cotton yield and quality since its emergence in 1912. In Pakistan, a crucial cotton producer, biotic stress from the Cotton Leaf Curl Virus (CLCuV) has led to nearly 50% production decline in a decade. This study proposes leveraging the plant microbiome as an eco-friendly method to suppress CLCuD in *Gossypium hirsutum*. By utilizing the naturally immune *Gossypium arboreum's* microbiome, diverse bacterial communities from *G. arboreum* (FDH228) were harnessed as Microbial Fraction (RMFs). This RMF was applied via soil drench to seedlings of naturally susceptible *G. hirsutum*, alongside a positive control using Salicylic Acid (SA) for defense induction. Microbial diversity was assessed by Illumina MiSeq 16S rRNA gene metabarcoding. Results demonstrated significant CLCuD suppression in *G. hirsutum* varieties treated with FDH228 (RMF), followed by pRMF and SMF. Phyllospheric MFs exhibited similar but milder suppression. This pioneering study underscores the plant microbiome's practical role in CLCuD suppression and represents a novel approach to combat a viral disease.

Key words: Cotton Leaf Curl Disease, Begomovirus, *Gossypium hirsutum*, Microbiome, *Gossypium arboreum*

OP-41

Metabolomic Analysis and Biotic Stress Tolerance Induced in Wheat by Cell Free Supernatant of Rhizospheric and Phyllospheric Bacteria

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Abstract

Wheat crop is a cornerstone of global as well as Pakistan agriculture. Cell-free supernatant is the liquid portion of a solution left after removing cells, often containing soluble metabolites or compounds with applications in biotechnology and research. Cell-Free Culture Supernatants (CFSs) of rhizospheric and phyllospheric bacteria are considered effective for the biotic stress tolerance and plant growth in wheat plants infected with powdery mildew and yellow stripe rust disease. Powdery mildew is a lethal plant disease caused by the fungus *Blumeria graminis*, whereas yellow stripe rust is caused by the fungus *Puccinia striiformis*. Rhizospheric and phyllospheric bacteria used in this study for CFS preparation include Serratia marcescens, and Fictibacillus spp. The study design uses Nuclear Magnetic Resonance (NMR) and R (version 4.3.0) package AlpsNMR to conduct a metabolomic analysis of the CFSs (Plant growth promoting bacteria) PGPBs. Our results exhibit the potential of CFS as an antifungal agent against *Blumeria graminis* and *Puccinia striiformis*. Furthermore, the CFS has been found to show a positive effect on plant growth characteristics such as plant height, number of leaves, and shoot and root length. A number of metabolites have been previously identified in CFS such as phytohormones, amino acids, volatile compounds, sugars, organic acids, and exopolysaccharides that stimulate plant growth and development. This study is a first and foremost to demonstrate the antifungal ability and disease suppressing potential of CFSs, through metabolomic analysis. Therefore, CFSs of PGPB have the potential to be used as a bio stimulant and biocontrol agent for sustainable agriculture practices.

Keywords: Cell Free Supernatant, Powdery mildew, yellow stripe rust, metabolomics Nuclear Magnetic Resonance, AlpsNMR

OP-42

Formulation and Evaluation of Functional Candies Fortified with Carrot Juice and Fennel Seed Extract: Nutritional and Sensory Properties

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Abstract

Carrot and fennel seeds are considered rich sources of antioxidants such as lutein, zeaxanthin, and β-carotene. The study aimed at formulating functional candies fortified with fennel seed extract and carrot juice. The candies can be used to improve the nutritive quality of confectionary products that could be healthy options for all age groups, particularly children. Fennel seed extract having the highest flavonoids and antioxidant capacity was selected to blend with carrot juice for hard candy formulation. Five different concentrations of fennel extract and carrot juice were added for the formulation of hard candy containing 30% (w/w) sugar, 30% (w/w) corn syrup, 0 to 40% (w/w) fennel seed extract, and 0 to 40%(w/w) carrot juice. The results showed the highest content of flavonoids in 40% (w/w) carrot juice formulation and the mixture of candies containing 10% (w/w) carrot juice and 30% (w/w) fennel extract, while the highest antioxidant activity was observed in candies containing 30% (w/w) carrot juice and 10% (w/w) fennel extract. The formulated candies showed a good sensory profile and can be utilized as a potential source of functional candies for improving the nutritional profile of children.

Keywords: Functional candies, Fennel seed extract, carrot juice, vision improvements

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OP-43

Computational Screening of Non-Synonymous SNPs from Human SQLE Gene to Assess Their Association with Multiple Cancer Types

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Abstract

Cancer is a complex disease triggered by various genetic alterations. Genes are the main drivers for the onset of cancer by inducing specific mutations. Recently, an oncogene SQLE has been reported to have a prominent role in multiple cancer types. Furthermore, many Genome-Wide Association Studies have highlighted SQLE as a genetic candidate to aggravate the cholesterol and steroid biosynthetic metabolism. In this study, a computational pipeline has been employed to scrutinize the pathogenic nsSNPs from SQLE and to assess the disease associations of selected nsSNPs. The combination of homology-based (SIFT, Provean, PolyPhen, and Mutation Assessor), machine learning-based (SuSPect, SNP&GO, PhD-SNP, MutPred, and PMut), and consensus-based tools (Meta SNP, Predict SNP, ConDel, and PON-P2) marked a total of 18 variants as significantly pathogenic. Among these 18, six variants, including E153G, L280R, G286R, R343P, R458T, and L473H, reside in evolutionarily conserved regions of the protein, as is evident by ConSurf analysis. Moreover, the sequence-based (I-Mutant, MuPro, and iStable2.0) and structure-based (SDM, DynaMut, PoPMusic, and FoldX) stability analysis tools revealed that these six mutations markedly affect protein stability. Finally, CHASM-3.1 predicted three variants (E153G, L280R, and G286R) to have a prominent role in multiple cancer types. The molecular docking analysis of wild-type and mutated protein models reveals that mutations bring conformational changes in native protein structure and thus affect its molecular interactions with other proteins in pathways. We, therefore, conclude that E153G, L280R, and G286R mutants of SQLE may contribute to oncogenic pathways by affecting the protein structure, stability, protein-protein interactions, and conformation of the native protein. These mutants need further wet lab validation.

Keywords: Non-synonymous SNPs, molecular dynamics simulations, functional assessments, cholesterol biosynthesis.

OP-44

Synergistic Effect of Multi-trait PSB for Osmotic Stress Alleviation

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Abstract

Drought is a significant abiotic stress that limits crop productivity worldwide. Water scarcity along with soil phosphorous deficiency adversy affects crop yield. Low mobility and high chelation rate make phosphate a limiting macronutrient in soil, therefore, farmers commonly resort to synthetic fertilizers to deal with phosphate requirements of plants, however, the excessive application of synthetic phosphate fertilizers has had detrimental effects on our ecosystem. Plant growth-promoting rhizobacteria (PGPR) especially, drought- tolerant phosphate solubilizing rhizobacteria (PSB) present a range of sustainable solutions to address these issues. These microbes colonize the roots and enhance plant resistivity through synergistic action of various mechanisms that assist plants in nutrient uptake through alteration in root morphology. In the present study, rhizobacteria with enhanced phosphate solubilization capabilities and the ability to withstand drought conditions were carefully chosen and their growth-promoting profile was thoroughly assessed. Phosphate solubilizing and drought resistance efficacy of these PSB was analyzed through HPLC and FTIR. The growth-promoting effects of these phosphate-solubilizing rhizobacteria were assessed using *Zea mays* L. Our findings indicated that these bacterial isolates demonstrated varying capabilities to solubilize phosphate under different physiological conditions. This data suggests that these bacterial strains hold promise as phosphate biofertilizers that can stimulate plant growth and enhance plant tolerance to water scarce conditions. Thus, use of such

biofertilizers for growth improvement may replace chemical phosphate fertilizers which will be a cost-effective strategy for promoting green agriculture.

Key Words: Drought tolerant, PSB, Phyto stimulation, HPLC, PGPR

OP-45

Anti-Microbial Sensitivity and Complicated Diseases Prevalence in Local Population of Sialkot Pakistan

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Abstract

A growing class of bacterial infections are at risk of being effectively prevented and treated due to antimicrobial resistance (AMR), which has emerged as one of the most important public health concerns of the 21 ST century. No longer vulnerable to the conventional pharmacological treatments that were once utilized to treat them are parasites, viruses, and fungus. The testing of large bacterial isolates for antimicrobial weak spots is a major task of the scientific laboratory for microbial technology. The goals of screening are to determine potential drug resistance in the same way that microorganisms do and to ensure drug resistance to the chosen medications for specific contaminations. To confirm incapacity to choose precise antimicrobial specialists or to identify competition in specific bacterial disengages, the presenting of antimicrobial therapy employing the academic microbial science studying facility is essential. We determine the prevalence of many complex diseases in the general populace of Sialkot, a city in Pakistan, using sensitivity testing and various parameters. Our research reveals gaps in neighborhood residents; knowledge of and attitudes towards AMR in the Sialkot District of Pakistan. The general public lack of understanding of AMR appears to be a major problem that has a negative impact on how antibiotics are used. We conclude that *E. coli* is mostly occurring organism in infected patients and ampicillin, amoxicillin is mostly resistant antibiotic among different infected patients.

Keywords: AMR, Anti-microbial sensitivity, Antibiotic, resistance, Ampicillin and Amoxicillin.

OP-46

Prevalence of Periodontitis Associated with Diabetes in Location Population in Sialkot, Pakistan.

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Abstract

Periodontitis is a commonly occurring bacterial infection that results in tooth loss. A high level of glucose in the mouth promotes bacterial growth. It is becoming more widely acknowledged that diabetes can lead to periodontitis, which involves long- term inflammation of the gums and tooth-supporting structures. It is crucial to gain insight into the prevalence of this disease and its risk factors in distinct populations to ensure effective healthcare management. This study investigated whether diabetes is connected to periodontitis in the local community of Sialkot, Pakistan. This cross-sectional study aimed to observe periodontitis prevalence and risk factors with and without diabetes. Furthermore, the study aimed to identify demographic factors that could impact periodontal health, such as age, gender, clinical attachment loss, HbA1c levels, and BMI. 169 participants participated in our study. A comprehensive oral examination, including CAL measurements, was conducted on participants to assess their periodontal health using a WHO probe. Demographic data analysis was done using SPSS 27, including HbA1c levels, age, gender, bleeding gums, and BMI. A significant association was found between periodontitis and HbA1c levels, CAL, age, gender, bleeding gums, and BMI. Individuals with higher HbA1c levels have a higher prevalence of periodontitis. The risk of developing periodontitis was higher in males than in females. People in Sialkot with diabetes have a higher risk of periodontitis. Personalized healthcare plans are essential for the best outcomes. Periodontitis is positively associated with HbA1c levels, CAL, age, gender, bleeding gums, and BMI.

Keywords: periodontitis, HbA1c, CAL, BMI, Bleeding gums, diabetes, bacterial infection.

POSTER PRESENTATIONS

PP-1

Molecular Detection and Analysis of Virulence Genes in *Escherichia coli* Isolated from Drinking Water and Raw Food

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Abstract

Developing nations have poor wastewater treatment and poor personal hygiene, which increases bacteria and other microbes in drinking water and raw food. These conditions favor *Escherichia coli*. The goal was to discover *E. coli* virulence factors and test antibiotic resistance in Kohat water and raw food samples. Twenty samples were collected and subjected to various tests, including biochemical assays and polymerase chain reaction (PCR) to identify *E. coli*. Antibiogram assays were performed using Kirby disc diffusion method. PCR was employed to identify virulence genes (Stx-1 and Stx-2).70% of samples were found to have bacteria in them, and the most common were *E. coli* and other Enterobacteriaceae. Additional testing of *E. coli*-positive samples confirmed positive TSI results but negative citrate and urease tests. Antibiotic susceptibility testing revealed that most of samples were completely resistant to penicillin, ampicillin, ceftazidime, and cefixime, while some samples showed susceptibility to amoxicillin plus clavulanic acid, cefoxitin, cefepime, cefoperazone + sulbactum, levofloxacin, ceftriaxone, ciprofloxacin, clarithromycin, azithromycin and doxycycline as per CLSI standards. PCR confirmed the presence of the Stx2 gene in all E. coli isolates, while Stx-1 was absent. Sequence analysis of Stx-2 gene showed >98% identity with GenBank sequences. In conclusion, this study employed a comprehensive approach to identify *E. coli* as a harmful pathogen in drinking water and raw food. The utilization of phylogenetic analysis, and virulence factor detection, along with antibiotic resistance profiling, enhances our understanding of *E. coli* contamination in resource-limited settings, highlighting the urgent need for improved wastewater management and hygiene practices.

Keywords: Antibiotic, *Escherichia coli*, raw food, virulence, antibiotic assay

PP-2

Prevalence of Metabolic Syndrome and Metabolically Healthy Obese in North West of Lahore: Interim Analysis

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Abstract

Metabolic syndrome (MetS) is a condition that increases the risk of diabetes and cardiovascular disease, It occurs due to the presence of different factors such as obesity, high blood pressure (BP), hypertriglyceridemia, low HDL cholesterol and hyperglycemia (fasting). Waist circumference more than 80 cm is considered obese for women and more than 90 cm for obese men. BP above 135/80 mmHg is regarded as hypertension. Hypertriglyceridemia refers to levels of triglycerides above 135 mg/dl in females and above 160 mg/dl for males. Hyperglycemia (fasting) is defined as serum glucose above 125mg/dl. Low HDL-cholesterol is the condition when levels of HDL fall below 40 mg/dl for males and less than 50 mg/dl for females. When there are abnormal values for 3 or more of the 5 factors, the person would be referred to as suffering from MetS, while metabolically healthy obese will have only one or none of the remaining 4 factors. To find out the prevalence of metabolic syndrome (MetS) and metabolically healthy obese in North West of Lahore. In a cross-sectional study, 300 healthy subjects from the working class in the North West of Lahore were recruited with informed consent. Eight CCs of blood were collected. The serum was analyzed for fasting glucose, triglyceride, HDL, and blood group type. BP and waist circumference were determined for each recruited subject. Using a modified Harmonized criteria for MetS, the prevalence of MetS and metabolically healthy obese was determined. There was a total of 94 males and 206 females (age range: 20-70 years). The prevalence of MetS in males was 51.1%, while in females it was 81.6%. The prevalence of metabolically healthy obese was 12.8% in males and 4.85% in females.

Keywords: Hyperglycemia, diabetes, cardiovascular disease, metabolic syndrome (MetS)

PP-3

Remediation of Pesticides through Microbiological Techniques

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Abstract

Pesticides play a significant role in modern agriculture by helping to protect crops from various pests, diseases, and weeds. While they can be effective in protecting crops and controlling disease vectors, pesticides can have a range of negative effects on the environment. They are major threat to biodiversity, as the survival of many aquatic organisms. There are several methods present for eliminating pesticides from the environment such as physical and chemical method but they lead toward production of secondary pollutant in environment. Contrary to physicochemical approaches, biological methods are cost effective and environment friendly. It involves the use of microorganism for eliminating pesticides from the environment. For the degradation process, bacteria use several metabolic pathways, which require some special enzymes (Esterases, Lyases, and Phosphatases). In conclusion, the use of bacteria for pesticides, offers a promising and sustainable approach to pest management in agriculture

Keywords: Pesticides, microorganisms, environment, degradation

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PP-4

Application of Bacterial Consortium to Decolorize Azo dyes

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Abstract

Although textile industry boosts up the country's economy but it is also known as for its high water consumption the release of untreated effluent in the main water bodies. Textile effluents can be significant and pose environmental challenges. In the current study, two bacterial strains SZ1 (*Bacillus* sp. and LGW6 were evaluated for their potential to remediate the textile azo dyes (Synozol Red and Synozol Yellow). The decolorization analysis was carried out using the supernatant recovered from centrifugation via spectrophotometrically. In single dye degradation, SZ1 degraded yellow dye 32% while LGW6 degraded 14% while in consortium, strains degraded 67% yellow dye. In red dye degradation SZ1 degrade 25%, LGW6 degrade 22% and in consortium degrade 89%. Furthermore, phytotoxicity analysis using *zea mays* was performed to evaluate efficiency of each treatment. Samples with bacterial consortium improved the root length, shoot length and total length as compared to control samples. The results have revealed that

both SZ1 and LGW6 could decolorize azo dyes efficiently. In conclusion, both the bacterial strains could be used in further research to in pilot and industrial scale

Keywords*:* Dye decolorization, biodegradation, azo dyes

PP-5

Computational analysis of phytochemicals against beak and feather disease virus

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Abstract

The virus replicates by infecting cells of the host and making copies by using components of the host cell. Circovirus is one of the most common viruses present in various animals including pigs, pigeons, parrots, etc. It belongs to the Circoviridae family and is a single-stranded DNA virus (ssDNA). It is characterized by various symptoms like diarrhea, weight loss, anemia, allergy, etc. To date, there is no direct treatment available for this virus. BFDV is a type of circovirus and affects pigeons and parrots. Getting active compounds or phytochemicals from plants to use for various diseases is a very common process. Various phytochemicals obtained from plant fruits, grains, etc. can be used as a cure for various diseases without causing any damage to the hosts. In the study, the families of plant Meliaceae, Moraceae, Moringaceae, Ranunculaceae, Zingiberaceae, Fabaceae, Aceraceae, Apocynaceae, Asteraceae, Polygonaceae, and Poaceae or Graminae are being targeted as they proved to have highest medicinal properties among all plant families. The basic target is to activate the immune system for the invasion of the virus by not harming the host. Various bioinformatics tools including PDB, Dr. Duke, modeler 10.1, chimera 1.15, PubChem, server, FTsite server NCBI, BLAST, swiss model, clustalW, and protein molecular weight are used in the research too. Further, the ability of the phytochemicals to be used as drugs is confirmed by verifying their various characteristics like Blood Brain Barrier (BBB), Gastrointestinal absorption (GI Absorption), solubility, Lipinski's rule of 5, toxicity, carcinogenicity, and mutagenicity. The docking process showed the interactions between proteins of causing agent and the phytochemicals. DFT confirmed the energy gaps and verified the results. After screening more than 3000 phytochemicals and selecting 224, Luteolin-7-o-beta-d-glucopyranoside proved to be the best phytochemical to inhibit BFDV isolates.

Keywords: Circovirus, Gastrointestinal absorption, DNA virus, BLAST

PP-6

Synthesis, Characterization and Biological Evaluation of Iron Oxide Nanoparticles Synthesized from *Apis mellifera* Honey

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Abstract

Infectious diseases of humans associated with debilitating conditions are on the rampage globally. Green approaches for nanoparticle synthesis have emerged as biocompatible, economical, and environment-friendly alternative to salvage the menace of microbial drug resistance. This study engaged *Apis mellifera* honey as a reducing and capping agent for synthesis of iron oxide nanoparticles (Fe2O3-NPs). In UV-Vis spectroscopic analysis, the absorption band ascribed to surface plasmon resonance peak was observed at 450 nm. XRD analysis confirmed the crystalline nature of Fe2O3-NPs and crystal size was deduced to be 40 nm. Elemental analysis by EDX validated the presence of iron coupled with oxygen in the form of nanostructures. Morphological properties of Fe2O3-NPs divulged by SEM demonstrated that their average size was 50 nm. The antibacterial activity of Fe2O3-NPs was ascertained against 30 clinical isolates of *Klebsiella pneumoniae* by well-diffusion method. They manifested antibacterial effect against all isolates with the largest inhibition zone recorded being 10 mm. MIC value for Fe2O3-NPs was 30 µg/ml. However, when mingled with three selected antibiotics, Fe2O3-NPs did not effectuate any antibacterial activity. Momentous antioxidant activity of Fe2O3-NPs (IC50 = 22 µg/ml) was discerned in comparison with standard at various concentrations. The anti-inflammatory activity of Fe2O3-NPs (IC50 = 70 µg/ml) was also noteworthy and superior to that of standard at different concentrations. Both the antioxidant and anti-inflammatory properties of Fe2O3-NPs escalated with their increasing concentration. Consequently, honey-mediated Fe2O3-NP synthesis may serve as a substitute to orthodox antimicrobial drugs and may be explored for prospective biomedical applications.

Keywords: Nanoparticles, iron oxide, honey, antibacterial, *K. pneumoniae*

PP-7

In-Silico Comparative Analysis of Microbial Communities of Microbial Fuel Cells

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Abstract

Traditional fossil fuel-based energy production has taken a toll on the environment and is insufficient to meet the world's growing energy needs. Microbial fuel cells (MFCs) offer an innovative alternative, converting chemical energy into electrical energy using bacterial communities. This study focused on understanding the diversity and abundance of bacteria in various MFC combinations, with a specific interest in identifying the most prevalent species associated with high power generation. Metagenomic analysis of 16S *rRNA* genes from MFCs was performed using data from the NCBI SRA database and Mothur software via the Galaxy web server. The analysis included sequence alignment, clustering into operational taxonomic units (OTUs), and alpha and beta diversity assessments. The results revealed significant species diversity among MFC samples, with certain bacterial groups, such as Bacteroidales, Clostridiales, Selenomonadales, Synergistales, Desulfuromonadales, and Rhizobiales, being abundant in MFCs that produced high energy output. Statistical tests confirmed the meaningful differences in microbial communities between high and low energy-producing MFCs. The presence of these abundant bacterial groups in high energy-producing MFCs suggests their essential roles in energy production. Further research and targeted studies on these microbes hold the potential to enhance power generation in MFCs, opening new avenues for sustainable energy production.

Keywords: Microbial fuel cells, galaxy, microbial communities, metagenomics, mothur, power output

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PP-8

Magnetotactic Bacteria: A Sustainable Solution for Heavy Metal Bioremediation

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Abstract

Magnetotactic bacteria (MTB) are a group of microorganisms that have the unique ability to align themselves along the Earths magnetic field lines. MTB have the potential to play a significant role in bioremediation, including the removal of heavy metals such as arsenic, chromium, mercury, cobalt, tellurium, and many others from contaminated environments. In this study, MTB were isolated from industrial waste water of H.M.D Tanneries Din Ghar Kasur. The samples were enriched using magnetic enrichment technique and its temperature and pH were optimized. MTB were collected using Racetrack method. The bacteria were cultured on Activated Charcoal Agar (ACA) under anaerobic conditions. Bacteria's magnetic movement was confirmed through microscopy under the influence of a magnetic field. Their movement was observed towards the magnets in a trajectory akin to the magnetic field lines. The susceptibility of these bacteria was tested to elevated concentrations of heavy metals including mercury, arsenic, cadmium, nickel and chromium. These bacteria were found to be resistant against As^{5+} up to 30mM as well as to As^{3+}, Hg, Ni, Cd and Cr up to concentrations of 20mM. These MTB can find various applications in bioremediation, including bioaugmentation, biostimulation, and chelation. Engineered magnetotactic bacteria with enhanced metal-binding capabilities can also be created while considering several factors such as environmental conditions, bacterial strains used, and the specific contaminants present for successful implementation in real-world remediation projects.

Keywords: Magnetotactic Bacteria; Racetrack; Magnetic field; Bioremediation; Arsenic; Chromium.

PP--9

Determination of Antifungal Activity of Different Medicinal Plants against Candida Species from Clinical Origin

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Abstract

The aim of the current study was to evaluate the *in vitro* antifungal ability of *Parthenium hysterophorus*, *Datura stramonium*, *Calotropis procera* and *Origanum vulgare* leaves extract using distilled water, N-hexane, chloroform, ethanol and ethyl acetate as solvent against Candida isolates. Morphological identification was performed by lectophenol and Gram staining procedure. Chromagar was used as differential media for *Candida* species identification. The antifungal assay and MIC were performed by using well diffusion method. All selected plants exhibited antifungal ability except *Calotropis procera*. From the selected specimens, *Parthenium hysterophorus* showed the maximum zone of inhibition (ZI) against B0, *Datura stramonium* against B9 and *Origanum vulgare* against Sp2 isolates. In chloroform and distilled water extracts of *Parthenium hysterophorus* and *Datura stramonium*, maximum ZI was measured in solvents like ethyl acetate, ethanol and n-hexane. MIC for each plant was performed at 25, 50, 100, and 200 mg/ml. Furthermore, MIC and MFC was also checked to confirm fungicide and inhibitory concentration. MIC and MFC of *Origanum vulgare* exhibited that the extracts at 100 and 200 mg/ml concentration completely killed the growth of SP2 isolate in distilled water, N-hexane, chloroform, ethanol where in ethyl acetate showed inhibitory concentration. *Datura stramonium* indicated that the extracts at 100 and 200 mg/ml concentration completely killed the growth of B9, T.A isolate in all extracts, whereas, at 200mg/ml concentration, all extracts of

Datura showed MFC against BO and Sp2 isolates. And the isolates of U9 specimens showed MIC in all solvents at 100 and 200 mg/ml except C at 200 mg/ml. *Parthenium hysterophorus* completely killed the growth of B9 isolate in all solvents at 200 mg/ml concentration while in BL showed MIC except at 200mg/ml.

Keywords: Antifungal ability, *Parthenium hysterophorus,* Chromagar, zone of inhibition

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PP-10

Bacterial Assisted Phytoremediation of Selenite in Mung Bean Plants

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Abstract

Heavy metals causing environmental pollution have become the severe threat for the world and the accumulation of these metals in soil is the major risk for human health. Bioremediation is the most accepted, time consuming, nondestructive technique and exists as natural process for remediation of soil. Besides this, the use of plants for cure of polluted soil or to reduce the toxic effects in environment, an efficient, environment friendly, low cost, approximately having 5% of clean method a technique called phytoremediation is in practice. The target is to reduce selenium toxicity in the environment by the efficient plant microbe interaction. The study examines the protein content, plant chlorophyll content, comparison of plant dry weight and fresh weight, and yield parameters (such as number of pots and weight of grains per pot) in mung bean plants treated with selenium and inoculated with selenium resistant bacterial strains, compared to plants inoculated with bacterial strains without salt supplementation. Almost an increase of 50% protein content, 43% pigment production, 61% fresh weight, 95% dry weight, 72% number of pots, 90% weight of grains has been reported in the plants treated with selenium salts as compared to the controls. The selenium resistant strains C3, F6, G7, H8, I9, N14, Q17, and R18 appeared as key organisms showing remarkable increase in every component of plant when supplemented with selenium. The findings support the absorption of selenium into the plants, which improves both the yield and growth parameters being examined. In future, this study will enable to utilize phytoremediation at commercial scale to produce crops with improved nutritional value in non-contaminated land as plants that contain selenium may be used for phytoremediation of selenium contaminants and as fortified food.

Keywords: Phytoremediation, heavy metal toxicity, selenium resistant strains, selenium supplemented, mung bean plants

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PP-11

Harnessing Purple Non-Sulphur Bacteria as a Single Cell Protein Source

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Abstract
Since single-cell proteins (SCP) are generated from unicellular organisms such as yeast, bacteria, protists, and microalgae, they are also known as microbial proteins. Certain SCPs can also be extracted from multicellular microorganisms such as macro algae and filamentous fungus. Purple non-sulphur bacteria (PNSB) are a family of phototrophic bacteria that have lately come to light as a promising solution for resource recovery, wastewater treatment, and SCP generation. PNSB can flourish in a variety of waste streams because they have a flexible metabolism and are tolerant of a broad range of environmental factors. Typically, these microorganisms are grown in organic carbon substrates, such as the fermented leftovers of agricultural and industrial wastewater, where microbial biomass is generated, collected, and processed. Certain microorganisms have entire or dried cells that have been shown to be high in essential amino acids (AA) and protein, which makes SCPs a good source of supplements or replacements for protein for both humans and animals. Because of its distinct metabolism and adaptability, PNSB can be easily enriched in a variety of wastewater sources under anaerobic or microaerobic lighting conditions. In an anaerobic wastewater treatment process utilizing purple non-sulfur bacteria, protein contents were sufficient independent of timing control of wastewater feeding and withdrawal.

Keywords*:* Single Cell Protein, Purple Non-Sulphur Bacteria, Cultivation, Protein Content, Wastewater.

PP-12

Relationship of Metabolic Syndrome with ABO Blood Groups in Okara and Lahore: Interim Analysis

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Abstract
Metabolic syndrome (MetS) is a condition that increases the risk of diabetes and cardiovascular disease. It occurs due to the presence of different factors such as obesity, high blood pressure (BP), hypertriglyceridemia, low HDL-cholesterol and hyperglycemia (fasting). There is some evidence indicating association of ABO blood groups with

MetS in certain populations of the world, however there is hardly any study carried out in Pakistan on this association/relationship. MetS according to Harmonized criteria is defined as presence of 3 or more of the 5 above mentioned factors. A waist circumference more than 80 cm is considered obese for women and more than 90 cm for obese men. High BP is defined as values above 135/80 mmHg. Hypertriglyceridemia refers to levels of triglycerides above 135 mg/dl in females and above 160 mg/dl for males. Hyperglycemia (fasting) is referred to as fasting blood glucose level above 125mg/dl. Low HDL -cholesterol is the condition when levels of HDL fall below 40 mg/dl in males and less than 50 mg/dl in females. To find out the prevalence of MetS in our population and determine its relationship with ABO blood groups. Methodology: In a cross-sectional study 290 healthy subjects in North Lahore and Okara were recruited with informed consent. Eight ml blood was collected in fasting state. Serum was analyzed for glucose, triglyceride and HDL. BP and waist circumference were recorded for each recruited subject. The prevalence of MetS was determined. Moreover, the relationship of ABO blood groups with MetS was also studied. There were a total of 101 males and females (age range: 20-70 years). The prevalence of MetS in males was 30.69 %, while in females it was 44.68%. No significant relationship was found between ABO blood groups and MetS.

Keywords*:* Metabolic syndrome, hyperglycemia, hypertriglyceridemia

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PP-13

Different Strategies to Identify Identical Twins

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Abstract

Identical twins are also called as monozygotic that originate from same zygote as they possess identical heritage. To discriminate identical monozygotic twins' short tandem repeats were not useful, therefore, various techniques including next generation sequences was applied. Monozygotic twins can be identified through germ line genomes, speech using deep learning network and epigenetic analysis. Fingerprint analysis is used to distinguish identical twins as all the human beings have unique fingerprints. The advance techniques help to identify genetic changes through sequencing, DNA methylation among monozygotic twins. For greater precision and accurate results, we have to focus on possibilities for future development to identify monozygotic twins.

Keywords: Identical twins, monozygotic, DNA methylation

PP-14

Exploring the Molecular Intricacies of Immune Reactions to *Naegleria fowleri* in Conjunction with Gut Microbiota for Novel Therapeutic Advancements

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Abstract

Naegleria fowleri, a pathogenic amoeba found on all continents except Antarctica, causes GIs infection with 95% fatality rate, predominantly affecting healthy children. Research on Naegleria's biology and behavior intensified as efforts to develop prevention and treatment strategies continue. Public health authorities conduct awareness campaigns to inform communities about risks and potential preventive measures. Despite low GIs infection cases in Africa and South America, monitoring and vigilance are crucial to detect and respond to outbreaks, safeguarding vulnerable populations worldwide *Naegleria fowleri* has been develop infection in gut microbiota. Collaborative efforts are vital to combat this deadly infection effectively. Different data bases were used to collect the data for article in systematics pattern. The globally epidemiologically surgery was performed to analysis the risk factor, death rate and consequence of viral load in community especially in gut disease and corresponding infections. Risk factors which also add the water resources and cultural practice are expressing the main cause of virus spreading. Boolean formula was applied to evaluate the research article. The defense mechanism of the human body against viral load involves the participation of both humoral and innate immunity intimate with gut bacterial colonization. These two components of the immune system work together to counteract the effects of viral infections. The humoral immunity, also known as the antibody-mediated immunity, is responsible for producing antibodies that specifically target and neutralize viruses. On the other hand, the innate immunity, also referred to as the non-specific immunity, provides a rapid response to viral infections through the activation of various cells and molecules. This collaboration between the humoral and innate immunity ensures a comprehensive defense against viral load in gut microbiota. Molecular characterization was done with particular immunogenic mechanism. The social collaboration among different communities is found an effective agenda to reduce the risk of disease and death rate as well by developing gut infection.

Keywords: Nagleria, virus, gut infection, health, molecular genetics, awareness.

PP-15

Computational Prediction of *Olea europaea* Compounds as Inhibitor of Main-Peptidase of SARS-CoV2

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Abstract

In December 2019, Severe Acute Respiratory Syndrome Novel Coronavirus 2 (SARS-nCOV2) was identified as potential causative agent for COVID-19 in the Wuhan City of China. This disease spread around the whole globe, thus WHO declared it as a pandemic by March 11, 2020. Due to rapid mutation rate, lack of specific genomic knowledge and treatment modalities against this RNA based virus, world scientific community urges to work for vaccine production, treatments options and alternative remedies including eastern herbs as potential anti-viral agents. *Olea europaea* (Olive) was found highly beneficial on the basis of its previous therapeutic applications. So, in the current study, its five different compounds (Catechin, Cynaroside, Elenolic Acid, Hydroxytyrosol, and Oleuropein) were chosen according to Lipinski physiochemical parameters, which were compared with already clinically used five anti-viral drugs (Ribavirin, Niclosamide, Nelfinavir, S-Nitroso-N-acetyl penicillamine, Chloroquine) against the Main-Peptidase (PDB ID:2GTB) of SARS-nCoV2 using Molecular Operating Environment (MOE) software. Among the chosen compounds of *Olea europae*a which were docked on the active site of ain Peptidase, Oleuropein provide the best minimum binding energy of -8.3201kcal/mol followed by Cynaroside with -7.2121kcal/mol. These two energy complexes are considered to have better drug potential in this initial studies as compare to the already commercially used drug agents e.g. Chloroquine, Ribavirin, Niclosamide and S Nitroso-N-acetyl Penicillamine having binding energy of -6.7168, -5.8171, -6.3361 and -5.4219kcal/mol respectively. Other three agents from olive were also docked to compare the binding energy of aforementioned clinically used drugs. Oleuropein and Cynaroside are considered to be the most compelling compounds as a drug agent against coronavirus2 infection. Further, molecular dynamic simulations and in-vivo investigations are needed to endorse the current findings of these compounds as potential drugs.

Keywords: Coronavirus, *Olea europaea,* WHO

PP-16

Analysis of Nutritional Awareness and Dietary Habits of University Students in Lahore and Adjacent Areas

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Abstract

Maintaining a balanced diet in middle-income countries like Pakistan is difficult due to inflation and increasing trends of consumption of junk and fast foods. The aim of this study is to find whether global trends regarding poor dietary habits and physical inactivity are also prevalent amongst Pakistan's university-aged population and to bring to light the effects of such trends on one's health. A cross-sectional study was conducted among 502 university students, ranging from the age of 18-30, from January 2023 to July 2023. Data collection was conducted in the form of a self-reported, semi-structured questionnaire which was cleaned up and analyzed in IBM SPSS version 22. The prevalence of overweight/obesity among male and female university students was 22%. Of the participating students only 155 (31%) were aware of my nutritional plate plan while the remaining 347 (69%) were unaware.432 (86%) agreed that their eating habits got worse upon coming to university. Similarly, 428 (85%) claimed that it is harder to maintain a balanced diet at university.76% of the participants said that they felt lethargic and 75% said that they still felt sleepy after a long night's sleep. The present study demonstrates that students lack a comprehensive knowledge about relevant and current nutritional trends, furthermore unavailability of cheap, healthy, and nutritional food and cultural and social trends makes it harder to maintain proper eating habits during university. Leading to an increase in side effects associated with nutritional deficiencies and non-communicable diseases.

Keywords: My nutritional plate plan, nutritional deficiency, BMI, obesity, lethargy

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PP-17

How Machine Learning and Neuroscience are Interconnected?

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Abstract

Understanding the complex and intricate system of cognitive thinking patters and the realm of unconscious mind allows us to translate our information into developing better machine learning codes. What would computers accomplish if they mimic and simulate neurons and biophysical details? Inspirational insights on how nature operates, help us imagine what can be done to develop better algorithms for computers to operate systemically. This is biologically feasible computing. Where biologically feasible computing, expands new horizons in the digital world, it also helps us explore neuroscience in depth. Once better computers that are better brain models are developed, they develop better simulations, which in turn help develop better neuroscience hypothesis to understand mental processes.

Keywords: cognitive thinking, simulations, algorithms

PP-18

Enhancing Insect Resistance: Incorporating Azadirachtin into Non-Repellent Plant Varieties

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Abstract

Azadirachtin, derived from neem and recognized as one of its primary active components, serves as the primary agent in combating insects. It is responsible for approximately 90 percent of the impact on the majority of pests. Introducing azadirachtin, a natural insecticidal compound found in neem, into non-insect repellent plants could potentially confer insect-repelling properties to those plants. Azadirachtin disrupts the feeding and growth of insects, acting as a deterrent and, in some cases, as an insect growth regulator. While azadirachtin is also considered relatively safe for humans, animals, and many beneficial insects. Therefore, its introduction into non-insect repellent plants at an optimal concentration, which does not adversely affect the plant's physiology, can result in various advantageous outcomes.

Keywords: Azadirachtin, pests, insecticidal compound, plants

PP-19

Microbial Harmony: Unraveling the Interplay of Microbiota, Lipid Metabolism, and Pathogens in Host Health and Antibiotic Resistance

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Abstract

Research in the field of bacterial utilization of different lipid sources and its impact on host lipogenesis reveals critical gaps. While extracellular pathogen lipid metabolism and exploitation are incompletely understood, the effects of specific fatty acids on gut microbiota remain unknown. Additionally, the interaction between lipids, especially when combined with other nutrients like dietary fibers, and its influence on gut microbiota needs exploration. Understanding these aspects is crucial for comprehending molecular pathogenesis and identifying therapeutic targets, especially in the context of emerging antibiotic resistance. The unresolved questions pose challenges in developing antibacterial strategies by targeting host lipids hijacked by bacteria. Although this approach could combat bacterial infections, the potential side effects on host homeostasis necessitate cautious consideration. Addressing these gaps is imperative for advancing research on the dynamics between host lipids and bacterial infections. Furthermore, in-depth studies on the intestinal microbiome underscore the importance of targeting it for treating lipid metabolism-related diseases. Unraveling metabolic interactions between the gut microbiota and the host is pivotal for personalized therapeutic strategies. This includes the development of novel prebiotics, probiotics, and synbiotics to prevent or treat conditions like obesity, metabolic disorders, and associated cardiovascular diseases. Overall, filling these knowledge voids is essential for advancing both the understanding of microbial dynamics and the development of effective therapeutic interventions.

Keywords: Microbiota, lipids, probiotics, prebiotics, synbiotics

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PP-20

Synthesis of Polymeric Nanocarrier for Doxorubicin Delivery in Cancer Cells

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Abstract:

The delivery of therapeutic compounds to the desired site is a major issue. Cancer is the second biggest cause of death globally. Though chemotherapy is successful to some extent, the drawbacks of chemotherapy are the inadequate accessibility of drugs to the tumor tissues requiring high doses, development of multiple drug resistance and their non-specific targeting. Most of the anti cancer drugs are hydrophobic and when they are administered in body, they get clear from the blood. That's why polymeric nanoparticles are used for delivering the anti cancer drugs to targeted site. As PEG is hydrophilic, drug is loaded to PEG core and converted into hydrophilic form. Polymeric nanoparticles are emerging as attractive treatment options for cancer. We developed PEG-PLGA nanoparticles for the delivery of DOX to cancerous cells. PEG-PLGA has ability to be used as carrier in drug delivery system due to its complete biodegradability and ability to self-assemble into nanometric micelles that are able to entrap small molecules like drugs and to release them into body in a time-dependent manner. The successful synthesis of PEG-PLGA was confirmed by its 1H NMR spectrum. The hydrodynamic diameter of NPs evaluated by DLS was approximately ~115 nm with zeta potentials -18.5mV. According to TEM images, all nanoparticles exhibited individual spherical morphology and size is around 100 nm. Drug release from DOX@NPs showed sustained drug release. DOX@NPs are more toxic to cancerous cells as compared to free DOX at lower concentration. Our developed drug delivery system can enhance the efficacy of hydrophilic drugs. Keywords: DOX, cancer, drug delivery, polymeric nanoparticles

Keywords: Anti-cancer, PEG-PLGA, multiple drug resistance

PP-21

Synergistic Remediation of Textile Effluent Polluted using Floating Treatment Wetlands Integrated with Plants and Bacteria

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Abstract

The mitigation of water pollution caused by textile effluents remains a critical environmental challenge. Floating wetlands (FTWs) is a cost effective and environment friendly technology for textile wastewater treatment. The FTWs, employing buoyant mats vegetated with plant, displayed notable efficacy in pollutant reduction. However, the inclusion of the bacterial consortium substantially augments the remediation process. The introduced bacterial strains not only reduce pollutants such as dyes, organic matter, nutrients, heavy metals, from the wastewater but also foster enhanced plant growth, evidenced by notable increases in root length, shoot length, and overall biomass production. Plants species with wide-ranging roots and biomass are suggested for vegetation in FTWs. The pollutant elimination effectiveness can be improved by the correct selection of plants and bacterial strains.

Keywords: Floating treatment wetlands, textile effluent, pollution

PP-22

Isolation and Characterization of Lignin and Phenol Degrading Bacteria

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Abstract

Lignin and chlorophenols have adverse effect on human health and environment as they can pose cytotoxic, mutagenic, endocrine-disrupting and carcinogenic effects. The present study aimed to 1) isolate, purify and characterize lignin and phenol degrading bacteria from pulp and paper mill effluent, 2) in-vitro screening for antifungal and phosphate solubilization activity and 3) estimation of degradation of lignin and phenol through spectrophotometer. Eight lignin and six phenol degrading bacteria were isolated and purified from pulp and paper mill effluent. LGW1, LGW4, LGW5 and LGW6 have the potential to utilize lignin as sole carbon source while PHW1, PHW2, PHW3 and PHW4 can utilize phenol as sole carbon and energy source. LGW5 showed 76%, LGW6 73% and PHW2 71% color reduction in wastewater. Estimation of lignin and phenol degradation was checked through spectrophotometer. Physiochemical analysis of wastewater was performed both before and after treatment and pH reduced to 7, EC reduced 44.04%, BOD and COD reduced 68.30% and 70.98% respectively, TDS 46.89%, lignin, color and phenol were reduced 70.27%, 76% and 71.50% respectively. On the basis of results, we conclude that LGW5, LGW6 and PHW2 have the bioremediation potential and can be applied at industrial scale.

Keywords*:* Lignin, phenol, bioremediation

PP-23

Long Reads Shotgun Metagenomics Binning and Annotation of Saline Soil Metagenome

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Abstract

Extreme environments are fascinating regions on Earth where organisms have adapted to survive and thrive under extreme conditions that are generally inhospitable to most life forms. It is estimated that 1 gram of soil contains billions of microbial species and reporting of only 1-2% of those can be cultured using standard methods. Metagenomics approach is used to study both the culturable and non-culturable microbial diversity of different environments. Metagenomics in combination with next generation sequencing technologies has made possible the discovery of a number of new microbial species. In this study, hypersaline soil samples were collected from the Khewra region. The samples were pooled together and metagenomic DNA was extracted using MO BIO's PowerSoil DNA Isolation Kit. The total DNA was sequenced from University of Minnesota, Genomics Center, using PacBio SMRT sequencing technology. The reads obtained were further processed for quality control and trimming. After assembly, 965 contigs were found with 65 percent GC content. The structural and functional annotation was done through IMG JGI database system. The binning and phylogenetic analysis was done through Busybee Web for comprehensive and differential composition-based metagenomic binning. It was found out that there were 186 RNA genes and 19909 protein coding genes. Functional annotation showed a large fraction of protein coding genes that have functions in inorganic ions transport and metabolism, and cell wall/envelope biogenesis all of which help the microbes survive in extreme saline conditions. The distribution of halophiles such as *Haloterrigena, Halorubrum, Streptomyces, Paraoceanicella, Mesorhizobium,* and *Natronomonas* across the saline habitat suggested their important role in this environment. Further pathway analysis output showed involvement of genes in different pathways such as energy metabolism, amino acid metabolism, xenobiotics degradation, and motility. These genes could be cloned further for practical applications such as bioremediation.

Keywords: Assembly, hypersaline, phylogenetics, taxonomy, PacBio sequencing technology

PP-24

Computational Analysis Predicting Deleterious Variants in Fbxo31 Gene

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Abstract

Mutation in FBXO31 gene is linked to intellectual developmental disorder. This study utilized *in silico* analysis to predict the highly pathogenic missense and splice site variants of FBXO31 that cause deregulation of Skp/Cullin/F-box (SCF) ubiquitin E3 ligase complex. This complex is significant for axonal identity and neuronal morphogenesis. It is also involved in proteasome-dependent degradation of various regulatory proteins such as cyclin D1. A total of 592 variants were retrieved from GnomAD, Variation Viewer, and dbSNP databases and further analyzed by CADD. 520 missense variants with PHRED score ≥ 20 were further analyzed by CAPICE and META-SNP and 89 variants were predicted to be highly pathogenic. Moreover, *in silico* stability analysis was done by different tools like DynaMut and DUET, and 8 variants were predicted as highly destabilizing on the basis of Gibbs free energy. The functional analysis was done by the Mutpred and 85 variants were predicted to disturb the function of the protein. UCSF chimera was utilized to check the clashes in the structure of the protein and 21 variants had clashes with their surrounding residues. Our results suggested that the structure of protein was significantly deleterious and protein motif and function were changed. Furthermore, the Consurf tool predicted 42% amino acid residues of FBXO31 as conserved. We further used the Scan Prosite and NetSurf2.0 databases to forecast the post-translation modification sites and it was noted that 4 variants significantly disturb the PTM sites of FBXO31. Splice analysis was conducted by SPiCE v2.1, Splice AI, and Mutation Taster, 6 variants predicted to affect the splicing mechanism. Overall, this study exhibited that identified variants of the FBXO31 gene have a significant role in the deregulation of FBXO31 complex that leads to intellectual disability.

Keywords: FBXO31, intellectual disability, *in silico*, scf ubiquitin e3 ligase complex

PP-25

In-Silico Designing of Bi-Functional Enzyme Constructs (Cellulase and Bglucosidase) for Enhanced Hydrolysis of Lignicellulosic Biomass

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Abstract

The rapid depletion of fossil fuels and the escalating environmental concerns have fueled the exploration of renewable energy sources, such as lignocellulosic biomass, for biofuel production. The hydrolysis of lignocellulosic biomass into fermentable sugars is a critical step in this process, and enzymatic approaches using cellulase and beta-glucosidase enzymes have shown promise. However, the suboptimal catalytic efficiency and synergistic interactions between these enzymes limit the hydrolysis yield. This thesis presents an innovative approach to enhance the hydrolysis of lignocellulosic biomass by employing *in silico* design of bifunctional enzyme constructs. The genetic sequences responsible for cellulase from *Bacillus altitudinis* and β-glucosidase from *Periconia* sp. were combined through fusion and subsequently introduced for expression within *E. coli* K12 bacterial strain. This fusion enzyme was stable at 60 °C for 2 h. Molecular docking simulations were utilized to predict potential binding sites and interactions between the enzymes, enabling the identification of suitable fusion points. Optimum pH for both cellulase and β-glucosidase activities was found to be 6.0. Optimum temperature for cellulase and β-glucosidase activities was found to be 60-65°C, respectively. In future, the docked complexes of stable fusion constructs would be evaluated using molecular dynamic simulations to assess conformational stability in dynamic environment. Combining cellulase and β-glucosidase makes it easier to channel one enzyme's output as a substrate to the other, improving the total efficiency of biomass hydrolysis. Therefore, these fusion enzymes might be useful in industrial applications

Keywords: Fusion enzymes, cellulase, b-glucosidase, *in-silico* analysis

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PP-26

Exploring the Impact of Combined BMI and HbA1c Levels on Pre-Diabetes Risk

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Abstract

Globally the prevalence of pre-diabetes is increasing day by day. The progression of which could lead to Type 2 Diabetes mellitus. This study deals with the combined effect of BMI and HbA1c levels on the risk of developing pre-diabetes. Alongside, evaluating body fat percentage, blood glucose testing, physical activity patterns and dietary choices gives a comprehensive approach to understand the pathophysiological pathway underlining pre-diabetes. It is explanatory research following a multi-quantitative methodology and for the sampling strategy, a simple random sampling technique was employed. After the informed consent, experimental data was collected according to the standardized procedures including HbA1c testing, BMI, body fat percentage and blood glucose levels. For the survey study, questioners related to food and physical activity were distributed via WhatsApp. The hypothesized results suggest that participants having high BMI and elevated levels of HbA1c are more likely to have pre-diabetes. It is because of poor diet and lack of physical activity along with high body fat percentage and elevated blood glucose levels. On the basis of the hypothesized results, it was concluded that high BMI and elevated levels of HbA1c commonly causing glucose dysregulation leads to pre-diabetes condition.

Keywords: Pre-diabetes, BMI (Body Mass Index), HbA1c levels, combined risk factors, Insulin sensitivity, Blood sugar monitoring, Food choices, Physical activity, and pathophysiological pathways.

PP-27

Effect of Water and Detergent Washings on Detection of Saliva Stains from Commonly Used Natural and Synthetic Clothes.

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Abstract

Forensic science plays important role in criminal justice system. In sexual assault cases, blood, semen and saliva commonly attained from crime scene. Culprit often tries to remove these biological stains through washing the crime scene. With that thought, the study was undertaken to observe the effect of water and detergent wash on natural and synthetic clothes and to extract, detect and quantify the amount of DNA from these clothes. However, both types of clothes gave positive results under various presumptive tests. Both types of clothes demonstrate different ranges of diameter after water wash till three washings. Furthermore, saliva was retained from laundered natural clothes till ten washings after processing with detergent while synthetic clothes after surfactant treatment could not efficiently retain saliva. Extracted DNA from both types of clothes analyzed under UV spectrophotometer and it was found that the amount of DNA was good enough to generate the DNA profile.

Keywords*:* Detergent, diameter, synthetic, natural, clothes

PP-28

Impact of Green Nano Fertilizers and Nano Pesticides on Plants

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Abstract

Nanotechnology is a new field of study that investigates the unique physicochemical features of the nanoparticles and their applications in various fields such as agriculture. Various techniques have been used to synthesize nanoparticles, including chemical, physical, photochemical, and biological approaches. In addition to being employed as nano-fertilizers that promote plant growth, these nanoparticles also serve as nano-pesticides, preventing various insects and pests from attacking plants. The synthesis of plant-based nanoparticles is an excellent approach due to their low cost, non-pathogenic factor, non-toxic phytochemical constituents, flexibility in reaction parameters, and biochemical diversity of plant extract. The impacts of ecofriendly and bio-based Zn NPs should be tested on different plants and agriculture crops. It not only enhances seed germination and plant growth, but also improves the quantum efficiency of the photosynthetic process. Zn NPs play a vital role in agriculture by having several applications that are crucial for ensuring food security and improving crop production. The aim of this research is to discuss the recent advances achieved in the field of plant biotechnology by utilizing nanoparticles and the impact these particles have made in soil fertility, seed germination and crop yield.

Keywords: Seed germination and crop yield, Zinc nanoparticles, nano pesticides, crops

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PP-29

In silico Drug Analysis of Colorectal Cancer using KRAS, MAPK14, and Ruvbl1 Gene

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Abstract

Overexpression in KRAS, MAPK14, and Ruvbl1 genes are linked to the colorectal cancer. The aim of our study is *in silico* analysis of certain overexpressed genes to predict the structure function sequence length, ligation. We use different computational technique/tools to explore how certain phytochemicals interact with three important genes linked to colorectal cancer. The methods adopted in this study having different aspects, encompassing molecular docking simulations and dynamic analysis. And then by using these simulations, it can help us to predict and

understand how phytochemicals interact with the KRAS, MAPK14, and Ruvbl1 genes. By understanding the detailed interactions between phytochemicals and genes, we aim to provide insights that might help design new substances or find new uses for existing ones.

Keywords: KRAS, MAPK14, Ruvbl1, Colorectal cancer, *in silico*

PP-30

Study on the Use of 6-hydroxyflavone (6-HF) as a Neuroprotective Agent against Induced Parkinson Disease (PD) in Mice

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Abstract

Parkinson's disease (PD) is the highly dominant neuro degenerative disorder and is manifested by the loss of dopamine neuronal cells and accumulation of protein called alpha synclein in the brain. It is more common in old people and is a multiple factor disorder having a number of heredity and natural aspects and distinguished by a number of features. The current study was conducted to explore the mechanistic potential of 6-hydroxy flavone (6-HF) in MPTP induced PD animal models. Male adult albino mice were randomly divided into three groups i.e. control, MPTP and MPTP plus 6-HF. The control animal received 0.9% saline solution while MPTP was administered at a dose of 30mg/kg and 6-HF at a dose of 10mg/kg intraperitonealy. MPTP administration on alternate day for two weeks cause memory dysfunction accompanied by activation of neuroinflammatory and neurodegenerative markers in the mice brain. On the other hand, 6-HF not only improved pre and post synapse but also improved MPTP induced memory dysfunction. Furthermore, 6-HF significantly acts as an anti-apoptotic agent by reducing oxidative damage and neuroinflammation in adult mice brain. Most importantly 6-HF inhibits NF-κB/ Caspase-3 signaling pathways in mice brain. In conclusion 6-HF is a novel therapeutic drug candidate in MPTP induced PD mice model. Further research is warranted to know the mechanism of neuro therapeutic action of 6-HF in several other neurological disorders.

Keywords: MPTP, NF-κB, Caspase-3, Parkinson, anti-apoptotic Proteins

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PP-31

Study on the Neuroprotective Effect of 6-Monohydroxyflavone (6-HF) in Pentylenetetrazole (PTZ) Induced Animal Model of Epilepsy

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Abstract

Oxidative stress has been implicated in several neuro-degenerative diseases. Oxidative stress further triggers neuro-inflammation and ultimately neuronal cell death. The purpose of the current study was to evaluate the anti-oxidant potential of 6-Hydroxyflavone (6-HF) against pentylenetetrazole (PTZ) induced oxidative stress in epileptic mice model. Experiment was conducted on adult albino male mice weighing between 30 to 32 g and about 7 to 8 weeks old of strain BALB/C were obtained from Veterinary Research Institute (VRI), Peshawar, KP.A total 30 mice were randomly classified into three experimental groups (n=10). As 1.Control group treated with 0.9 % saline 2.PTZ treated (35 mg/kg i.p.) 3. PTZ (35 mg/kg) and 6-hydroxy flavone (30 mg/kg) treated.Morris Water Maze (MWM) and Y-maze tests and western blot techniques were used. The results indicate that 6-HF significantly reversed the expression of proteins involved in neuro-inflammation and neuro-degeneration mediated memory dysfunction assist through in adult mice. Interestingly, the results revealed that 6-HF stimulated NrF2/TNF-α/Caspase-3 signaling pathway to inhibit β-Secretase (BACE-1) to delay PTZ induced amyloid beta (Aβ) production in mice brain. In summary, this study reveals anti-oxidant, anti-epileptic and neuro-protective capability of 6-HF in PTZ-induced mice model. Further in detail study is required to highlight the therapeutic potential of 6-HF in neurodegenerative diseases.

Keywords: Oxidative stress, pentylenetetrazole, 6-hydroxyflavone, caspase-3, y-maze test.

PP-32

In vitro Screening and Metabolomics Profiling of Soil Derived Actinobacteria for Potential Antitumor and Antibacterial Compounds

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Abstract

Many times the available cancer treatments become ineffective and have side effects. Also antibiotic resistance is a growing health concern these days hence new and effective drugs are needed. Actinobacteria are widely known to produce most of the commercially available medicinal compounds. Several novel bioactive compounds have also been reported from actinobacterial origin. This study aimed to investigate the antitumor and antibacterial activities of actinobacterial metabolites. 35 actinobacterial strains were isolated from 9 soil samples. After the morphological and biochemical characterization methanolic extracts of actinobacteria containing secondary metabolites were obtained. The extracts were screened for cytotoxic activity against brine shrimp larvae and *in vitro* antitumor activity against A549 lung cancer cell line. The antibacterial activity of the extracts was determined against Gram-positive and Gram-negative bacteria by agar well diffusion and microtiter plate assays. The chemical analysis of the extracts of was done by Thin Layer Chromatography (TLC) and Liquid Chromatography-Mass Spectrometry (LC-MS) which showed the presence of various compounds. The taxonomic identification of the selected strains was done by 16S rRNA gene sequencing. The extract from the strain identified as *Streptomyces bacillaris* showed more than 70% reduction in A549 lung cancer cells in 24 hours. The same extract showed about 30% OD reduction of methicillin-resistant *Staphylococcus aureus* (MRSA). The extract from another strain identified as *Amycolatpsis lurida* (a rare actinobacteria) showed zones of inhibition >14 mm and >20 mm in 48 hours and 72 hours of incubation respectively against *Mycobacterium fortuitum* which is a non-tuberculosis mycobacterium used in the process of discovery of drugs against Mycobacterium tuberculosis. This study proves to be beneficial in the field of pharmacology in discovery of novel and effective drug candidates for the treatment of cancer and various infectious diseases.

Keywords*:* Antitumor, antimycobacterial activity, actinobacteria, metabolomics profiling

PP-33

Study on Therapeutic Potential of Vitamin B6 against Lipopolysaccharide (LPS) Induced Neurodegenerative Disorders in Albino Mice

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Abstract

Alzheimer's disease (AD) is characterized by extensive loss of neurons in the brain of AD patients. Intracellular accumulation of beta-amyloid peptide (Aβ) has also shown to occur in AD. Neuro-inflammation has been known to play a role in the pathogenesis of AD. The present research work was conducted for the evaluation of neuroprotective activity of vitamin B6 against Lipopolysaccharide (LPS) induced over activation of neuroglial cells including astrocytes and microglial cells accompanied with presynapse and post synapse memory dysfunction in albino mice. LPS at dose of 250 µg/kg for 16 days consecutively injected in albino mice through intraperitoneal cavity. On contrary co-treatment of vitamin B6 at dose of 300µg/kg was injected to Albino mice for the last 10 days. Then mice were allowed to Morris Water Maze (MWM) and Y-Maze Tests to assess short-term and long-term memory mutilation after the administration of endotoxin. The percentage of spontaneous alternation for escape latency and probe test of LPS-administered mice was found less in comparison to normal Albino mice. Secondly co-treatment of mice with vitamin B6 at dose of 300µg/kg has improved memory and behavior after allowing them to behavioral tests i.e. Morris Water Maze (MWM) and Y-Maze tests. After performing behavioral tests the western blotting technique was carried out which confirmed that endotoxin administration caused the up regulation of neurodegeneration and neuroinflammatory proteins in the brain of mice such as amyloid beta (Aβ), beta-site APP cleaving enzyme 1 (BACE1), Nuclear Factor kappa B (NF-Kb), Tumor necrosis factor alpha (TNF-α), Ionized calcium binding adaptor molecule (Iba-1), Glial fibrillary acidic protein (GFAP) and interleukin 1 beta (IL-1β). Administration of vitamin B6 at dose of 300µg/kg has not only reduced neuroglial cells activation but also attenuated the level of pro inflammatory cytokines and chemokines in adult mice brain and eventually neurodegenerative disorders were suppressed. At the end of experimental work the results revealed that Lipopolysaccharide is a neurotoxic agent which causes neurodegeneration, memory dysfunction and it makes the neuroglial cells active at high level. While on the other hand vitamin B6 reduces the over activation of neuroglial cells in brain and it is considered to be the neuroprotective agent against lipopolysaccharide

Keywords*:* Endotoxin (LPS), neuroprotective agent (vitamin b6), neurodegeneration, pre and post synapse memory dysfunction

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PP-34

Investigating the Neuroprotective Capability of Vitamin B6 (Pyridoxine) Against Traumatic Brain Injury in Adult Mice

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Abstract

Traumatic brain injury is one of the most persistent diseases that is major reason of demise and infirmity globally. The main aims of study were to investigate neuroprotective potential of vitamin B6 against TBI induced oxidative stress mediated synaptic dysfunction and neuroinflammation along with memory impairment in adult albino mice. TBI was induced which caused oxidative stress, neuroinflammation followed by synaptic deficits and most importantly memory impairment in the adult albino mice. On the other hand vitamin B6 intraperitoneal administration (5mg/kg) post TBI was done for five consecutive days. Two well-known behavior tests (Y-maze & Morris water maze) were conducted to analyze the beneficial effect of vitamin B6 on memory dysfunction. Proteins expression was assessed through protein immunoblotting technique. Both Y-maze & Morris water results revealed that vitamin B6 significantly improved both short & long term spatial memory in adult mice. Furthermore different protein markers including pre and post synapse, endogenous antioxidant protein (Nrf-2), neuro-inflammatory markers (NFκ-B, TNF- α) and signaling protein (p-AKT). All these results of protein immunoblotting displayed that vitamin B6 reduced TBI induced oxidative stress associated neuroinflammation accompanied by both pre and post synapse dysfunction. This study also demonstrated that vitamin B6 stimulated p-AKT/Nrf-2 signaling against TBI. All these results loudly say that vitamin B6 is one of the natural safe and potent neuro-therapeutic drug candidates in neurological disorders

Keywords*:* Traumatic brain injury (TBI), vitamin B6, behavior tests.

PP-35

Determination of Antioxidant Potential, Bacterial Diversity, and Growth Performance of *Carassius Auratus* Fed on Polyherbal Formulation under Stress

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Abstract

Tremendous rise of aquaculture necessitates an urgent demand for its optimisation through scientific methods. It will increase fish health and growth while minimising environmental impact. Medicinal herbs are magical in their ability to improve immunity and health in aquaculture. This study investigated the effects of polyherbal aqueous extract in *Carassius auratus* under normal and stressed environmental conditions. Improved growth indices were observed with supplemented diet under thermal and salinity stress. Moreover, Fishes with supplemented diet not only maintained their normal microbial flora but also showed more microbial diversity compared to normal diet under stress conditions. Histopathologies of heart and gills were also compared under these stresses. Different variation level in antioxidant activities impart significant impact on enzymes like catalase and lipid peroxidase and showed a significant antioxidant potential under temperature and ammonia stress when fed with polyherbal diet. Medicinal properties of plants provide additional nutritional supplementation to fish for surviving in harsh environments.

Keywords: *Carassius auratus*, polyherbal formulation, temperature stress, ammonia stress, growth performance

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PP-36

Identification and Evaluation of Most Prevalent Thermophilic Fungi from Composting Process

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Abstract

Composting is bio degradative and aerobic process of organic constituents, which results in more stable organic products. The microbial communities present in the soil play a significant role in the accessibility of nutrients to plants by the decomposition of organic material. Samples of organic waste (compost) were obtained from Lahore compost Pvt. Ltd Pakistan at thermophilic stage of composting and subjected to PDA and potato glucose broth for evaluation at different pH, and Temperature. The genomic DNA was extracted and confirmed using phenol chloroform extraction method and gel electrophoresis. PCR was performed on extracted DNA using 18S universal primers for sequencing by 1st Base, Malaysia. The phylogenetic analysis was done through MEGA X and the analysis revealed that our fungal isolate under study belongs to *Leiothecium* genera. The inoculum can serve as soil conditioner and fertilizer for rapid growth of plants and further experimentation is needed to check the effect of consortium of bacteria and fungi isolated from compost on plants.

Keywords: Composting, gel electrophoresis, MEGA X

PP-37

Biodegradation of Crude oil from Oil contaminated sites

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Abstract

This study explores the use of bioremediation as a promising solution to mitigate the environmental impact of crude oil spills. Seven bacterial isolates from mechanic shop soil were characterized and evaluated for their ability to break down crude oil and promote plant growth. The bacteria were cultivated in minimal salt media with crude oil as the main carbon source, and their growth was monitored over time. Results indicate that these oil-degrading bacteria have the potential for effective bioremediation, showing an increase in optical density. Importantly, the presence of these bacteria did not negatively impact plant growth; instead, it supported it. The study emphasizes the synergy between ecological restoration and plant growth, offering a holistic approach to addressing environmental and agricultural challenges. Harnessing the natural strengths of these bacteria could contribute to reducing hydrocarbon pollution, restoring agricultural productivity, and improving soil health.

Keywords: biodegradation, oil-contaminated sites, hydrovarbon, ecology

PP-38

Feathered Residents: A Study of Bird Diversity in Sub-Urban and Urban Habitats

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Abstract

This study aims to assess bird richness and distribution in these disparate environments by presenting the findings of a thorough avian survey carried out in both urban (university campus) and relatively natural regions. Line transect approach was used during the course of year-round surveys, 36 bird species from 20 families and 8 orders were identified. The findings show significant differences in the richness and abundance of bird species across the two studied environments. A total of 1,296 birds were counted throughout the summer months, from March until the end of august. On the other hand, 598 birds were spotted throughout the winter, from October to late February. Seasonal variations in bird populations are a sign of the influence of food sources, migration patterns, and environmental conditions. The results showed that urban areas can have similar avian species diversity if are properly maintained and planted with mixed natural vegetation. Average Shanon-Weiner diversity index in summer was 2.31 while in winter was 2.22. In human settlement it was 2.12 and in suburban area was 2.42 throughout the year. The study highlights how crucial it is to properly understand and protect bird variety in both urban and relatively wild areas. In order to maintain local bird populations, such studies can help with the development of efficient conservation measures, habitat management, and urban planning. Long-term monitoring, habitat restoration, public awareness campaigns, migration studies, and the influence of climate change are some of the future research recommendations.

Keywords: Urbanization effects, line transect method, biodiversity assessment, environmental impact, bird populations, urban development, and conservation strategies.

PP-39

A Study on Freshwater Turtles Basking Behavior at Okara, Punjab, Pakistan

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Abstract

The study sheds insight on the nutritional preferences, feeding habits, and ecological functions of two particular species, the Brown River Turtle and Indian flap shell turtle, within the area. Samples were taken from certain water bodies using stomach flushing procedures, and examination of the samples revealed a variety of prey items, including as insects, worms, snails, plant parts, algae, soil particles, and unknown things. The study also highlights the serious global conservation challenges that these species face, with 40% of turtle species in Pakistan classified as internationally endangered. Conservation efforts are vital given numerous problems brought about by habitat loss, trade, and insufficient safety precautions. The study highlights the information gap that prevents effective conservation measures by highlighting the lack of thorough data on the range, abundance, and ecological needs of freshwater turtles in the Punjab area. It is advised that further research be done to examine population dynamics, habitat preferences, and dispersion patterns. Additionally, the study explores the physical traits, eating patterns, and seasonal differences in the diet of freshwater turtles, emphasizing the omnivorous nature of these creatures and their dependence on plant matter and fondness for insects. Sample size restrictions and geographic coverage, limits the results and makes recommendations for more research. These consist of expanding sample sizes, putting in place long-term monitoring plans, carrying out genetic research, evaluating habitat conditions, and dealing with the effects of climate change. Furthermore, community involvement, cooperative partnerships, conservation education, and policy change advocacy are highlighted as essential elements for the effective conservation of freshwater turtles in Pakistan.

Keywords: Freshwater turtles, basking behavior, nutritional preferences, ecological functions, conservation challenges, endangered species.

PP-40

A Study on Molecular Characterization of Black Rat (*Rattus rattus*) by 16S rRNA Gene in Lahore

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Abstract

The genetic variety and evolutionary background of the black rat (*Rattus rattus*) in Lahore are the main topics of this work, which explores the molecular characterization of this species. *Rattus rattus*'s family tree and genetic make-up will be uncovered through the use of the 16S *rRNA* gene, which will also shed light on the species' evolutionary changes and adaptations. The study examines morphological changes, hereditary variation, and adaptive evolutionary tendencies in order to provide a comprehensive knowledge of the species dynamics. The study shows anatomical and behavioural differences between various populations of *Rattus rattus* based on hereditary and natural variances. Phylogenetic relationship analysis establishes the evolutionary links between *Rattus rattus* and related species using unique labels like SNP and mtDNA sequences. Black rat hybridization across different species sheds light on the genetic mechanisms and results of interspecies mating. The results demonstrate that because of human movement and trade, *Rattus rattus* originated in the Indian subcontinent and spread throughout the world. The thesis also examines adaptive evolutionary trends that may be reactions to outside stressors in immunity, metabolism, and redundancy-related genes. Current advancements in genome sequencing technologies enable a thorough examination of the population structure and inheritance variety of *Rattus rattus*. Roof rat populations have morphological variations that are indicative of environmental adaptations. These variations include variations in body size, colour, pattern, skull shape, branch structure, and tail length. In this article, the role of morphological alterations and stiffness in intraspecies speciation and diversification is further explored. The small sample size and the requirement to combine genetic and morphological data are among the study's acknowledged shortcomings. One of the suggestions for further studies to deepen our comprehension of the phylogenetics of black rats is to overcome these constraints. In summary, this thesis sheds light on the intricate mechanisms that have moulded *Rattus rattus* over geological time by revealing information about the species' genetic diversity, evolutionary history, and morphological adaptation.

Keywords*:* Intraspecies speciation, morphological changes, genome sequencing, genetic diversity, 16S *rRNA* gene, *Rattus rattus*, and evolutionary history.

PP-41

A Study on Phylogenetic analysis of Rattus norvegicus by 16s rRNA as Reservoir of Zoonotic Diseases

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Abstract

This study does a comprehensive phylogenetic analysis of *Rattus norvegicus*, commonly known as the brown rat, using the 16S *rRNA* gene as a molecular marker. The project aims to provide knowledge on the evolutionary relationships, potential public health effects, and function of *Rattus norvegicus* as a reservoir for zoonotic diseases. The study collects genetic data from populations of *Rattus norvegicus* using 16S *rRNA* gene sequences for phylogenetic reconstruction. Using phylogenetic analysis, the study outlines the genetic relationships among different populations of brown rats, providing information about their evolutionary history and potential for the transmission of zoonotic illnesses. Using the 16S *rRNA* gene as a molecular marker, this work does a thorough phylogenetic analysis of *Rattus norvegicus*, often known as the brown rat. The project's objectives are to disseminate information regarding the evolutionary connections, possible implications for public health, and role of *Rattus norvegicus* as a zoonotic disease reservoir. In order to perform phylogenetic reconstruction, the study uses 16S *rRNA* gene sequences to gather genetic data from populations of *Rattus norvegicus*. The work uses phylogenetic analysis to show the genetic links between various brown rat populations, revealing details about their evolutionary background and potential for zoonotic disease transmission.

Keywords: *Rattus norvegicus,* phylogenetic analysis, 16S *rRNA* gene, zoonotic diseases, public health, genetic diversity, disease transmission, epidemiology

PP-42

A Study on Distribution on Norway Rats (*Rattus Norvegicus*) in District Sahiwal as a Reservoir of Zoonosis

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Abstract

This study explores the distribution patterns of Norway rats (*Rattus norvegicus*) in the Sahiwal district, focusing on their potential role as zoonotic disease carriers. The research utilises a comprehensive approach to understand the regional distribution of Norway rats and assess the implications for the propagation of zoonotic illnesses in the region. By employing field surveys and trapping methods, information about the spread of Norway rats in the Sahiwal district was achieved. In the genetic analysis, molecular markers were utilised to ascertain the presence of discrete rat populations and their potential association with zoonotic illnesses. The study shows that Norway rats are resilient to the environment since they are widely dispersed throughout the Sahiwal district. It is less likely that rat populations could act as reservoirs for zoonotic disease outbreaks when their variety and connectivity are better understood through genetic studies. The findings point to the necessity of more stringent oversight and control measures in order to lessen the possibility of zoonotic disease transmission linked to Norway rats in Sahiwal. The study's conclusions provide important information for public health initiatives to manage and prevent zoonotic illnesses associated with rodent populations.

Keywords: Norway rats (*Rattus norvegicus*), zoonosis, spatial patterns, reservoirs, zoonotic disease transmission, public health, rodent control.

PP-43

A Study on Phylogenetic Analysis of Brown Rat *Rattus Norvagicus* from Peshawar KPK by 16s rRNA Gene

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Abstract

Using the 16S rRNA gene as a molecular marker, this work performs a phylogenetic analysis of the brown rat (*Rattus norvegicus*) populations in Peshawar, Khyber Pakhtunkhwa (KPK). The purpose of the study is to clarify the evolutionary links and genetic diversity among brown rat populations in the designated area. Brown rat specimens were gathered by field surveys, and the 16S rRNA gene was extracted and sequenced using molecular methods. To investigate the genetic divergence and linkages among the tested brown rat populations, phylogenetic analysis was carried out. The brown rat populations in Peshawar, KPK, have a complex phylogenetic structure, according to the findings. The evolutionary dynamics and possible migration patterns of these rodents in the area can be understood through genetic diversity and clustering patterns. Given that *Rattus norvegicus* is recognised to be a reservoir for a number of zoonotic diseases, it is imperative for public health to comprehend the phylogenetic relationships of brown rats in Peshawar. The present study enhances the existing body of knowledge regarding the genetic diversity and population dynamics of brown rats. It highlights the significance of monitoring and management tactics in the successful control of diseases transmitted by rodents.

Keywords: Brown rat (*Rattus norvegicus*), phylogenetic analysis, 16s rRNA gene, genetic diversity, evolutionary relationships, Khyber Pakhtunkhwa (KPK), rodent-borne diseases, population dynamics.

PP-44

A Study of Public Attitude and Threats to Indian Flying Fox (Chiroptera: Pteropodidae) as A Pest Animal

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Abstract

In addition to examining perceived dangers related to the Indian Flying Fox's status as a nuisance animal, this study looks at public sentiments towards the species (*Chiroptera: Pteropodidae*). Despite its ecological value, the huge fruit bat known as the Indian Flying Fox is frequently regarded as a nuisance because of its effects on public areas and agriculture. This study intends to comprehend the intricate interactions between public perceptions, attitudes, and the perceived risks posed by Indian Flying Foxes through a combination of surveys, interviews, and ecological evaluations. The survey indicates a wide range of public opinions regarding the Indian Flying Fox, from awareness of conservation issues to worries about potential financial losses and health hazards. Individual experiences with the species, knowledge levels, and sociodemographic factors all have an impact on these sentiments. Perceived concerns linked to Indian Flying Foxes include crop damage, disease transfer, and nuisance in urban areas, as identified by the research. It is essential to comprehend public attitudes and worries in order to create socially acceptable and successful management plans for Indian Flying Fox populations. The study's findings provide valuable insight into the struggle between humans and environment that this species faces and emphasize the need of community engagement and education in easing tensions and promoting cohabitation.

Keywords*:* Indian Flying Fox, pteropodidae, public attitudes, pest animal, human-wildlife conflict, conservation, socio-demographic variables, crop damage, disease transmission, community engagement.

PP-45

A Study on Morphometric & Phylogenetic Analysis of *Rattus kandianus* from District Lahore, Pakistan

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Abstract

An in-depth analysis of the morphometric and phylogenetic traits that distinguish Pakistani District Lahore populations of *Rattus kandianus* is done in this article. The study intends to characterize the morphological variations and genetic links among *Rattus kandianus* specimens in the chosen location using morphometric measurements and molecular approaches. To have a complete understanding of intraspecies diversity, morphometric analysis is the systematic evaluation of important external features like body size, tail length, and skull morphology. The phylogenetic analysis of the 16S rRNA gene simultaneously shows the genetic diversity and evolutionary links among the populations of *Rattus kandianus*. Based on the results of the morphometric research, the *Rattus kandianus* individuals in District Lahore differed significantly in terms of size, shape, and length of tail. Phylogenetic research contributes significantly to our understanding of the dynamics of local rodent populations by providing valuable insights into the genetic composition and evolutionary history of these populations. This study not only advances our understanding of the intraspecies variation of *Rattus kandianus*, but also opens the door to potential uses in disease ecology and population management. The findings emphasize the need for continued study to inform effective conservation and management strategies as well as the need of combining morphological and genomic approaches to perform a full examination of rodent species.

Keywords*:* *Rattus kandianus,* Morphometric analysis, Phylogenetic analysis, District Lahore, Intraspecies diversity, Rodent dynamics, Disease ecology, Population management.

PP-46

Molecular Characterization of Black Rat (*Rattus Rattus*) By 16s rRNA Gene

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Abstract

The study focuses on the molecular characterization of the black rat (*Rattus rattus*) using the 16S rRNA gene as a molecular marker. Using molecular techniques, the 16S rRNA gene was extracted and sequenced from black rat specimens in an attempt to shed light on the genetic diversity and composition of different populations of *Rattus rattus*. The study employs phylogenetic analysis to investigate the evolutionary links between populations of black rats based on the 16S rRNA gene sequences. By detecting distinct genomic variations and clusters, the data provide insight into the evolutionary dynamics and genetic diversity of the species. The discovery offers significant new insights into the molecular characteristics of the species, laying the foundation for further research into the ecological and evolutionary significance of *Rattus rattus*. The findings have consequences for the ecology of disease, population control, and more general conservation strategies.

Keywords*:* Black rat (*Rattus rattus*), 16S rRNA gene, genetic diversity, phylogenetic analysis, evolutionary relationships, disease ecology, population management, conservation strategies.

PP-47

A Study on the Phylogenetic Relationship of Indian Flapshell Turtles from Depalpur, Punjab, Pakistan

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Abstract

The evolutionary links between Indian Flapshell Turtles (*Lissemys punctata*) in the Punjab, Pakistani region of Depalpur are examined in this study. The study uses both molecular and morphological analysis to clarify the evolutionary relationships and genetic diversity among the turtle populations in this particular area. The findings shed light on the distinctive genetic traits of the Depalpur population and provide context for the evolutionary background and geographic divergence of Indian Flapshell Turtles. Subsequent investigations could examine the financial importance of these turtles, emphasising their benefits to regional tourism, research prospects, and the preservation of their environment. Prioritizing habitat restoration in Depalpur is advised for conservation initiatives, with an emphasis on maintaining and restoring natural ecosystems that are essential to the turtles' long-term survival. A key element that advocates for local communities' education and involvement in habitat protection and biodiversity awareness is community engagement. It is suggested to use continuous genetic monitoring to follow population dynamics, providing important information on how populations react to changes in their environment and human influences.

Keywords*:* Indian Flapshell Turtles, phylogenetic relationships, *lissemys punctata*, depalpur, punjab, genetic diversity, habitat restoration, community engagement.

PP-48

Evaluation of Growth in C*irrhinus mrigala* after Inclusion of Black Pepper in Fish Feed.

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Abstract

The present study aimed to evaluate black pepper's effect on *Cirhinus mrigala* growth performance and to evaluate the effects of black pepper as immunostimulants via haematological and Histopathological studies and to find out optimum level of supplemented black pepper diets with canola meal based diet for *C. mrigala* fingerlings. The black pepper at 0%, 1.5%, 3%, and 4.5% were included in the fish feed as an additive. The fingerlings were obtained from the Satiana Road Fish Seed Hatchery in Faisalabad and transported to the Research Laboratory Department of Zoology in Faisalabad. The fingerlings were washed, disinfected, and then acclimatized for two weeks. The experiment was conducted in triplicate. The thirty *C. mrigala* fingerlings were added in each treatment; the 0% was considered as control. The fingerlings were fed at a rate of 3% of their live wet body weight. The duration of the experiment was of three months. The water quality parameters, such as dissolved oxygen, pH, and water temperature, were observed on a regular basis. In contrast, the rest of the parameters of water quality were calculated on a fortnightly basis. The morphometric parameters were studied on a monthly basis. The results of this research revealed that, compared to the control group in T_3, a canola meal-based diet supplemented with black pepper enhanced *C. mrigala* growth, hematology and histopathology in all diets, T_3 levels demonstrated superior growth, hematology and histopathology of muscles, gills, liver and kidney. As we compare T_3 diet to T_1 diet, show better growth higher SGR, low FCR and enhance immunity in T_3 diet level. The Data was subjected to one-way Analysis of Variance (ANOVA). The means was considered significant at $p<0.05$.

Keywords*:* Black Pepper, Temperature, Growth, Triplicate, Fingerlings

PP-49

Chimeric Antigen Receptor T-Cell Therapy in Multiple Myeloma: Progress, Current Limitations and Future Perspectives

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Abstract

Chimeric antigen receptor (CAR) T-cell therapy is a novel approach that has demonstrated promising efficacy in the treatment of relapsed, refractory multiple myeloma (RRMM). Chimeric antigen receptors (CAR) are engineered fusion proteins designed to target T cells for the antigens expressed on cancer cells. CAR-T therapy has achieved FDA approval for treating blood cancers like B-cell acute lymphoblastic leukemia, large B-cell lymphoma, and multiple myeloma by targeting CD-19 and B-cell maturation antigens. Ongoing research efforts are attempting to improve the durability of immune responses after CAR T-cell therapy. Several approaches including improved patient selection, novel CAR designs targeting multiple antigens, and modifications to the manufacturing process are being considered. The most common long-term adverse effects observed thus far are B-cell depletion (aplasia), hypogammaglobulinaemia, cytopenias and other related infections. Despite success in blood cancers, CAR-T technology faces challenges in solid tumors, including lack of reliable tumor-associated antigens, hypoxic cores, immunosuppressive tumor environments, enhanced reactive oxygen species, and decreased T-cell infiltration. To overcome these challenges, current research aims to identify reliable tumor-associated antigens and develop cost-effective, tumor microenvironment-specific CAR-T cells.

Keywords: Chimeric antigen receptor, CAR T-cell therapy, B-cell depletion

PP-50

Ajwa (*Phoenix dactylifera*) Seed Ameliorate the Effect of High Fat diet on C-Reactive Protein, Lipid profile and Cardiac Histopathology in Rabbits

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Abstract

High fat diet causes oxidation of accumulated fat cells which leads to Atherosclerosis. The inflammatory marker C-reactive protein has recently been identified as an independent predictor of future coronary heart disease. The inflammatory marker C-reactive protein has recently been identified as an independent predictor of future coronary heart disease. Present study evaluated the cardioprotective role of *Ajwa seed paste* on lipid profile and C-reactive protein (CRP) level in rabbits. 7 months old rabbits (n=15) for 30 days were kept in animal house school under standard laboratory conditions. Rabbits were divided into three groups (n=5). Group1 served as control group fed basal diet, group 2 fed high fat diet, group 3 fed high fat diet supplemented with 6gm ajwa seed paste. Feed consumption ratio was determined in all groups on daily basis. Feed consumption ratio showed significant ($P>0.05$) decrease in group 2and 3 fed high fat diet. In this study, lipid profile (cholesterol, triglyceride, LDL and VLDL) values were increased in group 2 compared to control group. It was found that significant ($P>0.05$) decrease in the level of bad cholesterol (LDL, VLDL) in group 3 (fed ajwa seed supplemented diet). HDL value showed significant ($P>0.05$) increase in group 3. HDL is good cholesterol and increased the level of HDL protect against the stroke and heart attack. and increase the level of good cholesterol (HDL). HDL takes the cholesterol from the body and back to liver where liver removes the bad cholesterol. The value of CRP is higher in group 2 due to the consumption of HFD and CRP level in group 3 showed significant ($P>0.05$) reduction. It is concluded from present study that ajwa seed paste is beneficial for heart health.

Keywords: Atherosclerosis, C-reactive protein, HDL

PP-51

Protective Potential of Vitamin B1 against Cisplatin Induced Nephrotoxicity

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Abstract

Chemotherapy toxicity is a common and unfortunate consequence of therapy that can occur even at usual doses. Chemotherapy acts by damaging cancer cells; however, normal cells are susceptible to damage as well, and when this occurs chemotherapy toxicity ensues. This study examind for the first time the therapeutic potential of Vitamin B1 (Thiamine) against Cisplatin (CisP) induced oxidative stress mediated inflammation and apoptosis in the kidneys of adult albino mice. Male adult albino mice of 8 weeks old were randomly divided into four different experimental groups i.e. 1. Control animals (0.9% normal saline treated), 2. CisP 3. CisP $^+$ Vita. B1 (300 µg/kg of body weight) and 4. Vita. B1 (300 µg/kg of body weight) treated respectively. Oxidative stress was measured with antioxidant enzymes assays and western blotting technique was used to evaluate the anti-inflammatory and anti-apoptotic efficacy of Vita. B1 against CisP induced nephrotoxicity in male adult mice. The results of antioxidant enzymes assays reveal that, Vita. B1 significantly stimulated antioxidant enzymes such as Catalase and GSH as inhibited by CisP while decreased LPO functions in the kidney homogenates of male adult mice. Additionally, Vita. B1 significantly inhibited phosphorylated JNK and NF-kB proteins to reduce CisP induced inflammation and Caspase-3 and PARP-1 (being apoptotic markers) in male adult mice. In summary, these findings show that Vita. B1 significantly restored antioxidant enzymes decreasing oxidative stress mediated inflammation and apoptosis induced by CisP in the kidneys of male adult mice. Further in depth study is warranted to report in detail the mechanism of nephrotoxicity in mice.

Keywords: Cisplatin (CisP), Vitamin B1, Catalase, GSH, p-JNK, NF-kB.

PP-52

A Systematic Perspective of Neurotoxicity in Adult Mice by Sudan-1 Dye

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Abstract

Industrial revolution has turned around the globe into a hell due to its continuous secretion of toxic pollutants into the environment. These pollutants are basically environmental toxins and they may exist as a particulate matter and gases as well. These toxic pollutants can cause damage to the human body in different ways and through different mechanisms. Among these toxins one of the major pollutants are the organic synthetic dyes which can easily contaminate water bodies and can cause serious health issues in human bodies when they find a way to enter into it. Because humans use all states of water for different purposes so they become the victims of these pollutants. For this reason in the current study we have examined the harmful effects of Sudan-1(Phenylazo-2-naphthol) dye on male Albino mice BAL/BAC. The male adult mice were randomly divided into three groups including normal, chronically exposed to sudan-1 dye and acutely exposed to sudan-1 dye. The chronic duration was for 10 weeks and the acute duration was for one week or seven days. Sudan-1 dye was dissolved in normal saline solution (0.9% NaCl solution) and was administered intraperitonealy at a dose of 3.6 mg/kg thrice a week. After completion of the injections the experimental mice were subjected to the behavioral tests including Morris Water Maze and Y-maze. The results of these tests indicates that both exposures of sudan-1 dye either for longer period (chronic) or shorter period (acute) of time induced impairment of the memory and behavior. Additionally the western blot result indicates that either exposure is neurotoxic to the experimental mice. Both exposures stimulated P-JNK/ TLR4 signaling pathway there by inducing Nf-Kb, caspase-3 and parp-1 proteins as a downstream markers of inflammation and neurodegeneration respectively. In summary the current study results indicates that organic dye sudan-1 is more toxic and lethal to the laboratory animals. A study with a full mechanism of the sudan-1 dye neurotoxicity is warranted in the future.

Keywords: Toxins, neuroscience, morris water maze, inflammation, neurodegeneration

PP-53

Vitamin B6 Via p-JNK/Nrf-2/NF-κB Signalling Ameliorates Cadmium Chloride-Induced Oxidative Stress Mediated Memory Deficits in Mice Hippocampus

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Abstract

Cadmium chloride (Cd) is a prominent heavy metal pollutant in the environment known to induce mitochondrial dysfunction, memory loss, and genetic disorder, leading to neurological disorders, especially Alzheimer's disease (AD). This study examined the neurotherapeutic potential of vitamin B6 (Vit. B6) in mitigating Cd-induced oxidative stress and neuroinflammation-mediated synaptic and memory dysfunction. Male adult albino mice were randomly divided into 4 groups: Control (saline-treated), Cd-treated, Cd+Vit. B6-treated, and Vit. B6 alone-treated. Cd and Vit. B6 were administered intraperitonealy. Behavior tests, including Morris Water Maze (MWM) and Y-Maze, were conducted, followed by western blotting, antioxidant assays, blood glucose and hyperlipidemia. Cd-treated mice exhibited impaired cognitive function, while Cd^+ Vit. B6-treated mice showed significant improvement. Cd-induced neurotoxic effects, including oxidative stress and neuroinflammation, were observed, with disruptions in synaptic proteins (SYP and PSD95) and activation of p-JNK. Vit. B6 administration mitigated these effects, restoring synaptic and memory deficits. Molecular docking and MD simulation studies explored the binding affinity of Vit. B6 with IL-1β, NRF2, and p-JNK proteins and confirmed VitB6's inhibitory effect underscored by experimental confirmation. These results highlight the potential of Vit. B6 as a safe therapeutic supplement to mitigate neurodegenerative disorders. This study underscores the importance of assessing the safety and potential benefits of nutritional interventions in combating environmental neurotoxicity for public health.

Keywords: neurotherapeutic, Vit. B6, memory dysfunction

PP-54

Punica Granatum Extracts Reduced the Proteins Expression Involved in Neuroinflammation Induced by Ethanol in the Developing Brain

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Abstract:
Ethanol is very toxic to the brain, and its excess usage can trigger apoptosis in the neuronal cells of brain. Similarly this ethanol consumption can also induces neuroinflammation in the brain. In the current study we have evaluated the potential of *Punica Granatum* (PG) plant flower extracts (Methanolic and n-Hexane) against ethanol-induced oxidative stress, neuroinflammation and neurodegeneration in postnatal day 7 (PND-7) rat pups. On 7th day of rat's birth the pups were randomly divided into four groups. 1. Control, 2. Ethanol, 3. Ethanol plus PG Methanolic extract and 4. Ethanol plus PG n-Hexane extract. Ethanol was administered sub cutaneously (s.c.) 5g/kg body weight, while control group were treated with saline solution. Along with ethanol exposure, the rats were cotreated with 30mg/kg body weight of plant extracts subcutaneously. After 4 hours of cotreatment the rats were sacrificed and their brain was removed carefully. The brain sample were homogenized and then centrifuged to separate the supernatants. The supernatants of all the groups were subjected to western blot technique. The results indicates that ethanol significantly induced oxidative stress, by decreasing nrf2 protein expression) followed by activated p-JNK (phospho) mediated neuroinflammation i.e. Nuclear Factor Kappa-light-chain-enhancer of activated B cell, (NFKβ), Tumor Necrosis Factor alpha (TNFα) and interleukin 1 beta (IL1β) and accompanied by neurodegeneration (increased ratio of by Bax/Bcl2, enhanced expressions of Caspase 3 and PARP1 proteins). In contrast, the PG plant extracts (both Methanolic and n-hexane) significantly activated Nrf-2 expression to inhibit p-JNK and its downstream signaling such neuroinflammation and neurodegeneration in the PND7 brain.In summary the current study reveals that both Methanolic and n-hexane PG extracts have antioxidant properties and can be used as potential agent against neurodegenerative diseases.

Keywords: Ethanol, *punica granatum*, caspase-3, nf-kb, parp-1.

PP-55

Investigation of Heavy Metals Accumulation and their Hematatoxicological Impact in Blood of Contaminated Water Drinkers of Different Localities of District Abbottabad

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Abstract

The quality of water is a vital concern for mankind, since it is directly linked with human welfare. It is a matter of history that fiscal pollution of drinking water cause water borne diseases which wiped out entire population of these cities. The present study aims to study to access the bioaccumulation of heavy metals concentration in blood of contaminated water drinkers and to evaluate the impact of heavy metals on blood hematology of contaminated water drinkers. Blood samples of non-contaminated water drinkers were collected and analyzed for heavy metals like Zn, Ni, Cr, Cu, Cd and Pb and compared with contaminated water drinkers. 3ml of the blood were taken from the selected people who are utilizing water since 20 years. The blood is then transferred to 5ml capacity EDTA plastic bottle and K1EDTA as anticoagulant. The estimation of heavy metal was done by tissue digestion with slightly modified method which was used previously so instead of 10ml nitric acid and 5ml per chloric acid, 5ml of nitric acid and 1 ml of chloric acid is used. After completion of procedure dense white fume indicate tissue digestion. To know the exact concentration of the heavy metal Atomic Spectrophotometer was used. Blood analysis was done by using whole blood on digital system on automated hematology analyzer. Heavy metal in non-exposed people show less content as compare to exposed one. The sequence of the heavy metal in the blood of control group were Ni>Pb>Cu>Zn>Zn>Cd>Cr. This showed that Ni (12.0 + 0.5ug/L) was the highest and Cr (5.6+0.8 ug/L) was the lowest parameter. The order for heavy metal analysis in exposed group was Zn>Ni>Cr>Pb>Cu>Cd. This highlighted that Zn with mean value of 19.6 + 1.7 ug/L was more and Cd with 14.0 + 1.5ug/L was less parameter. Blood parameter of control group showed less level as compared to blood level of exposed one. The sequence of all these parameter were MCV>NEUT>LYMP>MCH>HGB>MONO>MPV>WBC>RBC>PLT. The MCV (86.2+0.1fL) was high and PLT (3.1+0.5 (x10.e 3/ul) was low for control one. Similarly for exposed group MCV (83.4 +8.5 fL) was more and PLT (3.1 + 0.5 (x 10.e 3/ul) was less. Overall results showed that in control group the highest accumulatin metal was Nickle (Ni) and lowest metal was Chromium (Cr). In exposed group highest accumulating metal was zinc (Zn) and lowest metal was cadmium (Cd). Similarly in borh control and exposed group mean cell volume (MCV) has maximum value and Platelets has minimum value.

Keywords: Heavy metal, heamatological impact, contaminated water

PP-56

Antibiofilm potential of Tetracycline Loaded Titanium Nanoparticles

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Abstract

Biofilms are communities of microorganisms that are embedded in a self-produced matrix and adhered to surfaces. Biofilms are tough-to-treat microbial communities that resist antibiotics. Tetracycline-loaded nanoparticles effectively inhibit biofilm formation and eradicate mature biofilms due to their prolonged drug release, potentially reducing antibiotic resistance. This study aimed to investigate the antibiofilm potential of tetracycline-loaded titanium nanoparticles against various bacterial strains, including antibiotic-resistant ones. The specific objectives were to: Evaluate the antibiofilm efficacy of the nanoparticles against *E. coli*, *Providencia vermicola*, and *Enterobacter kobei* biofilms using different concentrations (10, 50,100µg/ml). Assess the impact of nanoparticle concentration on biofilm inhibition. The long-term effect of tetracycline release from nanoparticles on biofilm eradication and the potential of nanoparticles to reduce antibiotic requirements were evaluated. The study employed a sol-gel method to synthesize tetracycline-loaded titanium nanoparticles. The nanoparticles were characterized using UV, and Fourier-transform infrared spectroscopy (FTIR) to determine their size, shape, and drug-loading capacity. *In vitro* biofilm models were established using *E. coli*, *Providencia vermicola*, and *Enterobacter kobei* bacterial strains. The antibiofilm efficacy of nanoparticles loaded with tetracycline at different concentrations (10, 50, and 100µg/ml) was assessed using crystal violet staining, Microtiter tube assay, microtitre plate assay, and slime production assay techniques. The synthesized nanoparticles exhibited a high drug-loading capacity, enabling prolonged tetracycline release. Biofilm inhibition studies demonstrated the strong antibiofilm effectiveness of the nanoparticles against a variety of bacteria. Biofilm development was inhibited in a concentration-dependent manner, with higher nanoparticle concentrations resulting in increased antibiofilm efficacy of *Providencia vermicola*, and *Enterobacter kobei* bacteria. Tetracycline-loaded titanium nanoparticles have the potential to be a valuable tool for biofilm control. Their high drug-loading capacity, prolonged tetracycline release, and broad-spectrum antibiofilm activity make them promising candidates for further development and clinical applications.

Keywords: Biofilms, antibiofilm, nanoparticles, tetracycline

PP-57

A Chromium Resistant Bacteria Isolated from an Industrially Contaminated Sites in Kasur

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Abstract

Chromium, a transition metal renowned for its broad spectrum of industrial applications, can cause so many medical conditions in human beings. In order to shed insight on the complexities of microbial adaptation to this heavy metal contamination, this study focuses on the isolation and characterization of chromium-resistant bacteria from an industrial site in Kasur. Chromium's dual nature—it exists in two or more oxidation states—contributes to its complex behavior in natural ecosystems. Hexavalent chromium (Cr (VI)), a hazardous and carcinogenic form that is frequently found in wastewaters and in industrial effluents, is of special concern. Initially, we isolated several strains from an industrially contaminated site in Kasur, Pakistan. These isolates were then cultivated with different concentrations of chromium. Many other toxic metals were also analyzed such as Arsenate. Out of all strains only three strains show growth at 20mM arsenate concentration. To identify the growing patterns of these isolates over time, a standard growth curve analysis was carried out concurrently. Our research aims to expand knowledge of chromium's effects on ecosystems, highlighting the significance of creative approaches and sustainable methods for dealing with chromium pollution in industrial settings. Additionally, we will explore the microbial ecology of chromium-contaminated environments, taking into account the role that bacteria play in adapting to and possibly cleaning up heavy metal pollution.

Keywords: Chromium; heavy metals; bacteria; bioremediation; arsenic

PP-58

Multi-Metal Resistant Bacteria Isolated from Industrially Contaminated Site in Kasur

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Abstract

The current research focused on the isolation of Heavy Metal Resistant Bacteria (HMRB) from the Kasur industrial site, with a particular emphasis on resistance to arsenic. The main objectives of this research are to investigate the potential application of arsenic resistant bacteria in bioremediation processes. Arsenic resistant bacteria were found in samples taken from the Kasur Industrial site, and their resistance against different metals was analyzed. The bacteria showed resistance against several metals including arsenate and arsenite. Different concentrations of metals were also tested against bacteria. The enzymatic activities of these bacteria aid in the conversion of arsenate [As(V)] to arsenite [As(III)]. The bacteria are able to overcome the negative effects of arsenate exposure through this reduction mechanism, which is mediated by arsenate reductase enzyme. To examine arsenic reduction, several assays were carried out. The color change in qualitative assay indicated the degree of arsenic reduction, with a more pronounced change indicating higher reduction. For a quantitative assay, we measured the absorbance before and after reduction using a spectrophotometer. The decrease in absorbance correlated with the extent of arsenic reduction. After thorough analysis, the results taken from different assays and standard curves proved valuable insights into the arsenate resistance capabilities of bacteria. Considering this research, future prospects could include using these bacteria to build specific bioremediation techniques.

Keywords: Heavy metals; Chromium; Arsenic; Bacteria; Bioremediation

PP-59

Differential Expression and Bioinformatic Analysis of Circular RNA in Diabetes and Potential Therapeutics

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Abstract

The goal of our study is to find the core genes and its corresponding CircRNA that are associated with Diabetes. GEO contains datasets of circRNAs that are associated with Diabetes. Four datasets were downloaded from GEO database i.e. GSE 114248, GSE 182737, GSE 206041, GSE 209612 that contain differentially expressed circRNA associated with diabetes. They are further analyzed through GEO2R. Datasets contain the sample of diabetic patients and controls. The next step is to find the corresponding genes for the particular circRNAs. Functional enrichment analysis was performed to extract rational information from a set of genes. This provided us with the possible pathways being affected by the change of gene expression indiseased samples. The database named Database for Annotation, Visualization, and Integrated Discovery has been used to perform functional enrichment analysis. DAVID annotates the provided set of genes into the most affected processes such as Biological Processes (BP), Molecular Functions (MF), and Cellular Components (CC). Then KEGG is used to find detailed information about functional and biological systems pathways. Furthermore, we are aiming to perform Protein- Protein interaction to extract the gene that are interacting with each other. Then use MCC method to calculate hub genes. To find the hub genes in network and their differential expression in diabetes, we will use GEPIA. Our objective is to find the new genes that are involved in the pathogenies of Diabetes. These genes and their corresponding circRNA can be used for therapeutic purpose and as a biomarker for diabetes that could promote selective molecular therapy for Diabetes.

Keywords: Bioinformatics; Diabetes, Expressional analysis; Circular RNA

PP-60

In-Silico Analysis of Potential Anticancer Drug for *NEK7* and *PPP1CA* Proteins Overexpressed in Pancreatic Ductal Adenocarcinoma

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Abstract

The proteins overexpressed in pancreatic ductal adenocarcinoma, which is the most common type of pancreatic cancer, are NIMA-related kinase 7 (*NEK7*) and phosphoprotein phosphatase 1 catalytic subunit alpha (*PPP1CA*). The goal of the current investigation was to identify a possible *NEK7* and *PPP1CA* therapeutic inhibitor. For this investigation, 5000 compounds were retrieved from the IMPPAT library of phytochemicals, which were docked with our respective target proteins. Also, a reference compound, which is a Food and Drug Administration (FDA) approved drug, gemcitabine, was docked with the target proteins. The binding energy, of the reference compound for both the targeted proteins, is -6.5 kcal/mol. The common ligand with the lowest binding energy for both targets is Boeravinone B (PubChem ID: 14018348) with -9.2 kcal/mol of NEK7 and -7.6 kcal/mol for *PPP1CA*. For further analysis of drug reactivity density functional theory was performed for the 10 ligands with the lowest binding energies after molecular docking, and the ligand Boeravinone B was further studied for molecular dynamics simulation for analyzing the stability.

Keywords: Pancreatic ductal adenocarcinoma, NIMA-related kinase 7, IMPPAT, phytochemicals

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PP-61

Isolation of Arsenic Resistant Bacteria from Industrial Wastewater

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Abstract

Arsenic (As) is released into the environment due to various anthropogenic activities in the form of arsenate As (V) and arsenite As (III). In this study sample was collected from a textile industry in Faisalabad, Pakistan. This study aims to optimize the growth conditions of As-resistant isolates to assess their bioremediation ability. The bacterial strains were subjected to microscopic analysis. Furthermore, antibiotic resistance, cross-metal resistance, and minimum inhibitory concentration for As (V) and As (III) was checked. The isolates exhibiting higher resistance against As (V) and As (III) were subjected to the determination of As reduction- oxidation assays. Some biochemical tests including catalase, oxidase, carbon source utilization and gas production were also performed for their biochemical characterization.

Keywords: Arsenic, bioremediation, reduction, oxidation.

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