UMT | SSC
School of Science

2nd UMT INTERNATIONAL CONFERENCE ON LIFE SCIENCES

Translating Research into Impactful Solutions

April 10-12, 2025

Abstract Book

Organized by: **Department of Life Sciences, School of Science, UMT**

2nd UMT INTERNATIONAL CONFERENCE ON LIFE SCIENCES

Translating Research into Impactful Solutions

April 10-12 (Thursday-Saturday), 2025

UMT | SSC
School of Science

ABSTRACT BOOK

PAKISTAN ACADEMY OF SCIENCES

UNIVERSITY OF MANAGEMENT AND TECHNOLOGY
Estd. 1990
UMT

Preface

Pakistan Academy of Sciences (PAS) and Department of Life Sciences, School of Science, University of Management and Technology (UMT) Lahore Pakistan jointly organized the 2st UMT International Conference on Life Sciences, "*Translating Research into Impactful Solutions*" on April 10-12, 2025 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 USA, Canada, Turkey, Italy, China and Morocco. Over one hundred and sixty 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 33 invited/keynote speakers, 24 oral presenters and 65 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. Maria Dagla (Italy), Prof Dr. Yi Zhang (China), Dr. Hyung Goo Kim (USA), Dr. Hammad Ullah (China), Dr. Maria Vittoria Morone (Italy), Dr. Ningbo Chen (China), Dr. Temitope Fadipe (USA), Dr. Wasiq Ikram (Morocco) and Prof. Dr. Sami Simsek (Turkey), Dr. Ian Will (Canada), Ms. Nawshin TB Alim (Canada) inspired the young scientists with their intellectual lectures and fostered a very rich environment that prompted critical thinking in the audience.

Honorable Prof. Emiritus Dr. M. Waheed Akhtar (T.I) (Fellow and Secretary of Pakistan Academy of Sciences, Punjab Chapter) 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 Ahmad Abdullah awarded souvenirs and certificates at concluding ceremony.

CONFERENCE PATRONS

Ibrahim Hassan Murad

President, UMT

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

Rector, UMT

Ahmad Abdullah

DG, UMT

Prof. Dr. Sammia Shahid
(Dean, SSC)

Dr. Imran Tipu
(Chairperson, DLS)

CONFERENCE SECRETARY

Dr. Muhammad Ali

Organizing Committee


Prof. Dr. M. Perwaiz Iqbal


Dr. M. Sohail Afzal


Dr. Yasir Rehman


Dr. Kaneez Fatima


Dr. Iftikhar Ali


Dr. M. Irfan Fareed


Dr. M. Akram


Dr. Qurat ul Ain Hanif


Dr. Rana M. Mateen


Ms. Anam Amir


Ms. Nabiha Naeem


Mr. Ghadir Ali


Ms. Mehreen Fatima


Mr. M. Khurram


Mr. Aquib Nazar

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. BioScientific Review (BSR) is 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/
INVITED LECTURES

PLENARY / INVITED LECTURES

PL/IL-1

Importance of Fish in Human Health and Small-Scale Aquaculture

Dr. Muhammad Mudassar Shahzad
Department of Zoology, Division of Science and Technology, University of Education,
Township Campus Lahore.

*Corresponding Author:** drmudassarshahzad@gmail.com

Abstract

Fish play a crucial role in human health due to their rich nutritional profile, providing essential proteins, vitamins, and omega-3 fatty acids that are vital for growth, development, and disease prevention. Regular consumption of fish has been linked to improved heart health, cognitive function, and reduced risk of chronic diseases such as cardiovascular disorders and diabetes. In addition to their dietary significance, fish farming, or aquaculture, offers a sustainable method for food production, especially in regions with limited access to wild fish stocks. Small-scale aquaculture systems, such as backyard fish farming or community-based operations, are gaining attention for their potential to enhance local food security, create income-generating opportunities, and reduce the pressure on overfished natural resources. Despite challenges like disease management, water quality control, and limited technical knowledge, small-scale aquaculture can contribute to improved livelihoods and nutritional outcomes for communities. As demand for fish products continues to rise, promoting sustainable, small-scale aquaculture practices holds promise for meeting future food needs while supporting environmental conservation.

Keywords: Aquaculture, Fish, Farming, Food Security

PL/IL-2

Accelerating Wheat Variety Development: Innovative Strategies to Shorten Breeding Cycles

Fahim Ullah Khan
Department of Agriculture, Hazara University Mansehra Pakistan

*Corresponding Author:** fahimbiotech@hu.edu.pk

Abstract

The global demand for high-yielding, climate-resilient wheat varieties are growing due toincreasing population pressures, changing climatic conditions, and evolving disease threats. Traditional wheat breeding programs, which rely on lengthy selection cycles, face significantchallenges in delivering improved cultivars within a reasonable timeframe. We exploreinnovative strategies to accelerate wheat variety development by integrating cuttingedgebreeding techniques, advanced phenotyping, and data-driven approaches. Recent advancementsin genomic selection (GS), speed breeding, and high-throughput phenotyping (HTP) havesignificantly enhanced breeding efficiency. Genomic selection enables early and more accurateprediction of superior genotypes, reducing the reliance on multiple generations of field trials. Speed breeding techniques, leveraging controlled environment conditions, allow for up to sixgenerations per year, drastically shortening the breeding cycle. Additionally, the integration ofartificial intelligence (AI), machine learning (ML), and image-based phenotyping tools offersunprecedented opportunities for rapid and precise trait evaluation. Furthermore, genomic editingtechnologies, such as CRISPR-Cas9, provide targeted modifications to improve diseaseresistance, yield stability, and stress tolerance, expediting the development of climate-resilientwheat cultivars. The combination of these innovative strategies with optimized field evaluationand participatory breeding approaches ensures faster deployment of superior wheat varieties tofarmers. We will highlight successful case studies demonstrating the impact of these technologieson wheat breeding programs worldwide. By adopting an integrated approach that harnessesgenomics, digital agriculture, and accelerated breeding methods, we can effectively shortenbreeding cycles, enhance genetic gains, and ensure global food security in the face of futureagricultural challenges.

Keywords: Wheat breeding, Genomic Selection, Speed Breeding, Machine Learning, CRISPR, High-Throughput Phenotyping, Climate Resilience, Food Security

---

PL/IL-3

Food Supplements for Metabolic Health: Current Evidence and Future Directions

Hammad Ullah[1,2]*, Lorenza Francesca De Lellis[2], Daniele Giuseppe Buccato[2], Maria Vittoria Morone[3], Alessandro Di Minno[2,4], Danaè Larsen[5], Alessandra Baldi[2], Maria Daglia[2,6]

1. School of Medicine, Xi’an International Studies University, 710061 Xian, China
2. Department of Pharmacy, University of Naples Federico II, 80131 Naples, Italy
3. Department of Experimental Medicine, Section of Microbiology and Clinical Microbiology, University of Campania “L. Vanvitelli”, 80138 Naples, Italy
4. CEINGE-Biotecnologie Avanzate, Via Gaetano Salvatore 486, 80145 Naples, Italy
5. School of Chemical Sciences, The University of Auckland, Auckland 1010, New Zealand
6. International Research Center for Food Nutrition and Safety, Jiangsu University, Zhenjiang 212013, China

*Corresponding Author:** hammadrph@gmail.com; hammad.ullah@unina.it

Abstract

Metabolic disorders are a major global health concern, significantly increasing the risk of cardiovascular disease and other complications. While lifestyle modifications, including diet and exercise, serve as primary prevention strategies, adherence remains challenging. Nutraceuticals and food supplements have emerged as potential complementary

approaches; however, comprehensive evaluations of food-based interventions, particularly across diverse populations, are limited. This lecture aims to present the findings from our research studies on food bioactive ingredients for improving metabolic health, with a focus on red yeast rice, micronutrients, and extracts from *Zea mays* L., *Gymnema sylvestre* (Retz.) R.Br. ex Sm., brewer's spent grain (BSG), and *Prunus domestica* L. Methods and Key Findings: A series of studies were conducted to evaluate the efficacy of food-based interventions in improving metabolic parameters. A 3-month trial of a supplement containing monacolins, γ-oryzanol, and γ-aminobutyric acid significantly reduced low-density lipoprotein cholesterol (LDL-C) and total cholesterol (TC) while increasing high-density lipoprotein cholesterol (HDL-C) in subjects with mild dyslipidemia. Another 3-month study in participants with mildly impaired fasting blood glucose (FBG) found that a supplement containing *Z. mays, G. sylvestre*, zinc, and chromium significantly decreased FBG and glycosylated hemoglobin (HbA1c) at a lower dosage, with no additional benefit at higher doses. A crossover study demonstrated that a BSG extract-based supplement significantly reduced postprandial glycemia and insulinemia compared to placebo in normoglycemic subjects with mild glucose intolerance. Research on *P. domestica* extract revealed multiple benefits, including inhibition of metabolic enzymes, suppression of pro-inflammatory mediators, enhanced glucose uptake in liver and adipose tissues, downregulation of lipogenesis-related genes, and improvement in postprandial glycemia and insulinemia *in vivo*. Food bioactive ingredients offer promising benefits for metabolic health, particularly in individuals with mild metabolic disturbances. Future research should focus on optimizing formulations, evaluating long-term effects, and establishing clinical guidelines for their use

Keywords: Metabolic Health, Blood Glucose, *Zea mays* L., Glycosylated Hemoglobin

---

PL/IL-4

Unravelling the Genetic Etiology of Hereditary Disorders in Southern Kashmiri Population

Ansar Ahmed Abbasi[1,2], Madiha Shadab[1], Saiqa Khushal[1], Rabiah Shoukot [1], Nadine Krämer,[3] Na Li[4], Tauqeer Ahmed[1], Rameez Nisar[1], Sundas Farooq[1], Lena-Luise Becker[4], Xiang Fang[4], Hao Hu,[4] Barbara Vona [5,] Henry Houlden[6,] Reeza Morifan[6,] Zubair M Ahmed[7] and Angela M. Kaindal[3]

1 Department of Zoology Mirpur University of science and technology (MUST) Mirpur (10250), AJ&K Pakistan.
2 Department of Zoology University of Azad Jammu and Kashmir Muzaffarabad 13100, AJK, Pakistan
3 Institute of Cell Biology and Neurobiology and Center for Chronically Sick Children (SPZ), Charité – Universitätsmedizin Berlin, Augustenburger Platz 1, 13353 Berlin, Germany.
4 Laboratory of Medical Systems Biology, Guangzhou Women and Children's Medical Center, Guangzhou Medical University, Guangzhou, 510623, China
5 Institute for Auditory Neuroscience & InnerEar Lab, University Medical Center Göttingen
6 Department of Neuromuscular Diseases, Institute of Neurology, UCL UK.
7 Department of Otorhinolaryngology-Head & Neck Surgery School of Medicine, University of Maryland USA.

*[*] **Corresponding Author:** ansar.abbasi@ajku.edu.pk

Abstract

AJ&K (Azad Jammu and Kashmir), nestled in the picturesque Himalayas, is a region of breathtaking beauty and rich cultural heritage. Governed by its own president and prime minister, it enjoys semi-autonomous status within Pakistan. The southern districts of Azad Kashmir, include Bhimber, Kotli, and Mirpur. We assessed patients from multiple consanguineous families from Southern Districts of AJK, exhibiting non-syndromal intellectual disability postnatal microcephaly, Hearing loss Hereditary oculocutaneous albinism. With whole exome sequencing (WES) followed by Sanger sequencing and cosegregation analysis. WES analysis identified novel candidate genes, novel mutations in known genes linked with genetic disorders and previously reported mutations in known genes. Thus, our study expands the phenotypic spectrum of the genes linked with hereditary disorders in Kashmiri Population and hence contributed towards better understanding of mechanisms involved in these genetic disorders.

Keywords: Intellectual Disability*, Postnatal microcephaly, Candidate* Genes, Whole Exome Sequencing.

PL/IL-5

Scutellaria lateriflora L. as a Sleep Aid: A Controlled Study in Individuals with Primary Insomnia

Maria_Daglia[1,2,*], Hammad Ullah[1], Maria Vittoria Morone[3], Daniele Giuseppe Buccato[1], Lorenza Francesca De Lellis[1], Alessandro Di Minno[1,4], Alessandra Baldi[1], Roberto Sacchi[5]

1.Department of Pharmacy, University of Napoli Federico II, Via D. Montesano 49, 80131 Naples, Italy
2.International Research Center for Food Nutrition and Safety, Jiangsu University, Zhenjiang 212013, China
3.Department of Experimental Medicine, Section of Microbiology and Clinical Microbiology, University of Campania "L. Vanvitelli", 80138 Naples, Italy
4.CEINGE-Biotecnologie Avanzate, Via Gaetano Salvatore 486, 80145 Naples, Italy
5.Applied Statistic Unit, Department of Earth and Environmental Sciences, University of Pavia, Viale Taramelli 24, 27100 Pavia, Italy

Corresponding Author: maria.daglia@unina.it

Abstract

Primary insomnia is a sleep disorder characterised by persistent difficulties in initiating or maintaining sleep for at least one month, leading to significant distress or impairment in daily functioning, without an underlying medical, psychological, or environmental cause. This randomised, double-blind, placebo-controlled, crossover clinical trial investigated the efficacy and tolerability of a *Scutellaria lateriflora* L. extract-based food supplement in individuals with mild to moderate primary insomnia. Sixty-six participants (aged 18–70 years) were randomly assigned in a 1:1 ratio to receive either the food supplement (400 mg/day) or a placebo for 56 days, with a 28-day washout period between interventions. The primary outcome was assessed using the Pittsburgh Sleep Quality Index (PSQI), while secondary measures included sleep onset latency, sleep efficiency, total sleep time, and a Visual Analogue Scale (VAS) for subjective sleep quality. Supplementation with *S. lateriflora* resulted in significant improvements in sleep parameters, as evidenced by enhanced PSQI scores and secondary sleep-wake cycle measures. Importantly, no adverse effects were reported, supporting the supplement's safety profile. These findings indicate that *S. lateriflora* may represent a promising and well-tolerated intervention for improving sleep quality and restoring sleep-wake balance in individuals with primary insomnia.

Keywords: Primary insomnia; *Scutellaria lateriflora* L.; Sleep quality; Randomised controlled trial; Herbal supplement.

PL/IL-6

A Natural Approach to Dyslipidemia: A Randomized Clinical Trial to Evaluate the Efficacy of a Multi-Component Food Supplement

Maria Vittoria Morone[1,*], Hammad Ullah[2], Daniele Giuseppe Buccato[2], Lorenza Francesca De Lellis[2], Alessandro Di Minno[2,3], Alessandra Baldi[2], Roberto Sacchi[5], Maria Daglia[2,4]

1. Department of Experimental Medicine, Section of Microbiology and Clinical Microbiology,
2. University of Campania "L. Vanvitelli", 80138 Naples, Italy
3.Department of Pharmacy, University of Napoli Federico II, Via D. Montesano 49, 80131 Naples, Italy
4.CEINGE-Biotecnologie Avanzate, Via Gaetano Salvatore 486, 80145 Naples, Italy
5.International Research Center for Food Nutrition and Safety, Jiangsu University, Zhenjiang 212013, China
6. Applied Statistic Unit, Department of Earth and Environmental Sciences, University of Pavia, Viale Taramelli 24, 27100 Pavia, Italy; roberto.sacchi@unipv.it

Corresponding Author: mariavittoria.morone@unicampania.it

Abstract

Cardiovascular diseases (CVD) remain a leading cause of mortality worldwide, with hypercholesterolemia being a significant modifiable risk factor. Despite the widespread use of statins for cholesterol management, concerns over side effects and patient adherence highlight the need for alternative strategies. Dietary interventions and nutraceuticals have gained attention as promising approaches for maintaining lipid homeostasis. This study evaluated the efficacy of a novel food supplement containing *Mentha spicata* L. extract, *Amaranthus caudatus* L. seed flour, flavonoids (naringin, hesperidin), and B vitamins (B3, B6, B9, B12) in individuals with borderline dyslipidemia. In a randomised, double-blind, placebo-controlled clinical trial, 114 participants were assigned to three groups: low-dose supplement, high-dose supplement, or placebo, for 90 days. The primary outcome was the change in LDL cholesterol levels, with secondary outcomes including total cholesterol, HDL, triglycerides, inflammatory markers, and body composition parameters. The results demonstrated that the high-dose formulation significantly reduced LDL cholesterol and total cholesterol compared to placebo, while also increasing HDL cholesterol levels. The low-dose formulation showed a modest but positive effect on lipid parameters, whereas the placebo group exhibited a worsening lipid profile over time. No significant changes were observed in inflammatory markers or glucose metabolism, indicating that the intervention specifically influenced lipid homeostasis. In conclusion, this novel supplement, particularly at a higher dosage, appears to be an effective non-pharmacological strategy for managing borderline dyslipidemia. Given the growing interest in natural lipid-lowering interventions, these findings support further exploration of nutraceuticals as adjuncts to conventional cholesterol management.

Keywords: Dyslipidemia; *Mentha spicata* L.; *Amaranthus caudatus* L.; Flavonoids; B vitamins; Cardiovascular health.

PL/IL-7

Complete Genomic Landscape Reveals Hidden Evolutionary History and Selection Signature in Asian Water Buffaloes (*Bubalus bubalis*)

Yi Zhang

National Engineering Laboratory for Animal Breeding, Key Laboratory of Animal Genetics, Breeding and Reproduction of Ministry of Agriculture and Rural Affairs, College of Animal Science and Technology, China Agricultural University, Beijing 100193, China

Corresponding Author: yizhang@cau.edu.cn

Abstract

To identify the genetic determinants of domestication and productivity of Asian water buffaloes (*Bubalus bubalis*), we sequenced and integrated 470 genomes of domesticated river and swamp buffaloes along with their putative ancestors, the wild water buffaloes (*Bubalus arnee*). The swamp buffaloes inherit the morphology of the wild buffaloes. In contrast, most river buffaloes are unique in their morphology, but their genomes cluster with the wild buffaloes. The levels of genomic diversity in Italian river and Indonesian swamp buffaloes decrease at opposite extremes of their distribution range. Purifying selection prevented the accumulation of harmful loss-of-function variants in the Indonesian buffaloes. Genes that evolved rapidly (*e.g.*, *GKAP1*) following differential selections in the river and swamp buffaloes are all involved in their reproduction. Genes related to milk production (*e.g.*, *CSN2*) and coat color genetics (*e.g.*, *MC1R*) underwent strong selections in the river buffaloes specialized in milk production via soft and hard selective sweeps, respectively. The selective sweeps and single-cell RNA-seq data revealed the luminal cells as the key cell type in response to artificial selection for milk production of the dairy buffaloes. These findings show how artificial selection has been driving the evolutionary divergence and genetic differentiation in morphology and productivity of Asian water buffaloes.

Key words: Asian Water Buffaloes, Genomic Landscape, Single-Cell RNA-Seq

PL/IL-8

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

Wasiq Ikram[1] and Altaf Hussain[1]

[1]School of Botany, Minhaj University Lahore (MUL), Lahore, Pakistan

Corresponding Author: wasiq.bot@mul.edu.pk

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 were 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.

Key words: Phosphorus use Efficiency, Wheat, ^{32}P radio isotope, Citric acid

---

PL/IL-9

The Genomic Diversity, History, and Unique Evolutionary Adaptation of East Asian Cattle

Dr. Ningbo Chen

Northwest Agricultural and Forestry University, Yangling, China

Corresponding Author: ningbochen@nwafu.edu.cn

Abstract

Humpless taurine cattle (*B. taurus taurus*) and humped indicine or zebu cattle (*B. taurus indicus*) are two distinct but cross-fertile cattle subspecies, play a central role in the livelihood of pastoral communities across a wide range of

agro-ecosystems, from extremely cold and hot semiarid to hot humid tropical regions. However, their adaptive genetic changes and origin following the dispersal of these animals in East Asia, from the center of origin, remain poorly documented. The complex histories of East Asian cattle breeds warrant further investigation. East Asia is rich in bovine species resources, there are 55 native cattle breeds in China. Several bovine species including yak and gaur were also distributed in East Asia and adjacent regions, and hybridization of these species occurs frequency. All these events contributed to the complex genetic background and histories of East Asian cattle. Here, we used mitochondrial, Y chromosomal, autosomal, and ancient markers reveal the origin of East Asian cattle and extensive gene flow between East Asian cattle and other bovine species. East Asian cattle are mainly composed of three distinct ancestries, including an earlier East Asian taurine ancestry that reached China with Y2b paternal lineages, $T3_{119}$, $T3_{055}$, and T4 maternal lineages, a later introduced Eurasian taurine ancestry with Y2a paternal lineages and other maternal lineages, and East Asian indicine ancestry with Y3A paternal lineages and I1a maternal lineages. East Asian taurine cattle are known for their ability to tolerate harsh environments, such as the Tibetan plateau. The isolated Tibetan Plateau preserved unique prehistoric genetic resources of early East Asian taurine cattle. Our results revealed that recently selected and adaptive yak introgressed genes together contribute to the adaptation of QTP cattle to high-altitude environments. We found recently selected genes of QTP cattle related to body size and cold adaptation and clear signals of sympatric introgression from yak into Tibetan cattle at different altitudes, including several genes involved in the hypoxia response and UV radiation. Using high-quality whole-genome sequencing data from 354 indicine cattle of 57 breeds/populations, including indicine phylogeograhpic groups worldwide, we were able to characterize in fine detail indicine genetic diversity and population structure, and to show that their local environmental adaptation in Asia has benefitted from introgression of other bovine species. We identified distinct sets of loci that contain promising candidate genes for adaptation to hot semiarid and hot humid tropical ecosystems. Our results indicate that the rapid and successful adaptation of East Asian indicine cattle to hot humid environments was a direct consequence of a small number of genomic regions introgressed from banteng and/or gaur during an immigration of zebu along a coastal rather than inland routes. Our findings provide comprehensive, explanatory insights into the unique and successful evolutionary adaptation of East Asian cattle.

Keywords: Cattle and Related Species; Re-sequencing; Adaptation; Population Genomics; Introgression

---

PL/IL-10

Comparative Analysis of Microscopic and Molecular Methods for the Diagnosis and Post-Treatment Monitoring of *Echinococcus Granulosus Sensu Stricto* in Experimentally Infected Dogs

Muhammed Ahmed Selcuk[1, 2,] Figen Celik[1], Sami Simsek[1]

[1]Firat University, Faculty of Veterinary Medicine, Department of Parasitology, Elazig, Türkiye
[2]Siirt University, Faculty of Veterinary Medicine, Department of Parasitology, Siirt, Türkiye

Corresponding Author: ssimsek@firat.edu.tr

Abstract

Cystic echinococcosis (CE), caused by *Echinococcus granulosus*, is a significant zoonotic disease with profound public health and economic impacts. This study evaluated egg detection methods, molecular diagnostics, and post-treatment shedding dynamics in experimentally infected dogs. Three three-month-old male dogs were included in the study. Two experimental dogs (ED-1, ED-2) were orally infected with 20,000 *E. granulosus* protoscoleces, while one served as a control (CD). Stool samples were collected daily over 50 days post-infection and 30 days post-treatment. Detection of *E. granulosus* eggs was performed using the Fulleborn and sieving flotation methods. Genomic DNA was extracted, and molecular analysis was conducted via conventional PCR, Real-time PCR (RT-PCR), and digital PCR (dPCR). Egg detection in stool samples began on days 44-46 post-infection using flotation methods, while PCR detected parasite DNA as early as day 20. RT-PCR and dPCR provided consistent results, with dPCR demonstrating superior sensitivity detecting DNA even in samples with low egg counts. Treatment eliminated viable egg shedding within 2-4 days, but molecular tests intermittently detected residual DNA for up to 30 days post-treatment. This study highlights the efficacy of combining microscopic and molecular techniques for the detection and monitoring of *E. granulosus* in dogs. The findings support optimizing diagnostic and treatment protocols to mitigate the spread of CE in endemic regions.

Keywords: *Cystic echinococcosis*, Molecular Analysis, Real-time PCR, Diagnostic Protocols

---

PL/IL-11

Integrated Genomics in Disease Gene Discovery

Hyung-Goo Kim[1]

[1]Department of Neurosurgery, Robert Wood Johnson Medical School, Rutgers, the State University of New Jersey, USA

Corresponding Author: hk1047@rwjms.rutgers.edu

Abstract

The identification of canonical pathogenic variants will require the integration of different types of mutations affecting the same genes. Therefore, we plan to find convergent genomic evidence to identify novel ID genes from candidate loci of balanced chromosome translocations and microdeletions/microduplications in combination with the WES approach. We hypothesize that the positional candidate genes in these loci will have point mutations identified by WES. Our approach complements the gene discovery strategy using sole WES, which has become the norm in medical genetics. The validity of the causative gene will come from the accumulating evidence from each approach that collectively contributes to the identification of novel disease genes. The integration of different types of mutations affecting the same genes will offer a unique and powerful route to gene discovery. An illustrative example of this approach can be seen in the 1p32.3 microdeletion/microduplication syndrome, a contiguous genomic disorder characterized by intellectual disability (ID) and craniofacial anomalies (CFA). In this case, the combination of positional cloning techniques and next-generation sequencing (NGS) helped pinpoint a critical gene, SSBP3. By employing breakpoint mapping of two independent subjects with balanced translocations involving 1p32.3 and comparative mapping of 9 CNVs along with 6 intragenic variants in 8 individuals with matching phenotypes, we provided compelling evidence that the ID and CFA observed in this syndrome are both caused by disruption of the SSBP3 gene. This gene's involvement was further confirmed by functional studies in zebrafish and Drosophila, where knockdown of the respective SSBP3 orthologs led to distinct craniofacial and behavioral phenotypes. This example highlights how integrating positional cloning and NGS in combination can lead to the identification of novel disease genes, exemplifying the power of this approach in deciphering the genetic underpinnings of complex disorders.

Keywords: Integrated Genomics: Gene Discovery: Mutation

PL/IL-12

Identification of NS2B-NS3 Protease Inhibitors for Therapeutic Application in ZIKV Infection: A Pharmacophore-Based High-Throughput Virtual Screening and MD Simulations Approaches

Hafiz Muzzammel Rehman

School of Biochemistry & Biotechnology, University of the Punjab, Lahore, Pakistan.

Corresponding Author: muzzammel.phd.ibb@pu.edu.pk

Abstract

Zika virus (ZIKV) pandemic and its implication in congenital malformations and severe neurological disorders had created serious threats to global health. ZIKV is a mosquito-borne flavivirus which spread rapidly and infect a large number of people in a shorter time-span. Due to the lack of effective therapeutics, this had become paramount urgency to discover effective drug molecules to encounter the viral infection. Various anti-ZIKV drug discovery efforts during the past several years had been unsuccessful to develop an effective cure. The NS2B-NS3 protein was reported as an attractive therapeutic target for inhibiting viral proliferation, due to its central role in viral replication and maturation of non-structural viral proteins. Therefore, the current in silico drug exploration aimed to identify the novel inhibitors of Zika NS2B-NS3 protease by implementing an e-pharmacophore-based high-throughput virtual screening. A 3D e-pharmacophore model was generated based on the five-featured (ADPRR) pharmacophore hypothesis. Subsequently, the predicted model is further subjected to the high-throughput virtual screening to reveal top hit molecules from the various small molecule databases. Initial hits were examined in terms of binding free energies and ADME properties to identify the candidate hit exhibiting a favourable pharmacokinetic profile. Eventually, molecular dynamic (MD) simulations studies were conducted to evaluate the binding stability of the hit molecule inside the receptor cavity. The findings of the *in silico* analysis manifested affirmative evidence for three hit molecules with -64.28, -55.15 and -50.16 kcal/mol binding free energies, as potent inhibitors of Zika NS2B-NS3 protease. Hence, these molecules hold the promising potential to serve as a prospective candidate to design effective drugs against ZIKV and related viral infections. Keywords: ASINEX database; Zika virus; e-pharmacophore approach; high-throughput virtual screening; molecular dynamics simulation; prime MM-GBSA.

Keywords: Protease Inhibitors, Non-Structural Viral Proteins, Molecular Dynamic (MD) Simulations

PL/IL13

Homozygous Variant C.2861_2862del (P. K939Rfs*38) In *PRG4* Further Delineates the Phenotypic Spectrum in Camptodactyly-Arthropathy-Coxavara-Pericarditis Syndrome

Rana Muhammad Kamran Shabbir [1], Gökhan Nalbant [2], Sajid Malik [2], Aslıhan Tolun [3]

[1]Department of Zoology, Division of Science and Technology, University of Education Lahore, Punjab Pakistan
[2]Human Genetics Program, Department of Animal Sciences, Faculty of Biological Sciences, Quaid-i-Azam University, Islamabad, Pakistan.
[3]Department of Molecular Biology and Genetics, Boğaziçi University, Istanbul, Turkey.

Corresponding Author: kamran.shabbir@ue.edu.pk

Abstract

Camptodactyly arthropathy coxa-vara pericarditis (CACP; MIM 208250) syndrome is congenital autosomal recessive phenotype with lack of lubricin proteoglycan 4 due to mutations in *PRG4* gene in which, at least, 98 different mutations have been reported to cause CACP syndrome. Although CACP is, a rare genetic disorder but several cases described from different ethnic populations like Korean, Chinese, Pakistan, Indian, Saudi Arabian, Egyptian, Caucasian and Europeans. This study was aimed to determine the genetic cause of CACP syndrome in large Pakistani kindred with unreported clinically features. A large consanguineous family was studied showing camptodactyly, arthropathy of joints, coxa-vara, and cardiac defects, the primary features of CACP. More importantly, some patients born with brachydactyly and small nails, which have never been reported in any previously described case of CACP. Exome analysis revealed homozygous deletion c.2861_2862del (p. Lys939Argfs*38) in coding region of *PRG4* as causative reason. Conclusively, the study described the expanded clinical spectrum of CACP syndrome in a large consanguineous family. The newly reported clinical features were brachydactyly and small nails. The study results might be helpful to establish genotype-phenotype correlation of the CACP.

Key words: Camptodactyly, Mutation, Arthropathy, Homozygous

PL/IL14

Artificial Neural Networks-Powered Nanoinformatics Approach for Precision Medicine with Engineered Silver Nanoparticles

Muhammad Naveed

Department of Biotechnology, Faculty of Science and Technology, University of Central Punjab, Lahore.

Corresponding Author's Email: dr.naveed@ucp.edu.pk

Abstract

Nanomedicine, an emerging convergence of nanotechnology and healthcare, is set to transform diagnostics, treatment strategies, and drug delivery systems. At the core of this transformation is nano-informatics, a powerful tool that addresses the complex challenges of integrating nanoscale materials in healthcare. This study explores the use of nano-informatics in the design and application of engineered silver nanoparticles (AgNPs), focusing on their interaction with virulent and antibiotic-resistant genes in Staphylococcus aureus, a major contributor to multidrug resistance.Through advanced computational analysis, the binding affinities of AgNPs to four key virulence factors and resistance genes were assessed: spa, LukD, fmhA, and hld. High docking scores for spa (-7.16 kJ/mol), LukD (-6.5 kJ/mol), and fmhA (-6.45 kJ/mol) indicate strong interactions, showing significant potential in combating multidrug-resistant Staphylococcus strains. However, the smaller hld gene exhibited a lower binding score (-3.3 kJ/mol), likely due to its size. These findings highlight the efficacy of silver nanoparticles in disrupting antibiotic resistance mechanisms, offering new pathways for personalized nanomedicine.This study underscores the essential role of nano-informatics in precision nano-medicine, facilitating the design, analysis, and safety evaluation of nanoparticles. As nanomedicine continues to evolve, nano-informatics will be instrumental in advancing personalized healthcare by optimizing treatment precision and minimizing adverse effects. This approach opens novel strategies for addressing drug resistance and improving patient outcomes.

Keywords: Artificial Neural Networks, Nanoinformatics, Nanomedicines, Silver Nanoparticles, Personalized Medicine, Healthcare

PL/IL-15

Magnetic Affinity Purification of Proteins

Madeeha Shahzad Lodhi
Institute of Molecular Biology and Biotechnology, University of Lahore

Corresponding Author's Email: Madeeha.shahzad@imbb.uol.edu.pk

Abstract

Nanobiotechnology involves using nanoscale materials and devices to study and manipulate biological systems. Nanobiotechnology has the potential to revolutionize many areas of biology and medicine, such as drug delivery, gene therapy, tissue engineering, and diagnostics. However, using nanomaterials in protein purification is a newly emerging technique. Traditionally, chromatography and many other techniques have been used for protein isolation and purification in biosciences. These methods are lengthy, cumbersome, and involve combining different chromatography techniques. These methods have many limitations and hurdles due to time, purification efficiency, and percentage purity. The use of nanoparticles in protein purification incredibly magnetic affinity purification is an emerging technology and has the edge over the traditional techniques for purification. It involves fewer steps and fewer reagents. Comparatively, the time required for purification steps is short, and the yield is high compared to other lengthy conventional methods. Magnetic nanoparticles are being used in several biomedical applications, like imaging, thermal cancer therapy, and enzyme immobilization, due to their size-to-surface ratio, uniformity in size, and capacity to bind with linkers for different attachments of biomolecules. Magnetic nanoparticles were synthesized by hydrothermal method, fully characterized, and used to purify three different types of proteins: ligand protein transferrin, receptor protein folate, and an enzyme exo-polygalacturonase. The basic principle of the magnetic affinity purification technique is very simple and practical. Magnetic nanoparticles were modified according to the nature of the protein and applied for protein purification based on affinity. Magnetic nanoparticles were mixed in a protein source sample to get a protein complex with MNP under suitable conditions. This complex was separated by applying an external magnetic field. Proteins were collected from magnetic nanoparticles by adding elution buffers in the complex. The results indicated that the synthesized superparamagnetic MNP was suitable for the purification of proteins. A good yield of biologically active proteins was purified by this method. The purified proteins maintain their biological activities for a more extended period at low temperatures. Purified transferrin was used to synthesize the diagnostic probe and target theranostic nanomedicines, and tremendous results were achieved. Folate receptor antibodies were produced in rabbits and used in targeted nanomedicines. Exo-PG enzyme was purified 9.5-fold with a yield of 29.2%. The enzyme retained 98% activity in the presence of 20% glycerol at 4ºC. The purified exo-PG using MNPs yielded a 10-12% increase in juice production compared to without treated fruit juice. Many novel projects are underway to use nanotechnology for protein purification and application in different biological fields.

Keywords: Nanobiotechnology, Magnetic Nanoparticles, Protein Purification

PL/IL-16

Genomic Epidemiology of Dengue Virus in Punjab, Pakistan

Malik Ihsan Ullah Khan

Institute of Molecular Biology and Biotechnology, University of Lahore

Corresponding Author's Email: ihsan.ullah@imbb.uol.edu.pk

Abstract

Genomic epidemiology of Dengue virus (DENV) provides critical insights into viral transmission dynamics, evolution, and pathogenesis, informing strategies to mitigate outbreaks. This study investigates the genomic epidemiology of DENV in Punjab, Pakistan, focusing on serotype distribution, mutation patterns in structural and non-structural proteins, and their implications for public health. A cohort of 600 confirmed DENV patients (aged >13 years, no comorbidities) was analyzed, with demographic data indicating a predominance of males (average age: 32.5±9 years). Common symptoms included fever and body aches, while fatigue, vomiting, rashes, and bleeding were less frequent. Most cases originated in Lahore, with smaller clusters in Faisalabad and Sargodha. Genomic analysis of over 100 DENV isolates from tertiary hospitals yielded 20 whole genome sequences, revealing 1,169 non-synonymous mutations. The Envelope (E) protein exhibited the highest mutation frequency, followed by NS5 and NS4A, while NS2A was the most conserved. Novel mutations were identified across structural (E, prM) and non-structural (NS1, NS3, NS5) proteins, suggesting ongoing viral evolution and potential emergence of divergent strains. These findings highlight the dynamic genetic landscape of DENV in Punjab, driven by region-specific mutations that may influence viral fitness, antigenicity, and diagnostic accuracy. Regular genomic surveillance during outbreaks is essential to track emerging variants, refine therapeutic targets, and guide public health policies for epidemic preparedness. This study underscores the need for integrating genomic data into DENV management strategies in Pakistan to enhance outbreak response and mitigate future health crises.

Keywords: Genomic Epidemiology, Dengue Virus (DENV), DENV Management

PL/IL-17

The Role of Microbes in Corrosion: A Growing Challenge for Industries

Hafiz Zeshan Wadood

Department of Biology, Faculty of Basic Sciences, Lahore Garrison University, Lahore, Pakistan

Corresponding Author: dr.zeshanwadood@lgu.edu.pk

Abstract

Microbiologically influenced corrosion (MIC) is the influence of microorganisms on the kinetics of corrosion processes of metals, caused by microorganisms adhering to the surfaces in the form of a Biofilm. MIC is being increasingly acknowledged during the last few decades. The process of establishing the importance of MIC in equipment damage is very slow because of the limitation of analytical techniques to identify, localize and control the corrosion reactions. MIC is a fear to different industries like oil and gas industries, food processing units, aircraft and automobile industry, construction sector, water treatment and distribution plants and nuclear power plant. The investigation of MIC requires multidisciplinary awareness including electrochemistry, corrosion and chemical engineering along with microbiology and microscopy. Various bacterial groups are involved in the corrosion process. The biofilms of bacteria formed on the surface of metals can be beneficial or harmful for the underlying metals. These biofilms can accelerate the corrosion process or these can inhibit the corrosion of underlying metal.

Keywords: Microbiologically influenced corrosion, Biofilm, Industries, Electrochemistry, Microbiology

---

PL/IL-18

Isolation and Identification of *Clostridium Perfringens* and Its Toxins from Mutton in Lahore City, Punjab, Pakistan

Shahan Azeem

University of Veterinary and Animal Sciences (UVAS), Lahore, Pakistan

Corresponding Author's Email: sazeem@uvas.edu.pk

Abstract

The meat industry of Pakistan has demonstrated steady progress. Recently the country's meat exports have also exhibited a surge. *Clostridium perfringens* is commonly associated with meat contamination. The present study evaluated the presence of *C. perfringens* and its toxins in mutton samples collected from Lahore City, Punjab, Pakistan. Forty samples of minced and non-minced mutton were collected from local butcher and retail shops representing four areas (Islampura, Shadman, Ichhra, and Gulberg) of the city. The samples were subjected to ELISA for *C. perfringens*

alpha, beta, and epsilon toxins. The samples were simultaneously evaluated by bacterial isolation, biochemical testing, and a multiplex PCR targeting alpha, beta, and epsilon toxin genes. More samples were positive for alpha toxin gene of *C. perfringens*: 17.5%(7/40), compared to alpha toxins 10%(4/40). The samples collected from the local butcher shops were contaminated with *C. perfringens* and its toxins. Interestingly, no contamination was detected in any of the samples collected from retail meat shops. In conclusion, improper hygienic conditions at butcher shops could lead to the contamination of mutton with *C. perfringens* and its toxins.

Keywords: Meat Industry, Clostridium Perfringens, Toxins

PL/IL-19

Senescence Program Initiated by Cellular Cannibalism

Syed Qasim Raza[1-3], Guido Kroemer[2] and Jean-Luc Perfettini[3]

1.Institute of Biochemistry and Biotechnology, UVAS, Lahore
2.INSERM U848, Gustave Roussy Cancer Campus, F-94805 Villejuif, France
3.Laboratory of Molecular Radiotherapy, INSERM U1030, Gustave Roussy, Villejuif, France

Corresponding Author: qasim.raza@uvas.edu.pk

Abstract

The engulfment of live cells by other live cells, also known as cannibalism, can entail “entosis” *i.e.* the death of engulfed cells. Cyclin-dependent kinase inhibitor p21$^{WAF1/CIP1}$ (p21) triggers autophagy and favors the accumulation of E-cadherins on the surface of engulfing cells, thereby enhancing the capacity to engulf and eliminate live cells. Importantly, engulfing cells exhibited genomic instability and activated a p21-dependent, oxidative stress-dependent senescence program that suppressed tumor growth. Histopathological detection of Senescence in breast cancer tissues following the initiation of neoadjuvant chemotherapy was associated with a positive outcome with regard to treatment-induced tumor involution and patient survival. Inversely, the suppression of senescence favored the proliferation of aneuploid cannibal cells, the emergence of genomic instable daughter cancer cells with robust survival advantages and was associated with disease progression. Altogether, esults indicate that senescence induced internalization is a novel non-cell autonomous program of senescence that compromises the fitness of cannibal cells, thereby antagonizing their oncogenic potential

Keywords: Cyclin-dependent kinase inhibitor, Senescence, Cellular Cannibalism

PL/IL-20

E. Democracy in the European Union: Exploring the Potential of Digital Technology

Tasneem Sultana

Area Study Center of Europe, University of Karachi

Corresponding Author: tasneemsultana0766@gmail.com

Abstract

European Union is the largest liberal democracy, and strongest regional organization in the World, working on both supranational and intergovernmental lines. For Supranationalism EU establish institutions e.g. European Commission, European Parliament, European Council, European Court of Justice etc. Among all these institutions only the European Parliament is a directly elected body of 720 members, represents around 450 million people of 27 member states. The motto of European Union is Unity in Diversity thus, the European Parliament and European Courts operates in 24 languages, the Judges, the Members of the European Parliament (MEPs) speak and access documents in their preferred language. All the legislations, court decisions, and communications with EU institutions are also available in 24 languages. Translators use wide range of IT application tools and technologies for speedy and error free documents through computer-assisted translation (CAT) tools. The E. Parliament during its plenary sessions uses electronic voting machines. Moreover, before the 2024 E. Parliament elections, to safeguard the fundamental rights, the EU legislate the Digital Space including the AI Act (considered as the world's first comprehensive regulation on artificial intelligence), for online campaigning and elections to ensure fundamental rights; including democracy, the rule of law and environmental protection. To safeguard the harmful effects of the AI system, the Digital Service Act (DSA) covers several areas related to AI in elections, ensuring transparency, accountability, and the integrity of electoral processes; significantly curtail disinformation campaigns during elections. Some of the EU members already using E. votes and data-driven campaign technologies. This research paper focuses on the relationship between democracy and digital technology in Europe and the widespread presence of digital technology promote or undermine democracy in Europe.

Keywords: European Union, democracy, digital technology, AI, E. Parliament, diversity

PL/IL-21

Application of an Indigenous, Low-Cost, and Sustainable Floating Treatment Wetlands Technology for Wastewater Treatment and Reuse

Muhammad Afzal[1], Muhammad Shoaib Hassan[1], Salman Younus[1], Samina Iqbal[1]

National Institute for Biotechnology and Genetic Engineering Faisalabad Pakistan

Corresponding Author: manibge@yahoo.com

Abstract

In Pakistan, due to very high capital and operational costs of conventional technologies, > 99% wastewater is discharged in water bodies untreated. This wastewater contaminates the water, soil and food. To address this issue of high cost of wastewater treatment, a very low-cost floating treatment wetlands (FTWs) technology has been developed using locally designed and developed floating mat and available indigenous plants and microbes. FTWs is a low cost, sustainable, and environment friendly technology for wastewater treatment and reuse. It requires ~100 times lower capital investment than conventional technologies, without any operational cost. Until now 500,000 sq ft FTWs have been applied at more than 100 sites in Pakistan and it improves the quality of about 500 billion cubic meter wastewater annually, and sequesters 300 tons of carbon per year. It removes (up to 90%) both organic and inorganic pollutants from the wastewater, and treated water is being safely discharge in the environment or reuse in agriculture and horticulture.

Keywords: Floating Treatment Wetlands, Low cost, Wastewater Treatment

---

PL/IL-22

Coinfecting Parasites in A Warming World: Temperature Dependent Virulence and Microbial Competition in Nematode Hosts

Ian Will

University of British Columbia, Kayla King Group, Vancouver, Canada.

Corresponding Author: Ian.will@ubc.ca

Abstract

Different parasite species often coinfect individual hosts in nature, altering disease outcomes in ways not predicted by one-host one-parasite paradigms. Simultaneously, climate change subjects organisms to thermal stresses, which can modify pathogenicity and resistance. We performed laboratory experiments to test how these two major factors, coinfection and thermal stress, can shape disease together. We leveraged a model system using nematodes

(*Caenorhabditis elegans*) singly or co- infected by two *Leucobacter* bacteria species, which naturally coinfect *Caenorhabditis*. Hosts were infected across a range of temperatures that (i) spanned the host thermal optimum to past its reproductive viability and (ii) reflected the natural climate of these *Leucobacter* species. We found temperature controlled which parasite species was the primary driver of virulence, but that across temperatures, coinfection protected hosts from peak single-infection virulence. Our results contribute to exploring the “thermal mismatch hypothesis”, which relates fitness outcomes to relative host-parasite(s) performance at different temperatures.

Keywords: Climate Change; Nematodes; Host-Parasite; Virulence

---

PL/IL-23

Recombinant Dna Technology for Enzymes Production for Poultry Feed Industry

Muhammad Tayyab

Institute of Biochemistry and Biotechnology, University of Veterinary and Animal Sciences, Lahore, Pakistan

Corresponding Author: muhammad.tayyab@uvas.edu.pk

Abstract

Poultry sector is one of the major established industries of Pakistan that is committed to provide valuable meat to our community. Phytases, cellulases, xylanases and proteases are the main enzymes being added in the poultry feed. The addition of these enzymes is important because their addition in feed put a positive impact on the growth of poultry bird. Phytases are responsible for the availability of free phosphorus while the xylanases and cellulases are responsible for the availability of monomeric absorbable sugars for the growth of bird whereas proteases also involve for the improvement of digestion of proteins. In the absence of these enzymes the phytate, cellulose and xylan are not being digested by the poultry bird and these components of feed simply pass through the digestive track and are removed from the body with manure and contribute in environmental pollution. In the current study the phytase, cellulase and xylanase genes from hyper-thermophilic bacterium were amplified by using the PCR and ligated into the cloning vector pTZ57R/T. These vectors were transferred in the *E. coli* DH5α cells. The expression of phytase, cellulase and xylanase genes were analyzed in *E. coli* BL21CodonPlus cells with the help of pET expression system. Recombinant proteins were purified through different chromatographic techniques and their molecular masses were determined through SDS-PAGE. Recombinant proteins were characterized. The locally produced recombinant enzymes were utilized for supplementation of poultry feed to examine their effect on the growth of poultry birds. The supplementation of poultry feed with locally produced enzymes showed significant growth enhancing effect on poultry birds and improved the feed uptake and feed conversion ratio.

Key Words: Poultry Enzymes, Recombinant Proteins, Hyper-thermophilic Bacterium

PL/IL-24

Phage Therapy: A Targeted Approach to Control Poultry Colibacillosis

Atif Jamal[1], Liloma Shah[1], Muhsin Jamal[1,] * Muhammad Asif Nawaz [2], Muhamamd Ali [3]

1 Department of Microbiology, Abdul Wali Khan University, Garden Campus, Mardan, Pakistan
2 Department of Biotechnology, Shaheed Benazir Bhutto University, Sheringal, Dir (U), Pakistan
3 Department of Life Sciences, School of Science, University of Management and Technology, Lahore

Corresponding Author: muhsinjamal@awkum.edu.pk

Abstract

In poultry and livestock, massive economical losses are caused due to common veterinary infection termed as colibacillosis. Unrestrained usage of antibiotics accounted for the spread and appearance of MDR bacterial strains and has lowered the efficacy of conventional treatment regimes for infectious illnesses. This encouraged the renewed curiosity in phages amongst scientists since the start of the 21st century. Phages are prevalent in nature and go together with bacterial species within every setting they colonize, comprising the warm-blooded animals microbiota. The key objective of the current study was to isolate and characterize a phage infecting multi-drugs resistant (MDR) *E. coli.* A new phage named as MJ-DMR-1 was isolated from waste water against MDR *E. coli-3018*. Diverse characteristics of the phage MJ-DMR-1, such as one- step growth, pH stability, heat stability, host range, and effect of Mg^{2+} and Ca^{2+} ions on adsorption rate of phage to its host bacterial species were investigated. Well defined boundaries and clear plaques were made by the phage MJ-DMR-1 with size ranging from 2.0-3.6 mm having a narrower host range attacking very limited isolates of designated bacteria under study. Phage MJ-DMR-1 displayed an optimum multiplicity of infection of 0.1-1. Morphological investigation showed that phage MJ-DMR-1 belonged to *Myoviridae* family of order caudovirales, comprising a contractible tail 20 nm wide, 160 nm in length and a head of 65 nm. It was likewise stable at pH 7. Adsorption rate of phage to its host bacterial specie was boosted when bacterial specie was treated with solutions of $CaCl_2$ or $MgCl_2$ as liken to control. One-step growth curve investigation showed that, the latent time was about 32 minutes, and the burst size was round about 550 virions per cell. The phage MJ-DMR-1 showed a deleterious effect against *E. coli-3018* planktonic culture reducing bacterial growth significantly as compared to control (without phage). Consequently, we concluded from this study that MJ-DMR-1 was a lytic phage with high potential to be used as a therapeutic agent against bacterial infections in poultry caused by *E. coli.* These features could serve as a guideline for selecting potential candidates for phage therapy to control collibacillosis in poultry.

Keywords: Bacteriophage, Colibacillosis, Poultry, Antibiotic Resistant. Avian Pathogenic *Escherichia coli*

PL/IL-25

Leveraging System Biotechnology and Metagenomics Towards Sustainable and Optimized Production of Polyhydroxyalkanoates

*Temitope O. Fadipe[1,2], Blas Blázquez[2,3], Funmilayo T. Dada.[1], Olumide Afolabi [4], Folusho O. Oluwaloni[1] and Juan Nogales[2,3]

[1]*Biotechnology Department, Federal Institute of Industrial Research Oshodi, Lagos, Nigeria.*
[2]*Department of Systems Biology, Centro Nacional de Biotecnología, CSIC, Madrid, Spain.*
[3]*Interdisciplinary Platform for Sustainable Plastics towards a Circular Economy-Spanish National Research Council (SusPlast-CSIC), Madrid, Spain.*
[4]*Department of Biological Sciences, University of Africa, Toru- Orua, Sagbama,*
Bayelsa, Nigeria.

Corresponding Author: topesalaam@gmail.com

Abstract

Plastics are synthetic polymers and have become integral to meeting daily human domestic and industrial material needs due to their durability and thermal properties. However, their excessive utilization and non-degradability have been associated with negative impacts on human and animal health and ecosystem imbalance. This has led to increase in research and development of ecofriendly and sustainable biopolymers. Polyhydroxyalkanoates (PHAs) are intracellular biopolymers produced by some bacteria as energy storage under conditions of limiting nutrients and excess carbon. PHAs have comparable physical, chemical and mechanical properties to synthetic polymers and as a result are suitable candidate polymers for the production of ecofriendly bioplastics. Several PHA biosynthetic bacteria have been identified and classified based on their PHA polymerase type. Metagenomics has also greatly advanced the detection and identification of culturable and non-culturable PHA biosynthetic bacteria in environmental samples. With particular focus on the class IV PHA polymerases, we have expressed the PHA operon of *Bacillus pacificus* in *Escherichia coli* DH5α using the Golden Gate approach. We have also optimized a method for the transformation of *B. subtilis* 168 with pJL74 plasmid expressing the reporter gene, *gfp* and thus unlocking its potential as a novel microbial factory for PHA production. Furthermore, we employed 16S rRNA metagenomics approach to characterise the PHA bacterial communities in Olusosun landfill soil. With the Golden Gate approach, functionalized DNA parts including, *phaA, phaB, phaC* and *phaR* genes, promoter, ribosomal binding site and terminator were successfully cloned into plasmids (pSEVA182 and pICH41308) and transformed in *E. coli* DH5α. Such DNA parts were further used to construct transcriptional units of *phaA, phaB, phaC* and *phaR*. Afterwards, they were assembled in a synthetic polycistronic operon using the Golden Standard. The final cluster was successfully confirmed in *E. coli* DH5α. Positive green, fluorescent clones of *B. subtilis* 168 were obtained following transformation with pJL74-*gfp*. With respect to the detection and identification of PHA bacterial communities by metagenomics, the V3/V4 regions of the 16S rRNA gene of DNA isolated form Olusosun landfill soil was sequenced on the PacBio HiFi amplicon sequencing platform and analyzed on Qiime2 amplicon pipeline. The results revealed the presence of bacteria belonging to the four PHA biosynthetic classes. Identified bacteria include *Enterobacter* (class I), *Pseudomonas* (class II), *Paracoccus*, *Rhodococcus* (class III), *Priestia* and *Lysinibacillus* (class IV). In a nutshell, we have demonstrated that the Golden

Standard can be effectively utilized in the synthetic assembly of the PHA operon for further expression in model and non-model bacteria within the context of the industrial production of PHAs. We have also shown that the metagenomics approach was useful for the detection and characterization of novel PHA biosynthetic bacterial species from soil.

Keywords: Bacteria, Biopolymer, Polyhydroxyalkanoates, PHA polymerase, Golden Gate, Metagenomics

PL/IL-26

The Replication-Associated Protein Encoded by Cotton Leaf Curl Multan Alphasatellite Overcomes the Host's Transcriptional Gene Silencing Mechanism

Qamar Abbas

Department of Biology, Lahore Garrison University, Lahore

Corresponding Author: qamar92@lgu.edu.pk

Abstract

Alphasatellites are non-essential satellite-like entities associated with geminiviruses, though their exact role in enhancing geminivirus infection remains uncertain. The ability of the replication-associated protein (Rep) encoded by the cotton leaf curl Multan alphasatellite (CLCuMuA) to suppress transcriptional gene silencing (TGS) was studied using *Nicotiana benthamiana* line 16-TGS, which carries a transcriptionally silenced green fluorescent protein (GFP) transgene. When 16-TGS plants were inoculated with a recombinant Potato virus X (PVX) vector containing CLCuMuA Rep, GFP expression was restored. Northern blot analysis revealed that the GFP fluorescence observed correlated with GFP mRNA accumulation. Similar results were obtained with PVX vectors carrying Rep proteins encoded by six genetically distinct alphasatellites, demonstrating restored GFP expression in 16-TGS plants. These findings suggest that the alphasatellite-encoded Rep can reactivate the expression of transcriptionally silenced GFP transgenes in *N. benthamiana*, highlighting the role of alphasatellites in countering host defense mechanisms.

Kewwords: Alphasatellites, GFP Expression, Green Fluorescent Protein (GFP)

PL/IL-27

A Paradigm Shift: From Conventional Methods to AI Tools in Protein Structure Analysis

Muhammad Fayyaz ur Rehman

Institute of Chemistry, University of Sargodha

Corresponding Author: muhammad.fayyaz@uos.edu.pk

Abstract

Artificial intelligence (AI) has brought a paradigm shift in biochemistry, medicine and pharmaceutical research by increasing the efficiency, accuracy and reliability of protein structure modeling and drug discovery. AI-driven approaches can be combined with the existing protein structure analysis methods, including NMR, X-ray crystallography, Cryo-EM, ab-initio modelling, and molecular dynamics (MD) simulations. This merger is transforming our understanding of molecular interactions and accelerating the identification of potential therapeutic compounds. AI is helping researchers to forecast protein-ligand interactions accurately, assess toxicity, and conduct pharmacokinetic studies in a shorter time and at reduced costs compared to traditional approaches. MD simulations further strengthen these insights by sorting detailed snapshots of molecular behavior for a deeper exploration of conformational dynamics and stability, which is necessary for effective drug targeting. This talk will illustrate how the protein structure analysis is optimized by integrating NMR, mass spectrometry and conventional computational tools integrate with AI tools. By getting help from real-world cases, I will show the successful conventional approaches in drug development, starting from early virtual screening to lead optimization. By combining the theoretical frameworks and practical implementation, the aim is to encourage researchers to make possible ethical use of AI tools for protein structure, ligand interactions and MD simulations in their research. It also envisions a future where these complementary technologies are fully embedded within the biochemistry labs, molecular biology processes, and drug development lifecycle, revolutionizing how we conceptualize, design, and deliver next-generation therapies.

Kewwords: Artificial intelligence, Molecular Dynamics (MD) Simulations, X-ray Crystallography

PL/IL-28

Intrinsically Disordered Region of CDC14A is Essential for Hearing in Human and Mouse

Ayesha Imtiaz[1], Kanwal Shabbir[1], Derek Logan[2], Thomas B. Friedman[3]

[1]School of Biological Sciences, Punjab University, Lahore
[2]Lund Protein Production Platform (LP3), Lund, Sweden.
[3]National Institute on Deafness and Other Communication Disorders, NIH, Bethesda, USA.

Corresponding Author: ayeshasbs@gmail.com

Abstract

A large proportion of the proteins or their regions lack a defined 3D structure under physiological conditions, such proteins or regions are termed as intrinsically disordered proteins (IDP) or regions (IDR). Human CDC14A is a 623-residue protein, it comprises of a globular N-terminal catalytic domain and a long intrinsically disordered region (IDR) comprising of 278 amino acids at the C-terminus. Mutations affecting N-terminal globular domain cause hearing impairment infertile male syndrome (HIIMS) while mutation in the IDR cause isolated hearing loss. By biochemical structural and functional studies, we are trying to understand this phenotype-genotype correlations and importance of IDR of CDC14A in hearing.

Keyword: *CDC14A* (Cell Division Cycle 14A), hearing impairment infertile male syndrome (HIIMS), hearing loss, dual specificity phosphatase, Recombinant protein

---

PL/IL-29

Protein Engineering Approaches to Improve Catalytic Properties of Archael Lysophospholipases

Arshia Nazir, Muhammad Sajjad

School of Biological Sciences University of the Punjab

Corresponding Author: m_sajjad_khattak@yahoo.com; sajjad.sbs@pu.edu.pk

Abstract

In the first part of the study, detailed *in silico* analysis of wild-type LPL from *P. abyssi* was performed followed by its recombinant production in *Escherichia coli* using pET expression system. The recombinant enzyme was purified through affinity chromatography and characterized. The enzyme was remarkably thermostable at 65 to 85 °C. The enzymatic activity was independent of the metal ions tested. Kinetic parameters including K_m, V_max and k_{cat}) were also calculated for 4-nitrophenyl butyrate. In the second part of the study, protein engineering methods were employed to improve the thermostability and solubility of the recombinant enzyme, Pa-LPL. A truncated variant of LPL (tLPLΔ12) was constructed with deletion of a 12 amino acid residue loop to rigidify the 3D structure. The truncated enzyme was found to be more thermostable than the wild-type enzyme at 65 and 95 °C. The kinetic parameters have no significant differences between the two enzymes. Further, SUMO fusion technology was also used to check its effect on Pa-LPL activity, stability and solubility. Fusion of SUMO improved the thermostability at different temperatures tested.

Key words: Protein engineering, Archaeal enzymes, *Pyrococcus abyssi*, Lysophospholipase, Enzyme kinetics, Thermostability

---

PL/IL-30

Saccharification of Plant Biomass Utilizing Nano-Coupled Glucanase from *Clostridium Clariflavum* for Low-Cost Bioethanol Production

Muhammad Nauman Aftab

Institute of Industrial Biotechnology, Government College University Lahore

Corresponding Author: director.iib@gcu.edu.

IL-31

The Phage-like Gene Transfer Agent and its Receptor

Nawshin Alim

Department of Microbiology & Immunology, University of British Columbia

Corresponding Author: ntbalim@student.ubc.ca

Abstract

Horizontal gene transfer (HGT) in prokaryotes is responsible for important processes from antibiotic resistance transfer to rapid adaptation and speciation. The phage-like gene transfer agent (GTA) is a mobile genetic element that carry out HGT, but are distinct from those involved in transformation, transduction, or conjugation. Phage-mediated HGT (transduction) spreads antibiotic resistance and virulence genes in pathogens. Up to 109 /mL of phage-like particles, including GTAs, are found in aquatic environments. *Rhodobacter capsulatus* is a model organism and its archetype RcGTA is the most well-understood. Only <3% cells in any population of *R. capsulatus* produces RcGTA and these cells lyse to release the particles at stationary phase. While all living cells of recipient strains can receive genes via RcGTA, some environmental strains of *R. capsulatus* are not capable of receiving RcGTA-mediated genes. They make suitable candidates to study the RcGTA-receptor binding mechanism. Recent cryogenic electron microscopic analyses have revealed the complete RcGTA structure revealing a morphology that is analogous to those of tailed phages. Both the head and the tail have multiple receptor-binding proteins (RBPs). The goal of my project is to elucidate the binding mechanism of the RcGTA to recipient cells. The capsular polysaccharide (CPS) of recipient cells is understood to be the primary receptor that the RcGTA head spike binds to. I hypothesize that the head spike protein degrades the CPS to facilitate binding to a second receptor. The tail fiber protein, which has sequence and structural homologies with oligosaccharide-binding proteins, is predicted to bind the secondary receptor on the outer membrane and I hypothesize that this receptor is the lipopolysaccharide (LPS) of *R. capsulatus* recipient cells. Wild-type genome library complementation, screening LPS-mutants created by site-directed mutagenesis, and biochemical analysis of LPS and CPS are being employed in this study.

Keywords: Horizontal Gene Transfer, Bacteriophages, Gene Transfer Agents, Extracellular Polysaccharides, cryo-EM

PL/IL-32

Eco-Benign Silver Nanoparticles for Antimicrobial Applications

Hammad Arshad[1*], Umer Hassan[3,4] & Saima Sadaf[2]

[1] Department of Biology, Lahore Garrison University, Lahore, Pakistan
[2] School of Biochemistry & Biotechnology, University of the Punjab, Lahore. Pakistan
[3] Department of Electrical and Computer Engineering, School of Engineering, Rutgers the State University of New Jersey, Piscataway, NJ, USA
[4] Global Health Institute, Rutgers the State University of New Jersey, New Brunswick, NJ, USA

Corresponding Author: hammadarshad@lgu.edu.pk

Abstract

Antimicrobial resistance (AMR) is one of the top global health issue. One of the possible remedies for AMR is the use of silver nanoparticles (AgNPs) due to their exceptional anti-microbial properties. The current research presents an efficient strategy for the synthesis of biogenic AgNPs for biomedical applications. Contrary to the physical and chemical methods of synthesis, our approach entails the use of plant-based materials i.e., *Aloe vera* and *Salvadora persica*, hence both ecofriendly and cost-effective. The synthesis was optimized under variable conditions for fastest AgNPs preparation. The AgNPs were comprehensively characterized using UV-visible spectroscopy, FTIR, TEM, SEM DLS and ICP-OES. Further, the immobilization of the AgNPs onto cellulosic and non-cellulosic materials was studied. Antimicrobial efficacy of AgNPs and the immobilized materials was evaluated using Gram-positive *Staphylococcus aureus* and *Staphylococcus epidermidis*, Gram-negative *Escherichia coli*, *Acinetobacter baumannii, Pseudomonas aeruginosa*, and the fungus *Candida albicans* by Kirby-Bauer method and serial dilution method. The cytotoxicity of SpNPs was studied using freshly isolated human WBCs. Light induced AgNPs were synthesized robustly in 10 minutes at room temperature. All the AgNPs presented size range of <100 nm with spherical shape, crystalline structure and involvement of phytochemicals in reduction and capping of NPs. All AgNPs were effective against tested pathogens with or without MDR properties. LED-based and heat-based immobilization of AgNPs on filter paper presented promising microbial inhibitory effect. The lowest MIC and MBC was noted as <1.0 µg/mL in SpNPs. The green synthesized AgNPs are easy to synthesize and are a cost-effective alternative to inorganic AgNPs produced with reducing chemicals, with considerable antimicrobial activity, deserving further investigations for biomedical applications.

Keywords: Antimicrobial Resistance, Silver Nanoparticles, UV-visible spectroscopy

---

PL/IL-33

Resistance Strategies of *Microbacterium* sp. strain 1S1 against Heavy Metals and Its Potential Use to Clean Metal-Contaminated Wastewater

Abdul Rehman

Institute of Microbiology and Molecular Genetics, University of the Punjab, Lahore 54590, Pakistan

Corresponding Author: rehma.mmg@pu.edu.pk

Abstract

A multiple metal resistant *Microbacterium* sp. strain 1S1, which tolerated arsenite and arsenate upto 75 and 520 mM, was isolated from industrial wastewater. The arsenite surface adsorption and uptake into the bacterial cells, exposed to 15 mM arsenite, were confirmed through Scanning Electron Microscope (SEM), Energy Dispersive X-ray (EDX), and Fourier-transform infrared spectroscopy (FTIR) analyses. The cell physiology of strain 1S1 altered in arsenite exposure, and the percent increase in GSH/GSSG ratio and NPSHs concentration was up to 40.0 and 78.50%. Furthermore, a 240% increase in catalase proved that arsenite induces hydrogen peroxide mediating oxidative stress. The bacterial cells growing in a rich medium with 15 mM arsenite were able to oxidize 98% arsenite after 96 h of incubation, and the inactivated biomass of the bacterium at 1 g per liter removed 99% of 15 mM arsenite after 10 h of incubation. The harboring of multiple resistance strategies and appreciable arsenic oxidizing potential make strain 1S1 an impending foundation for green chemistry to exterminate environmental arsenite.

Keywords: Metal Resistant, Scanning Electron Microscope, Fourier-Transform Infrared Spectroscopy

ORAL PRESENTATIONS

ORAL PRESENTATIONS

OP-1

Harnessing Clinical and Lifestyle Factors: A Comprehensive Approach for Diabetes Classification and Prediction using Supervised Learning

Muhammad Ubaid Ur Rehman[1*]

[1]HITEC University, Taxila

[*]**Corresponding Author:** mubaid63@gmail.com

Abstract

Diabetes mellitus is a chronic disorder and metabolic disease that can cause severe complications in human body such as osteoporosis, cardiovascular diseases, diabetic neuropathy, diabetic retinopathy, blurred vision and limb loss etc. The common symptoms of diabetes include higher frequency of urination, increase in thrust and hunger, unexplainable weight gain or loss. The early detection and prediction of diabetes mellitus can save an individual from these complications. In scientific literature most of the earlier studies have addressed this issue however, there is a pressing need to develop more personalized model for early diabetes prediction and classification by incorporating relevant clinical and lifestyle factors alongside existing clinical data to further refine risk stratification and inform preventive measures. This study proposes an enhanced, innovative classification and personalized diabetes prediction model that utilizes machine learning to analyze clinical data of diabetes patients, enabling proactive prevention and intervention strategies to combat the rising diabetes epidemic within a community. The experimentation in this study is performed using multiple regression and classification algorithms such as Random Forest Regressor, Linear Regressor, Support Vector Regressor, Decision Tree Regressor, Ridge Regressor, KNeighbor Regressor, Xg Boost Regressor, Random Forest Classifier, Decision Tree Classifier, Naïve Bayes and Extra Tree Classifier. To evaluate effectiveness of each experimentation, there was a need of clinical data of diabetes patients. For that reason, authors collected a clinical data of 768 female patients from the National Institute of Diabetes and Digestive and Kidney Diseases. The selection of this dataset is two-fold because it is publicly available and it contains significant clinical data such as "No of Pregnancies", "Average Glucose Level", "Blood Pressure", "Skin Thickness", "Insulin Level", "Body Mass Index", "Weight", "Family History of Diabetes" and "Age of Patient". The study results have indicated that Linear Regressor can effectively determine accurate blood glucose level with a root mean square error of 0.2381 as compared with other implemented regressor algorithms. Similarly, Random Forest classifier can significantly classify diabetes instances with an accuracy of 0.84. The discussion in this study concludes that machine learning techniques can effectively analyze clinical data of diabetes patients to identify patterns and relationships between clinical factors and diabetes incidence. By utilizing these patterns, personalized prediction and classification models can be developed to empower individuals and healthcare providers to make informed decisions and implement strategies to prevent diabetes or delay its onset.

Keywords: Diabetes Mellitus; Diabetes Classification; Diabetes Prediction; Machine Learning; Supervised Learning.

OP-2

Comparison of Traditional and Probiotic Yogurt in Relation to their Impact on Pediatric Acute Diarrhea Patients

Izma Zahir [1*]
[1] University of Management and Technology

[*]**Corresponding Author:** izma.zahir@umt.edu.pk

Abstract

Yogurt itself is known to contain probiotic bacteria but the beneficial bacteria present in it does not survive during their passage from the gastrointestinal tract. Therefore, supplementing yogurt with a probiotic species can make it a functionally beneficial dairy product. The aim of this study was to develop traditional and probiotic yogurt, to assess its nutritional composition, and to evaluate its effectiveness in terms of treating diarrhea. Lyofast-LA3 strain of Lactobacillus acidophilus and Bifidobacterium bifidum BB04 were used to supplement yogurt prepared with the standard culture. The traditional yogurt was prepared in the conventional way. After that, proximate composition and clinical intervention were evaluated. The preparation stages represent a gradual improvement in the sensorial properties of both the yogurts. While the proximate analysis of traditional and probiotic yogurt indicated no significant difference in their nutritional composition. The intervention of probiotic and traditional yogurt, resulted in a significant difference between the two groups. After 72 h of administration of probiotic yogurt, only 8% of participants passed watery stool in the experimental group while in the control group, 48%, that is, almost half, of the subjects still passed watery stools. While the frequency remains the same in both groups, about 88% of children passed stool 1–3 times per day at the end of intervention.

Keywords: probiotic, Yogurt, *Lactobacillus acidophilus, Bifidobacterium bifidum*, nutrition

---

OP-3

Drug Discover in the Treatment of Esophageal Squamous Cell carcinoma.

Shahraiz Butt[1*]
[1] University of Management and Technology

[*]**Corresponding Author:** f2023254006@umt.edu.pk

Abstract

Keywords: Drug discovery, Cancer, Squamous cells, Treatment

OP-4

Isolation of Pectinase from *Bacillus Halotolerant Sp.* LC3 Utilizing *Persea Americana* Waste for Sustainable Enzyme Production

Laiba Abdul Manan[1*]

[1] Lahore College for Women University, Lahore

[*]**Corresponding Author:** laibamanan77@gmail.com

Abstract

With the rising demand for eco-friendly and cost-effective enzymes in industries such as textiles, food processing, pharmaceuticals, and paper and pulp manufacturing, researchers have increasingly turned to natural sources, including microorganisms like fungi, yeast, and bacteria, as well as plants. Among these, pectinase has gained significant attention due to its role in plant fiber processing, fruit juice clarification, and pectin wastewater treatment. In this study, a pectinolytic bacterium was successfully isolated from avocado (*Persea americana*) peel using the repeated streaking method. Molecular identification through 16S rRNA sequencing confirmed the strain as *Bacillus halotolerant sp.*, a potent pectinase producer. The enzyme exhibited optimal activity under specific conditions: a temperature of 40°C, an incubation period of 72 hours, pH 8, and a substrate concentration of 1.5% pectin. Furthermore, sucrose, yeast extract, and NaCl were identified as the most effective carbon, nitrogen, and metal ion sources, respectively, for bacterial growth and enzyme production. To purify the enzyme, ammonium sulfate precipitation was performed at different saturation levels. SDS-PAGE analysis was conducted to determine the molecular weight of the extracted protein, confirming its purity and structural characteristics. The findings of this research highlight the potential of avocado peel as a valuable waste-derived resource for enzyme production, contributing to sustainable biotechnological applications.

Keywords: Avocado, pectinase production, enzyme purification, sustainability, Bacillus

OP-5

Drug discovery for the treatment of monkey pox virus

Aiman Aftab [1*], Dr. Rana Muhammad Mateen[1], Dr Sohail Afzal[1]

[1] Department of Life Sciences, School of Science, University of Management and Technology

[*]**Corresponding Author:** f2023254009@umt.edu.pk

Abstract

Monkey pox is a double standard DNA enveloped virus caused by monkey pox virus. It is a zoonotic viral disease with symptoms similar to small pox that can be transmitted from animal to humans or human to human, an orthopoxvirus (OPXV). MPXV specifically belongs to Chrodopoxvirinae sub family and Poxviridae family member. The antiviral drugs and current vaccines are insufficient because of rapidly increasing MPXV outbreak. Currently, no drug has been specifically designed against MPXV that emphasized the urgent need of developing effective antiviral treatments. As a result, in- silico techniques have shown effectiveness in disease research and drug discovery. To discover medicines, modern techniques of drug designing such as drug repurposing may help to provide the more instant solutions. In this study, A42R, phosphatase H1 and mRNA capping enzyme regulatory subunit E12 of MPXV was chosen as an antiviral target. We used phytochemical library (IMMPAT) containing 17967 compounds that were screened out on the basis of ADMET criteria. After careful evaluation, the selected ligands were then virtually screened to identify the potential inhibitor against the target proteins of MPXV through molecular docking, density functional theory and MD simulation. Also, tecovirimat was used as reference compound for this study. It was approved by FDA as antiviral drug during 2022 outbreak. For the targeted proteins, the binding energy of reference compound was -8.3kcal/mol, -6.3kcal/mol and -7.0kcal/mol. The identified common ligand with the lowest binding energy for targets is Medicarpin 3-O-glucoside (PubChem ID: 23724664) with -9kcal/mol of A42R protein, Ceroptene (PubChem ID: 42607662) with -7.9kcal/mol of phosphatase H1 and Trichosetin (PubChem ID: 91819764) with -8.4kcal/mol of E12 subunit as potential compounds for the prevention and treatment of monkey pox virus disease.

Keywords: In-silico study; Monkeypox virus (MPXV); A42R profillin, Phosphatase H1; E12 subunit; molecular docking; Density functional theory (DFT); molecular dynamic (MD) simulation

OP-6

Title

Ayesha Malik [1*]

[1] University of Management and Technology

[*]**Corresponding Author:** F2021232015@umt.edu.pk

Abstract

Keywords:

OP-7

In-silico analysis of plant-derived secondary metabolites against thyroid disease

Kainat Shahid [1*]

[1] University of Management and Technology

[*]**Corresponding Author:** F2023254007@umt.edu.pk

Abstract

Keywords: Secondary metabolite, thyroidism, in-silico, plant-derived, treatment

---

OP-8

Teratogenic and Embryotoxic Effects of Pyrazinamide in Albino Mice

Ghulam Fatima Saleem[1*], Ata Ul Mustafa Fahid[1*], Zainab Akhtar[1], Sadia Ahmad[1], Chaman Ara[1], Asma chaudhary[2], Muhammad Amad Sarwar[3]

[1] 1Institute of Zoology, University of the Punjab, Lahore, Pakistan

[2]Department of Zoology, Division of Science and Technology, University of Education, Lahore, Pakistan

[3]School of Mathematics Nanjing University of Aeronautics and Astronautics, Jiangsu province, China

[*]**Corresponding Author:** gfsaleem99@gmail.com, fahidchaudhry786@gmail.com

Abstract

In this study, the embryotoxic effects of the anti-tuberculosis drug pyrazinamide were assessed in pregnant mice. Various concentrations of pyrazinamide (0.00, 4.00, 8.00, and 10.00 µg/g body weight) were administered orally to the pregnant mice on days 6 through 12 of gestation. On day 18 of gestation, the fetuses were recovered and subjected to morphological, morphometric, and histological examinations. The primary aim was to evaluate the potential toxicity of pyrazinamide on the developing embryos. Morphological analysis revealed a range of abnormalities, including hemorrhages, hydrocephaly (accumulation of fluid in the brain), microphthalmia (abnormally small eyes), and various limb deformities such as forelimb micromyelia (underdeveloped limbs), hyperextension, drooping wrists, low-set arms, and hindlimb dysplasia. Additionally, spinal abnormalities such as scoliosis (curved spine), sacral hygroma (fluid-filled sac near the spine), open eyelids, and curly tails were observed. These defects appeared to increase in severity with higher doses of the drug, suggesting a dose-dependent relationship. Morphometric studies also indicated significant reductions ($P<0.001$) in fetal body weight, crown-rump length (CR length), head circumference, eye circumference, forelimb and hindlimb size, and tail length compared to control fetuses. This reduction in growth parameters points to intrauterine growth retardation caused by the drug. Histological examination revealed neural tube defects, pericardial hemorrhage, and hepatic necrosis (liver cell death) as additional signs of toxicity. Based on the observed abnormalities in morphology, growth parameters, and histology, it is concluded that pyrazinamide is embryotoxic and potentially toxic to developing mice. This study highlights the importance of assessing the safety of drugs like pyrazinamide during pregnancy to minimize risks to fetal development.

Keywords: pyrazinamide, embryotoxic, retardation, intrauterine

---

OP-9

Antagonistic Effects of Aspirin and Pomegranate Juice Induced in Developing Mice

Zainab Akhtar[1*], Ata Ul Mustafa Fahid[1*], Ghulam Fatima Saleem[1], Sadia Ahmad[1], Chaman Ara[1], Asma chaudhary[2], Muhammad Amad Sarwar[3]

[1] Institute of Zoology, University of the Punjab, Lahore, Pakistan

[2] Department of Zoology, Division of Science and Technology, University of Education, Lahore, Pakistan

[3] School of Mathematics Nanjing University of Aeronautics and Astronautics, Jiangsu province, China

[*]**Corresponding Author:** zainabakhtar4157@gmail.com, fahidchaudhry786@gmail.com

Abstract

This study aimed to assess the fetotoxic effects of aspirin, a commonly used antihypertensive drug, during gestation, and to evaluate the ameliorative effects of pomegranate juice against its toxicity. Pregnant mice were administered aspirin by gavage in different doses: a high dose of 3.5 µg/g body weight (B.wt.) and a low dose of 2.65 µg/g (B.wt). The drug was administered daily from the 6th to the 12th day of gestation for a total of seven days. Throughout the study, several congenital abnormalities were observed in the fetuses, including hemorrhages, hygromas (fluid accumulation), resorbed fetuses, deformed and hyperextended limbs, hyperactive flexed limbs, distorted spinal axis, and signs of intrauterine growth retardation. These findings indicate that the administration of aspirin, especially during the critical organogenesis period, can have detrimental effects on fetal development. Additionally, the study investigated the potential protective role of pomegranate juice in mitigating these harmful effects. The results showed that pomegranate juice significantly reduced the severity of the detrimental effects caused by aspirin. This suggests that pomegranate juice may possess antioxidant or other protective properties that help counteract the toxicity induced by aspirin. In conclusion, while aspirin may pose risks to developing embryos, especially during organogenesis, the use of pomegranate juice may offer a promising avenue for ameliorating these adverse effects. This study emphasizes the need for careful consideration when administering antihypertensive drugs during pregnancy and highlights the potential therapeutic benefits of pomegranate juice in reducing drug-induced toxicity.

Keywords: aspirin, pomegranate juice, mice embryo

OP-10

Deleterious nsSNPs of EpCAM Gene (EPCAM-202): Insilico analysis of Structural and Functional Effects

Ubaid Ur Rehman[1]

[1] Minhaj University Lahore

*Corresponding Author:** m.ubaid.rehman007@gmail.com

Abstract

EpCAM is a transmembrane glycoprotein having a basic purpose of interactions, adhesion and structural integrity of epithelial tissue. It is highly expressed in colon, endometrium, gall bladder, liver, bile, pancreas, kidney and thyroid tissue of humans and its high expression is found in cancers of colon, pancreas, prostate, breast, gastric and head and neck cancer. The study aimed to highlight the most deleterious nsSNPs, and identify functional, structural and stability changes along with post translational modifications, phenotypic changes domains and interactions of EpCAM. About 37 bioinformatics tools and databases were used to find and analyze damaging nsSNPs. SNPs and their information was gathered from databases like Ensemble, NCBI and UniProt. 12 deleteriousness predicting tools were used including CADD v1.7, SIFT v6.2.1, PolyPhen-2 v2.2.3, REVEL, MetaLR, MutationAssessor v4.7, PROVEAN v1.1, MutPred2, SNPs&GO, PHD-SNP, E-SNPs&GO and PANTHER 19.0 which were followed by I-Mutant2.0 v0.7, INPS-MD, iStable and MUpro 1.0 for stability prediction. Addition of new or loss of post translational modification was predicted by GPS-MSP 3.0, NetPhos 3.1, NetNGlyc-1.0, NetOGlyc 4.0, MusiteDeep, PRmePRed, iPhoPred, PhosphoSVM, RUBI and GPS-Uber. ConSurf, InterPro v102.0, GeneMANIA and STRING v12.0 were used for conservation, domains, gene-gene and protein-protein interaction analysis respectively. Project HOPE v1.1.1, SWISS-MODEL, PROCHECK, ERRAT, PyMOL v3.0 and Discovery Studio were used for structure-related analysis. The study highlighted seven nsSNPs from EPCAM-202 which are the most highly deleterious nsSNPs as they are highly destabilizing, deleterious, cause PTM, phenotypic changes and show high deviation from the wild-type structure having a high probability of playing a role in cancers and syndromes. Studying these seven nsSNPs is highly significant as it can reveal the gene's association with cancers, syndromes, medicinal and therapeutic strategies. Further in-vitro analysis can reveal their relation and prevalence among the population.

Keywords: Glycoprotein, Cancer, in-vitro, Ep-CAM

OP-11

Environmental Challenges Faced by Pakistan's Tourism Sector: Impactful Solutions for Environmental Sustainability

Talat Rafi[1*], Tasneem Sultana[1]

[1] Area Study Centre for Europe, University of Karachi.

[*]**Corresponding Author:** talatrafirazakhan@gmail.com

Abstract

Environmental issues have been observed as extremely serious challenges all over the world and have accelerated during the mid-20th century. Scientists attribute this most noticeable trend to this period, where the rate of greenhouse gas (GHG) emissions has significantly increased. Many sectors such as tourism, agriculture, forestry, energy, health, fisheries, and industries, have been influenced by these challenges. Pakistan's tourism sector faces some noticeable challenges which threaten the industry's sustainability and reputation. Certain human activities in the tourists' hotspots such as burning of the fossil fuel causing deforestation, air pollution due to the overuse of plastic materials, food waste and overuse of transportation, consumption of electricity and oil, water contamination due to the throwing of garbage in the seas and rivers, noise pollution and loss of biodiversity due to the overuse of loudspeakers, use of pressure horns, loud music, bon fire etc., have all resulted into badly affecting the thriving tourism sector. Such activities are threats to the environment resulting into a great climate change like global warming, torrential rains, cloud bursts, floods and damage to the marine life, and coastal lines. This study aims to identify these challenges through a comprehensive literature review, media reports, and visual evidence from major tourists' locations in Pakistan. Furthermore, it explores some impactful solutions, such as ecotourism practices, sustainable transportation systems, effective waste management strategies, and targeted awareness campaigns to mitigate these environmental challenges. The descriptive study provides actionable recommendations for Pakistan's tourism industry stakeholders, policymakers, and tourists to promote sustainable environmental development, create a positive image of Pakistan's tourism industry and ensure environmental sustainability.

Keywords: Environmental, Challenges, Pakistan's Tourism, Activities, Sustainability, Solutions

OP-12

Title

Rida Ijaz[1*]

[1] University of Lahore

[*]**Corresponding Author:** rida55malik@gmail.com

Abstract

Keywords:

OP-13

Title

Rabiya Maham[1*]

[1] University of Management and Technology

[*]**Corresponding Author:** rabiyamaham12@gmail.com

Abstract

Keywords:

OP-14

Efficacy Of Organic Farming Against Charcoal Rot of Chickpea (Cicer Arietinum)

Sundus Akhtar, Asma Maryyum and Ayesha Shafqat

School of Biology (Botany Section), Minhaj University Lahore.

Abstract

Chickpea (*Cicer arietinum L.*)) is an important and most consumable legume crop cultivated in the arid region of Pakistan, the fourth highest producer of this crop in the world. Charcoal rot disease caused by *Macrophomina phaseolina* (MP) is an important disease affecting chickpea production. Fungicides are mostly used to control charcoal rot; however, these cause environmental pollution and pose adverse effects on the ecosystem. Therefore, ecofriendly management options are inevitable for the management of charcoal rot disease. The charcoal rot infestation was induced by inoculating the soil with M. phaseolina, and the impacts of the different treatments of farmyard manure (0.5 %, 1 %, 1.5 % and 2 %) were studied on the disease infestation, growth, yield, biochemistry and physiology of chickpea. The results revealed that farmyard manure used for the management of charcoal rot disease through regulating the antioxidant enzymes' activities and strengthening the immune system of chickpea plants. Farmyard manure also improved the soil physiochemical properties and beneficial microbes' activity which released antimicrobial protein- and plant defense- stimulating protein and in response to ROS (reactive oxygen species) signaling molecules plant susceptibility was reduced. The studied total chlorophyll content, soluble sugar, total protein content, catalase and peroxidase were significantly altered by the applied treatments. The findings of the experiment indicated that farmyard manure used to enhance the crop yield and manage charcoal rot disease in chickpea. This paper reports that the farmyard manure is easy-to-apply, cost-effective, ecofriendly and sustainable option for the management of charcoal rot disease in chickpea.

Keywords: farmyard manure, rot disease, ROS, chickpea

OP-15

Replacement of fishmeal with selected plant by- product artificial feed of *Labeo rohita*

Sadaf Aman[1]*, and Muhammad Ashraf[2]

[1] School of Zoology, Minhaj University Lahore, Pakistan

[2] Faculty of Fisheries and Wildlife, University of Veterinary and Animal Sciences Lahore,

***Corresponding Author:** sadafaman.zoology@mul.edu.pk

Abstract

This study was conducted to determine the effect of plant by products by replacing fish meal with soybean meal, sunflower meal cotton seed meal, guar meal and rice polish. Pelleted feed and powder feed were given to the fish and kept in fiberglass tanks. This experiment was continued for the 90 days. Control group was fed with Oryza feed organics having 30% CP. Treatment 1 was based on fishmeal powder while treatment 2 was without fishmeal powder. Treatment 3 and 4 were similar to diet 1 and 2 respectively but were pelleted. Physico-chemical parameters were monitored on daily basis but nitrate and phosphate were checked after three days and there was positive correlation between phosphates and nitrates with treatment T 1 and T 3. Growth rate were measured on every fortnightly survival and body weight increments were measured on every fortnight. In organoleptic test tenderness was high in fishmeal pellets (T 4) but significantly acceptable higher in treatment 1 (T 1). Red blood cells and white blood cells were significantly higher in Group T 1 than all its counterparts.

Keywords: Replacing fish meal, Plant based feed, Labeo Rohita, Growth performance

OP-16

Effect of nitrogen, phosphorus and potassium on the bio mass production of Spirogyra

Nadia Jabeen[1*], RimshaArshad[2], Muhammad Hammad Ashraf[3], Ishrat Fatima[4]

[1] School of Botany, Minhaj University Lahore

[2] Department of Botany, University of the Punjab, Lahore.

[3] Government Dyal Singh Graduate College Lahore

[4] Department of Biological Sciences, University of Veterinary and Animal Sciences

***Corresponding email:** drnadia.bot@mul.edu.pk

Abstract:

The current research investigated the effect of nitrogen, phosphorus, and potassium on the biomass production of Spirogyra hyaline cleve.Of all the nitrogen sources used [$(NH_4)SO_4$, NH_4Cl, $NaNO_3$, $Ca(NO_3)_2$, and $Co(NO_3).6H_2O$], $Ca(NO_3)_2$ gave the optimum biomass production (18.2 gL^{-1}).The volumetric rate of biomass production (3.9) and specific rate of biomass production (2.47) was significantly high than other nitrogen sources. Particularly, 2.0% of $Ca(NO_3)_2$ resulted in significantly high product yield coefficient (1.74), volumetric rate of biomass production (4.7) and specific rate of biomass production (1.54) . Further increase in the concentration decreased the biomass production. Among all the phosphorus sources [Na_3PO_4, $(NH_4)_3PO_4$ and K_2HPO_4], K_2HPO_4 yielded the optimum biomass production (20.4 $g\,L^{-1}$) with 0.5 $g\,L^{-1}$ resulted in maximum biomass production of 22.4 $g\,L^{-1}$. Further increase in the concentration insignificantly decreased the biomass production. Moreover, from various potassium sources [KNO_3, KH_2PO_4, $K_2Cr_2O_7$, and $KNaC_4H_4O_6$], KH_2PO_4 resulted in significantly high volumetric rate of biomass production (2.1) and specific rate of biomass (3.65), with 0.5$g\,L^{-1}$ showing the maximum biomass production of 18.6 $g\,L^{-1}$. Further increase in the concentration significantly decreased the biomass production. Additionally, when tested in modified and control media, the production of algal biomass was gradually increased in both media and reached optimum after 18 days of incubation (13.1 $g\,L^{-1}$ and 10.3$g\,L^{-1}$ respectively). Therefore, standard media gave better results and was selected for optimum biomass production of Spirogyra hyaline cleve.

Keywords: Algal biomass production, Impact of nutrients, Spirogyra.

OP-17

HPLC-Based Elucidation of Tannins from Leaf, Stem Seedling Tissue, and Callus Culture Extracts of Selected Medicinal Plants

Madieha Ambreen [1], Safdar Ali Mirza [2], Zahida Bano [3] And Muhammad [3]

[1] School of Biology, Botany section, Minhaj University, Lahore, Pakistan

[2] Department of Botany, GCU, Lahore, Pakistan

[3] University of Doha for Science and Technology

Corresponding author: madiha.ambreen@yahoo.com

Abstract

Optimized HPLC profiling is a powerful and effective analytical tool for standardizing plant samples and authenticating plant materials. In this study, three selected medicinal plants—Achyranthes aspera, Ipomoea hederacea, and Ocimum basilicum—were subjected to callus induction following seedling, leaf, and stem germination. The induced callus was subsequently dried, finely ground, and extracted using methanol and water for HPLC analysis. A validated procedure was employed to identify and separate the tannin content in seedling leaf, stem, and callus culture extracts. The highest callogenic response was observed in A. aspera leaf explants cultured on MS medium supplemented with 2.0 mg/L 2,4-D and 4.0 mg/L NAA. These callus cultures exhibited a green color and granular morphology. Conversely, the lowest callogenesis response was noted in I. hederacea stem explants grown on MS medium supplemented with 0.5 mg/L 2,4-D and 0.5 mg/L BAP, resulting in brown-colored, granular callus. HPLC fingerprinting was performed using a Shimadzu LC-20A system with a retention time of 2.9 minutes at 270 nm to ensure quality consistency in tannin analysis across different plant parts. Among all explants and callus culture samples, O. basilicum leaf callus culture extract exhibited the highest sample area (9365.56) and the highest tannin content (95.04%). Furthermore, the tannin content of O. basilicum (2.66) and A. aspera (7.81) leaf callus culture extracts demonstrated superior precision and accuracy in relative standard deviation values compared to stem seedling tissues and other callus culture extracts.HPLC profiling proves to be an accurate, efficient, and precise method for evaluating tannin content in selected plant samples. Moreover, these plants hold significant potential for isolating bioactive compounds in pure form, which could be harnessed for pharmaceutical applications. The optimized chromatographic fingerprint serves not only as an alternative analytical tool for authentication but also as a crucial method for standardizing the quality of medicinal plant compounds.

Key words: Medicinal plant, explants, callus culture, HPLC, analytical tool

---

OP-18

Title

Asifa Roohi[1]

Alumni UMT

Corresponding author: asifaroohi313@gmail.com

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 encapsidation 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 and two RNA SLs designated as B and H in the current study have significant role in MS2 encapsidation. 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 structure 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: Protein-protein interactions, protein-genome interactions, prediction, ssRNA viruses

OP- 19

Artificial Intelligence Based Diagnostic Solution for Newcastle Disease Detection in Poultry

Badar Un Nisa[1], Sohail Raza[1*], Arfan Ahmad[1], Muhammad Muddassir Ali[2], Muhammad Ilyas Riaz[1], Riasat Wasee Ullah[3]

[1]Institute of Microbiology, University of veterinary and animal sciences, Lahore.

[2]Institute of Biochemistry and Biotechnology, University of veterinary and animal sciences, Lahore.

[3]Food and Agricultre Organization of the United Nations (FAO), Islamabad

Corresponding author: sohail.raza@uvas.edu.pk

Abstract

Newcastle disease is one of the most widespread and devastating poultry diseases, causing a high mortality rate that leads to significant economic loss and reduced productivity worldwide. Early diagnosis is crucial to control its outbreaks; however, many farmers face challenges in accessing laboratories, particularly in rural settings. To address this issue a novel approach was developed using image-based classification for rapid, accurate, and most importantly accessible disease diagnostic tool. In this study, the Convolutional Neural Network Model (CNN) was trained using broiler-dropping images classified as healthy or diseased. A total of 1,345 samples were collected from broiler birds and confirmed via PCR targeting the F-gene to construct an image dataset. Approximately 700 images, obtained both from poultry farms and controlled trials, were selected to train the baseline 2D CNN model, which was subsequently fine-tuned for improved performance. The model demonstrates high performance, achieving an accuracy rate of 95% during testing and 85% validation accuracy. Based on these results, deploying a baseline 2D CNN model at the farm level is highly recommended for efficient and cost-effective Newcastle disease diagnosis, ensuring timely intervention and improved poultry health management. While the model has shown promising results, further refinements are possible. Expanding the dataset with additional samples from diverse regions with varying environmental conditions could enhance its accuracy and cost effectiveness making the model a more robust and reliable diagnostic tool.

Keywords: Artificial intelligence, Baseline 2D Convolutional Neural Network Model, Newcastle disease, Deep learning, diagnostic tool.

OP- 20

Platelet Indices and C Reactive Protein as a Biomarker for Diagnosing Sepsis Types in Neonates

Hira Arshad[1]

[1]University of veterinary and animal sciences, Lahore.

Corresponding author: arshadhira110@gmail.com

Abstract

OP- 21

Computer Aided Drug Discovery of Potential Inhibitors Against Fatty Acid Binding Protein (FABP4) Involved in Colorectal Adenocarcinoma

Aymen Yaseen[1]

[1] University of Management and Technology

Corresponding author: F2023253010@umt.edu.pk

Abstract

Keywords:

OP- 22

Formulation and Characterization of Functional Muffins Supplemented with Synbiotics

Bareera Najeeb[1], Hafiz Ubaid ur Rahman[1], Urwa Tariq[1], Hafiz Muhammad Arslan Ghous[1], Nauman Khaild[1]

[1]School of Food and Agricultural Sciences, University of Management and Technology, Lahore

Corresponding author: Hafiz Ubaid ur Rahman (ubaidurrahman@umt.edu.pk)

Abstract

The increasing consumer demand for good nutritional foods with long shelf life has initiated the development of numerous functional products. There is scientific evidence that prebiotics and probiotics can impart a range of health benefits if consumed regularly. The aim of this study was to prepare functional muffins with pomegranate peel as prebiotics, Bifidobacterium bifidum as probiotics, and their combination as synbiotic. The effect of the fortification on muffin quality was determined by measuring texture, color and volume after baking under controlled conditions.

Texture profile was evaluated on texture analyzer using the compression test. The L*, a* and b* color values were recorded and used to calculate the browning index and total color change. To study the joint variability of the attributes for which significant differences were found, principal component analysis was applied to average scores of all parameters. Results showed that, after baking, the satisfactory viability growth of B. bifidum was seen in T3 (3% of pomegranate peel and 6% of B. bifidum) which was 106CFU/mL T4 (3% of pomegranate peel and 8% of B. bifidum)

showed 108CFU/mL and decreased during storage (T3 had 103 CFU/mL and T4 104CFU/mL). The viability of B. bifidum in the in-vitro Gastro-intestinal tolerance test was 102 CFU/mL in T1 and 103 CFU/mL in T4. Texture profile analysis using a compression test on a texture analyzer revealed that muffins with probiotic and synbiotic formulations maintained better texture. However, the addition of prebiotics to muffins resulted in harder samples with darker colors. Although the color profile did not vary significantly among the treatments, browning increased during the storage period of 7 days.

Keywords: Commercial probiotics, Pomegranate peel, Encapsulation, Synbiotic

---

OP- 23

Halal Gelatin Extraction from Fish Waste and Potential Applications in the Food Sector

Muhammad Usman[1], Hafiz Ubaid Ur Rahman[1], Amna Sahar[2,3]Anam Ishaq[1]

[1]School of Food and Agricultural Sciences, University of Management and Technology, Lahore

[2]National Institute of Food Science and Technology, University of Agriculture, Faisalabad, 38000, Pakistan

[3]Department of Food Engineering, University of Agriculture, Faisalabad, 38000, Pakistan

Corresponding author: usmanmurtaz@gmail.com

Abstract

Gelatin is the hydrolytic product of animal collagen. It is produced mainly by partial hydrolysis of collagen material, which involves the breakdown of collagens' primary, secondary, and tertiary structure. It is used as a foaming agent, thickener, texture stabilizer, emulsifying agent, and others in various food items that include dairy, puddings, ice cream, jelly, meat products, and beverages. Out of the total gelatin market share, mammalian gelatin accounts for more than 90 % of the share. With the highest proportions from pig sources, it is almost impossible to meet the demand for gelatin in the Halal market. Gelatin acceptability depends upon the animal source through which it is extracted. Bovine and porcine gelatins have limited acceptability due to religious prohibitions. For example, gelatin obtained from haram animals (pig, horse, donkey, dog, and others) as well as gelatin obtained from halal animals, but not slaughtered in an Islamic way is also prohibited for Muslim communities. So, there is a need to look for alternative sources for gelatin production. Fish solid wastes include different by-products such as bones, scales, and hides that are high in collagen content and account for up to 75% of the total body weight. These wastes can be utilized for the extraction of different products such as gelatin that can be used in different food and pharmaceutical industries. Fish gelatin can be used as a replacement for mammalian gelatin due to its nutritional profile as it contains all the amino acids; essential and non-essential. Fish gelatin cannot only be used as a replacement for bovine and porcine gelatin, but it also increases the utilization of fish waste and reduces pollution.

Keywords: Fish gelatin, waste utilization, halal and haram, gelatin authenticity

OP- 24

Formulation and characterization of goat milk candies supplemented with fennel and chia seeds

Qindeel Asif [1], Anum Ishaq[1], Iram Aslam[1]

[1]School of Food and Agricultural Sciences, University of Management and Technology, Lahore.

Corresponding author: anum.ishaq@umt.edu.pk

Abstract

This study aimed to provide an overview of the most recent research on the impact of plant additives on the physicochemical, functional, microbiological, and sensory aspects of yoghurts and its products. For this purpose, yogurt from goat milk was made and then used to make candies with different concentrations of fennel and chia seeds to check the effect on the overall properties of the product in a storage study of a week. The highest acidity value was seen in T4 (0.88±0.02). The highest Ash % was seen in T4 (1.74±0.21). The highest value for protein % was observed in T4 (10.33±0.39). The highest fat % value was also seen in T4 (3.93±0.41). The highest Brix % was seen in T3 (74.15±1.4). The highest value for TS was seen in T4 (57.29±1.5). The highest value for total phenolic content was present in T5 (367.9±13.4 mg GAE/100g) while the highest mean value for DPPH (%) was present in T2 (68.0±1.6). Total flavonoid contents were also identified. The highest mean value was present in T5 (4.72±0.10 mg QE/g). The highest mean value for water activity was present in T_o (0.682±0.06). The highest value for texture was present in T4 (13.9±4.3). Total plate count indicated high levels in T_o (140±95) CFU/g (log10) though it was within the standard as prescribed by Thai community product standard, frozen dried jelly (No.520/2547). No coliform was detected in any sample.

Keywords: Fennel seeds, Chia seeds, Goat milk yogurt

POSTER PRESENTATIONS

POSTER PRESENTATIONS

PP-1

Eco-Friendly Hydrogels from Natural Polymers: Improving Water Retention and Crop Yield in Arid Agriculture

Muhammad Aman[1], Laiba[1], Zartasha Nadeem[1], Muhammad Asad Anwar[1]

[1]Department of Bioinformatics and Biosciences Capital University of Science & Technology

[*]**Corresponding Author:** amaneiddique456@gmail.com

Abstract

Hydrogels, which are three-dimensional, cross-linked polymer networks, have gained significant attention for their water absorption and retention capabilities, making them particularly valuable in agriculture. With the global population expected to rise by 2.3 billion by 2050, agricultural productivity faces immense pressure, particularly in arid and semi-arid regions where water scarcity is a critical concern. This study hypothesizes that seed gum-based polysaccharide hydrogels, composed of natural polymers such as guar gum, sodium alginate, and pectin, with bentonite clay as a cross-linker, can improve soil moisture retention and provide a controlled release of water. These hydrogels are expected to offer a sustainable alternative to synthetic water retention agents, which often pose environmental risk due to their non-biodegradable nature. The objective of this research is to develop and characterize these seed gum-based hydrogels, evaluating their swelling capacity, water retention ability, and mechanical properties. By leveraging the biodegradable and eco-friendly nature of natural polymers, the study aims to enhance soil moisture in water-scarce environments, thereby promoting plant growth and improving agricultural yields. Although experimental validation has not yet been conducted, the anticipated outcomes suggest that these hydrogels will enhance water use efficiency, reduce the frequency of irrigation, and offer a more sustainable approach to addressing the challenges of water scarcity in agriculture. The research aims to contribute to sustainable agricultural practices, particularly in countries like Pakistan, where water management and soil health are critical for food security.

Keywords: Seed gum-based hydrogels, Water retention, Sustainable agriculture, Arid soils, Biodegradable polymers.

PP-2

Unveiling the Power of Tio2 Doped Zno Nanomaterial as an Effective Antimicrobial Solution in the Leather Industry

Asma Irshad[1], **Rabbia Jawad**[2], Uzair Ishtiaq*[3,4], Nicolas Joly[5], Bochra Bejaoui[6,7], Naceur M'Hamdi[8], Patrick Martin**[9], Firdous Mubashar[1]

[1]School of Biochemistry and Biotechnology, University of the Punjab, Lahore, Pakistan
[2]School of Biological Sciences, University of the Punjab, Lahore, Pakistan
[3]Department of Research and Development, Paktex Industries, 2.5 KM Tatlay Road, Kamoke, Gujranwala, 52470, Pakistan
[4]Department of Life Sciences, University of Management and Technology, Lahore, Pakistan
[5]Unite Transformations & Agroresources-ULR7519, Univ. Artois, Unilasalle, F-62408, Bethune, France
[6]University of Carthage, National Institute of Research and Pysico-chemical analysis (INRAP), Laboratory of Useful Materials, Technopark of Sidi Thabet, Ariana, 2020, Tunisia
[7]University of Carthage, Faculty of Sciences of Bizerte, Department of Chemistry, 7021, Zarzouna, Bizerte, Tunisia
[8]University of Carthage, National Agronomic Institute of Tunisia, Research Laboratory of Ecosystems & Aquatic Resources, Tunisia

Corresponding author: rabbiajawad000@gmail.com

Abstract

The surface protection of leather supplies is a major concern worldwide due to its susceptibility to microbial growth. Different methods are employed to protect leather, their results end up with the environmental pollution and human safety issues. Nanoparticles with excellent antimicrobial potential can provide sustainable protection to leather accessories. The present work represented a comprehensive investigation into the preparation and characterization of titanium dioxidedoped zinc oxide (ZnO/TiO2 NPs) nanoparticles and their exploring as a potential antimicrobial agent in the leather industry. ZnO nanoparticles were synthesized through Sol-gel method by the reduction of zinc acetate dihydrate via black cardamom seed's extract and subsequently doped with TiO2. The optical, structural, and morphological features of nanoparticles were thoroughly scrutinized through UV–visible spectroscopy, XRD, FT-IR, and SEM-EDAX. The UV–visible spectrum showed enhanced performance between 300 and 350 nm and various peaks of the FT-IR spectrum, i.e. 3315.53, 1566.20, 1402.25, 1340.53, 1014.56, 921.97, 690.52, and 677.01 cm^{-1}, revealed chemical bonds that prove the correct doping of TiO2 in ZnO nanoparticles. The characteristic peaks obtained from XRD at 2Ɵ of 32◦, 35.5◦, 37.2◦, 47.9◦, 55.6◦ 63.51◦, and 70◦ intimated to the crystal planes of (100), (002), (101), (102), (110), (103), and (112), respectively. SEM-EDAX images revealed the roughly spherical but agglomerated structure of nanoparticles with size 45.44 nm. Furthermore, minimum inhibitory concentration (MIC), antimicrobial potential, and anti-biofilm potential analyses of nanoparticles, against all selected microorganisms (*Aspergillus niger*, *Staphylococcus aureus*, and *Escherichia coli*) provided valuable insights into physical and biological properties of the nanoparticles. The clear zones of inhibition (29–30 mm) against these pathogenic strains showed exceptional antimicrobial action of the ZnO/TiO2 NPs. Overall, these results provide an approachable method to synthesize ZnO/TiO2 nanoparticles and their antimicrobial ability will prove to be beneficial for the protection of leather materials from various microbial contaminations.

Keywords: Antimicrobial potential; Leather materials; Microbial degradation; Surface protection; TiO2 doped ZnO nanoparticles

PP-3

Synthesis of Guar Gum Beads for Drug Delivery Application

Maheen Noor[1*]

[1]Lahore College for Women University

[*]**Corresponding Author:** maheennoor118@gmail.com

Abstract

Tramadol is an analgesic that need repetitive administration due to un-controlled release and low bioavailability in the body. In this research work, Guar Gum beads were synthesized by precipitation method for loading Tramadol HCl. The structural confirmation of prepared beads was accomplished by FTIR, SEM and XRD analysis. The swelling studies revealed the pH responsive behaviour of beads and showed the sustained release of the drug up to 12h at pH 7.4 which proved these beads to be effective drug carriers. The prepared samples were biocompatible, biodegradable and cost-effective drug carriers for a variety of analgesic drugs.

Keywords: Drug, Guar Gum, FTIR, Tramadol, Beads

PP-4

Synthesis of Biogenic Silver Nanopropolis for Burn Wound Treatment

Tuba Sajjad*[1]
[1]Lahore College for Women University
[*]**Corresponding Author:** tubasajid610@gmail.com

Abstract

Burn wound healing remains a critical challenge, and there is an increasing need for effective and cost-efficient treatments. This study explores the synthesis of Silver nanopropolis via a green approach, for burn wound healing treatment. Bee propolis, sourced from northeast Punjab, Pakistan, was extracted using maceration and analyzed for its high phenolic content, and utilized to reduce silver ions to prepare nanoparticles. The synthesized nanopropolis was characterized by using UV-Visible Spectroscopy (UV-Vis), Fourier Transform Infrared Spectroscopy (FTIR), Scanning Electron Microscopy (SEM), and X-ray Diffraction (XRD). Nanopropolis showed significant antioxidant (0.4696 μg ml−1) and anti-inflammatory (0.3996 μg ml−1), and antibacterial activity. An ointment formulated with silver nanopropolis and hydrogels was studied to treat burn wounds in rabbits. The results showed faster wound healing and more collagen deposition silver nanopropolis treated wounds compared to the control group

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

PP-5

Phenotypic Characterization of Mbl Enzymes in Urinary Tract Infection Causing Pathogens

Ghadir Ali1*[1], Ayesha Ahmed[1], Shehzeen Usman[1], Bisma Ali[1]

[1]Department of life sciences, University of Management and Technology

Correspondence to: Ghadir_ali@umt.edu.pk

Abstract

One prevalent bacterial infection is urinary tract infections (UTIs). People of all ages and genders are susceptible to UTIs, which are among the most common bacterial diseases worldwide. The area, population demographics, access to healthcare, and reporting habits can all affect epidemiological data on UTIs. An enzyme called metallo-βlactamase is resistant to the majority of antibiotics, especially when it comes to gram-negative bacteria. The Life Science Laboratory at the University of Management and Technology in Lahore provided the glycerol stocks of the bacterial isolates used in this investigation. The culture was then reconstituted and screened on agar plates for the formation of MBL. Using disc diffusion techniques, the antibacterial resistance against meropenem in the presence or absence of EDTA was found. Biochemical testing was used to identify and distinguish MBL manufacturers. Additionally, this study used Graph Pad Prism software for statistical analysis, namely the Chi-square test. Klebsiella spp. were the most common species in the bacterial isolates of the suspected UTI patients in the current investigation (100%). Three of the twenty-five bacterial isolates were found to generate MBL. Males had a lower percentage of isolates that produced MBL (8.33%) than females (15.3%), and the variation was not statistically significant (P=0.587).

Keywords; UTIs, MBL, Antibacterial resistance

PP-6

Insilico Drug Designing against Mutated Huntington Disease HTT Protein

Khadija Zafar[1*], Maria Kalsoom[1], Rameesha Fiaz[1], Saira Khadim[1].

Department of life Sciences, University of Management and Technology

Corresponding Author: F2024254020@umt.edu.pk

Abstract

Huntington's disease (HD) is a neurodegenerative disorder caused by a CAG repeat expansion in the HTT gene, leading to an abnormal huntingtin (Htt) protein with elongated polyglutamine strands. These protein aggregates are toxic to neurons, causing severe brain damage. While complete recovery from such damage remains unattainable, peptide therapy presents a promising approach for mitigating the disease's effects. Peptide-based treatment strategies focus on two classes: polyglutamine (poly Q) peptides and non-polyglutamine (non-poly Q) peptides. Among non-poly Q peptides, several have demonstrated neuroprotective and therapeutic potential. For instance, QBP1 targets polyglutamine repeats to prevent toxic protein aggregation, thereby slowing disease progression. Similarly, p42 has shown neuroprotective properties, potentially shielding the brain from further damage. Exendin 4, originally used for diabetes treatment, promotes neurite outgrowth and enhances neuronal viability. Additionally, ED11 and calmodulin (CaM) play crucial roles in calcium signaling, which is vital for synaptic plasticity and neuronal function. Binding Immunoglobulin Protein (BiP) contributes to protein folding and stress response, while Leuprorelin, a hormone-regulating peptide, may also support brain recovery. This diverse peptide-based strategy aims to facilitate neuroprotection, reduce the impact of brain damage, and potentially restore neural tissues. A key approach in peptide therapy is designing peptides that selectively bind to the mutant Htt protein, preventing toxic aggregation. By masking aggregation-prone sites, these peptides may halt the disease's progression and alleviate symptoms. Our poster presentation focused on screening peptides with anti-aggregation properties, comparing their binding affinities to homology-modeled Htt protein, and designing novel peptides based on conservation analysis. By leveraging prior peptide therapies, our study has developed a promising therapeutic strategy for Huntington's disease, offering hope for improved patient outcomes.

Keywords: Huntington’s disease, HTT gene mutation, neurodegeneration, peptide therapy, poly Q & non-poly Q peptides, protein aggregation, neuroprotection, QBP1, p42, Exendin 4, ED11, CaM, BiP, Leuprorelin, neuronal recovery.

PP-7

Isolation and Characterization of Bacteria from Soil Samples and their Role in Plant Growth Promotion

Eisha Naveed*[1]

[1]Department of Life Sciences, University of Management and Technology

Corresponding Author: S2024254002@umt.edu.pk

Abstract

Soil enormous microbial diversity influences soil fertility and crop health through nutrient recycling and organic matter degradation. Our study aimed to 1) Isolate and purify bacteria from rhizosphere soil samples, 2) Morphological, biochemical characterization, and identification of isolated bacteria and 3) Screening of plant growth promoting capability of identified bacterial isolates. Seven bacteria, three from mint soil and four from lettuce rhizospheric soil, were isolated, purified, and characterized. Gram staining, endospore staining, and acid fast staining performed along with ten different biochemical tests for bacterial identification. Plant growth promoting potential of isolates was determine by their growth on Pikovskaya's agar medium and plant microbe interaction. Isolate Mnt1 showed phosphate solubilization ability. Isolate Mnt1 and Ltc4 showed the maximum increase in *Zea mays* plant growth compared to the control and other isolates application. Based on the results, isolate 1M has plant growth promoting potential that can be utilized to enhance crop yield at commercial scale. It can be used to produce effective biofertilizers of economic importance. Isolate Mnt1 showed increased plant width by 80% and Ltc4 showed 44% increased weight. Moreover, Isolate Mnt2 showed negative impact and reduced plant growth, reduced plant's weight by 53%.

Keywords: Soil sample from Mint and Lettuce rhizosphere, Bacterial Isolation, Purification, bacterial characterization, *Zea mays* plant growth, Biofertilizer

PP-8

Whole Genome Scan and Selection Signatures for Climate Adaption in Yanbian Cattle

Musab Rasool[*1], Usman Ali[1], Quratulain Hanif [1,2] Jiafei Shen[2], Yang Cao[2], Yongsheng Yu[2], Chuzhao Lei[2]

[1]Department of Life Sciences university of Management and Technology Lahore

[2]Northwest A&F University, China

[*]**Corresponding Author:** musabrasool57@gmail.com

Abstract

Yanbian cattle is inhabitant of North of China, exhibiting many phenotypic features, such as long, dense body hair, and abundant intramuscular fat, designed to combat the extreme cold climate adaption. In the current study, we studied the cold tolerance of nine Yanbian cattle by whole genome resequencing and compared with African tropical cattle, N'Dama, as a control group. Yanbian cattle was aligned to the Bos taurus reference genome (ARS-UCD1.2) yielding an average of 10.8-fold coverage. The positive selective sweep analysis for the cold adaption in Yanbian cattle were analyzed using composite likelihood ratio (CLR) and nucleotide diversity ($\theta\pi$), resulting in 292 overlapped genes. The strongest selective signal was found on BTA16 with potential mutation in CORT gene, a regulatory gene of primary hormone in the hypothalamic-pituitary-adrenal (HPA) axis, is reported to be associated with the cold stress, represented four missense mutations (c.269C > T, p.Lys90Ile; c.251A > G, p.Glu84Gly; c.112C > T, p.Pro38Ser; c.86G > A, p.Pro29His). Meanwhile another gene on BTA6, showed significantly higher selective sweep signals for a cold adapted trait for hair follicle and length development, FGF5 (fibroblast growth factor 5) with a missense mutation (c.191C > T, p.Ser64Phe). Moreover, cold adapted Yanbian cattle was statistically compared with the hot adapted N'Dama cattle, a taurine cattle reported to show superior heat tolerance than zebu cattle, making them better adapted to the hot regions of Africa. XP-CLR, Fst, and $\theta\pi$ ratio were used to compare both breeds, yielding 487, 924, and 346 genes respectively. Among the 12 overlapped genes, (CD36) (c.638A > G, p.Lys 213Arg) involved in fat digestion and absorption plays an important role in membrane transport of long-chain fatty acid and its expression could increase in cold exposure. Henceforth, our study provides a novel genetic insights into the cold climate adaptation of Yanbian cattle and identified three candidate genes (CORT, FGF5, and CD36), which can add to an understanding of the cold climate adaptation of Yanbian cattle.

Keywords: cold adaptability, positive selective, *CD36, CORT, FGF5*

PP-9

Global dispersal and adaptive evolution of domestic cattle: a genomic perspective

Qurat-ul-Ain Hanif,[1] Sofia Shehzad*[1]

[1]Department of Life Sciences, University of Management and Technology

Corresponding Author: sophia09shehzad@gmail.com

Abstract

Domestic cattle have spread across the globe and inhabit variable and unpredictable environments. They have been exposed to a plethora of selective pressures and have adapted to a variety of local ecological and management conditions, including UV exposure, diseases, and stall-feeding systems. These selective pressures have resulted in unique and important phenotypic and genetic differences among modern cattle breeds/populations. Ongoing efforts to sequence the genomes of local and commercial cattle breeds/populations, along with the growing availability of ancient bovid DNA data, have significantly advanced our understanding of the genomic architecture, recent evolution of complex traits, common diseases, and local adaptation in cattle. Here, we review the origin and spread of domestic cattle and illustrate the environmental adaptations of local cattle breeds/populations.

Keywords: UV exposure, Stall-feeding systems, local adaptation, Adaptive evolution

PP-10

Functional Foods: Shaping the Future of Nutrition and Health

Noor ul Huda[1], Anam Saquib[1]

[1]Quintech Centre for Applied Sciences (QCAS), Lahore

*Corresponding Author: noor.huda61100@gmail.com

Abstract

Functional foods manifest the convergence of nutrition and health, serving as bedrock of therapeutic nutrition. In recent years, functional foods have gained immense importance for combating significant health challenges such as nutritional deficiencies, cognitive and immunity-related disorders. Functional beverages are recognized as important segment of functional foods offering added nutraceutical value along with taste and hydration. These beverages encompass a range of healthier dietary alternatives as probiotic drinks, essential oil flavored drinks, fortified juices and organic vinegar infusions. Functional beverages exhibit additional health benefits due to vitamins, minerals and biologically active components, mainly based on terpenoids, flavonoids, phenols, aldehydes and ketones. Functional foods aligning with consumer dietary preferences not only improve human health but also supports sustainability, paving the impactful way to ensure zero hunger, good health and well-being. Therefore, scientific advancements in development of functional foods offer promising path towards evolving demand of personalized nutrition, disease prevention and sustainable food.

Keywords: Functional food, Nutraceutical product, Functional beverages, Personalized nutrition, Sustainable food

PP-11

Salmonella Bio-Burden Reduction in Commercial Broiler Birds by *Salmonella* Phage Therapy

Aman Ullah*[1], Anam Saquib[1]

[1]Quintech Centre for Applied Sciences (QCAS), Lahore

*Corresponding Author: amanullahkanjan3578@gmail.com

Abstract

Salmonella is a bacterium that is responsible for the most common gastrointestinal illnesses and can cause food-borne infections. The emergence of multi-drug resistant (MDR) in bacterial strains worldwide is a major threat, representing a major challenge in public health. To reduce its incidence, the One Health approach is required, and the development of new bio-control protocols will help eliminate or prevent the spread of *Salmonella*. The need for alternative bio-control methods has led to the use of bacteriophages or viruses that target bacteria, as promising tools. Thus, the aim of this study was to evaluate the efficacy of phages as a biocide against *Salmonella*. In this study seven *Salmonella* bacteriophages isolated and purified from the sewage and the feces of the broiler farm. Two phage, Spa4 and Salm8 were selected on the bases of both phage have no lytic activity against each other host strains. The phage cocktail was given to broilers raised in commercial conditions at a 9 log PFU/dose for eight doses, while naturally occurring Salmonella cells colonized in the gastrointestinal tract of broilers were significantly reduced as suggested by a considerably lower Salmonella prevalence after 4-5 days of phage treatment. Our findings suggest that a phage cocktail is an effective bio-control agent to reduce *Salmonella* present in the guts of broilers, which can be applied to improve food safety in broiler production.

Keywords: *Salmonella*, Multi-drug resistant (MDR), One Health approach, Bio-control, Bacteriophages, Phage cocktail

PP-12

In Silico Development of a Multi-Epitope Vaccine Against Nipah Virus Causing Fatal Encephalitis in Humans

Afeera Farooq*[1]

[1]Department of Life Sciences, University of Management and Technology

Corresponding Author: S2024254005@umt.edu.pk

Abstract

Prostate cancer is a cancer that occurs in the prostate gland. It is one of the common types of cancer in males as it affects one in seven men. This study is aimed to identify hub genes that have a role to play in the occurrence of cancer and to analyze their interaction levels with FDA approved drugs. To those means, used microarray datasets GSE46602 (36 PCa patients and 14 controls), GSE69223 (15 PCa patients and 15 controls), GSE30994 (3 PCa patients and 3 Controls) and a RNA seq dataset GSE104131 (16 PCa patients and 16 controls). By taking a Bioinformatics approach, I was able to identify ten hub genes (CAV1, GSTM3, GSTM4, CYP3A5, PRKCA. GJA1, PGR, S100A6, ACSS3 and AOX1). We took forward the top 3 of these genes and docked them with the FDA approved drugs we selected after screening them. As a result, achieved docking results with Bicalutamide, Estramustine, Enzalutamide, Rucaparib, Olaparib, Apalutamide and Darolutamide. As a result, I was able to conclude that the identified hub genes all have potential to act as biomarkers for localized prostate cancer, and that GSTM4 can be considered as a useful element in the prognosis of prostate cancer based on its significant interaction with the FDA approved drugs.

Keywords: Prostate cancer, mRNA, RNAseq, Hun genes, Biomarkers, Molecular docking, FDA approved drugs

PP-13

Comparative Analysis, Diversification, and Functional Validation of Plant Nucleotide-Binding Site Domain Genes

Ayesha Malik[1], Esha Imran[1], Aquib Nazar[1,3], Khirman Baloch[1], Athar Hussain[2,3*]

[1]Department of Life Sciences, University of Management & Technology, Lahore

[2]School of Food and Agricultural Sciences, University of Management & Technology, Lahore

[3]Genomics & Informatics Lab, Lahore

[*]**Corresponding Author:** athar.hussain@umt.edu.pk

Abstract

Nucleotide-binding site (NBS) domain genes are one of the super family of resistance genes involved in plant responses to pathogens. The current study identified 12,820 NBS-domain-containing genes across 34 species covering from mosses to monocots and dicots. These identified genes are classified into 168 classes with several novel domain architecture patterns encompassing significant diversity among plant species. Several classical (NBS, NBS-LRR, TIR-NBS, TIR-NBS-LRR, etc.) and species-specific structural patterns (TIR-NBS-TIR-Cupin_1-Cupin_1, TIR-NBS-Prenyltransf, Sugar_tr-NBS etc.) were discovered. We observed 603 orthogroups (OGs) with some core (most common orthogroups; OG0, OG1, OG2, etc.) and unique (highly specific to species; OG80, OG82, etc.) OGs with tandem duplications. The expression profiling presented the putative upregulation of OG2, OG6, and OG15 in different tissues under various biotic and abiotic stresses in susceptible and tolerant plants to cotton leaf curl disease (CLCuD). The genetic variation between susceptible (Coker 312) and tolerant (Mac7) Gossypium hirsutum accessions identified several unique variants in NBS genes of Mac7 (6583 variants) and Coker312 (5173 variants). The protein–ligand and proteins-protein interaction showed a strong interaction of some putative NBS proteins with ADP/ATP and different core proteins of the cotton leaf curl disease virus. The silencing of GaNBS (OG2) in resistant cotton through virus-induced gene silencing (VIGS) demonstrated its putative role in virus tittering. The presented study will be further helpful in understanding the plant adaptation mechanism.

Keywords: GaNBS, cotton, CLCuD, Nucleotide-binding site (NBS), abiotic stresses

PP-14

Biodegradation of Textile Effluent Azo Dyes Using Coriander Stems Coated with Adapted Bacteria

Hadia Yasir[1*], Kalsoom Moazam[1]

[1]Department of Life Sciences, University of Management and Technology

Corresponding Author: hadiayasir26@gmail.com

Abstract

Azo dyes are a class of synthetic dyes that are widely used in various industries such as textile, pharmaceutical and printing. They dyes are characterized by the presence of azo groups (-N=N-) in their molecular structure and are used because of their vibrant colors. But these dyes are known to have toxic or carcinogenic properties, that are threatening to both aquatic life and environment. Thus, it is essential to remove this pollutant from wastewater intended for discharge into water bodies. Traditional methods of using activated carbon adsorption or chemical treatment can be used but again, these are costly and challenging to environment. This study proposes a novel and eco- friendly approach of utilizing coriander stem coated with dye degrading bacteria as a bioactive filtration system for azo dye biodegradation. The method integrates both adsorption (by coriander stems) and biodegradation (by bacteria) to enhance dye removal efficiency. Hence coriander stem, typically regarded as an agriculture waste is a game-changer for this approach which have been previously reported for heavy metal remediation like arsenic and lead. In this proposed study, bacterial strains such as *Bacillus* and *Pseudomonas* were isolated from textile effluent samples and screened for their ability to degrade specific dyes. The planned methodology includes coating coriander stems with isolated bacteria and then introduced into azo dye-contaminated water, and decolorization efficiency will be evaluated using UV-Vis spectrophotometry. Control experiments with uncoated coriander and bacteria alone were conducted to compare performance. It is hypothesized that the bio-coated coriander system would achieve faster and more efficient dye removal than bacteria alone, owing to the dual action of adsorption and biodegradation. Furthermore, coriander stems would provide a stable support system for bacteria, preventing their washout in continuous water flow systems. Unlike synthetic carriers, coriander stems are biodegradable and can be easily removed post-treatment through filtration. Additionally, they can be composted or converted into biochar, reducing waste accumulation. This approach provides a low-cost, scalable, and environmentally sustainable alternative for textile wastewater treatment. Future research will explore optimizing bacterial strains and assessing long-term system stability. If successful, this approach could provide a practical and environmentally sustainable alternative to existing wastewater treatment methods.

Keywords: Azo dye biodegradation, coriander stems, bacterial biofilms, textile wastewater treatment, sustainable bioremediation.

PP-15

Biomechanical Stimulation in Stem Cell Culture: A Cost-Effective Alternative to Growth Factors

Aneshra Nabeel*[1], Faiza Qaisar Dar[1], Inshal Aamer[1]
[1]Department of Life Sciences University of Management and Technology

[1]**Corresponding Author:** aneshra.nabeel17@gmail.com

Abstract

Stem cell culture follows conventional procedures that use basic fibroblast growth factor (bFGF) to preserve pluripotency while supporting cell growth. The expensive nature of recombinant growth factors together with their unpredictable batch-to-batch variation creates major obstacles for using these factors in clinical practice and research applications. Research now investigates cost-effective alternatives through plant-based bFGF and advanced bioreactor systems. The plant-derived (bFGF) shows advantages with lower contamination risks and production expenses yet several scalability issues and quality consistency problems and long-term delivery requirements must be addressed. The controlled environment of bioreactor-based suspension cultures and perfusion systems provides conditions similar to in vivo conditions which leads to better stem cell proliferation and differentiation. The implementation of these systems faces restrictions due to their complexity and high operational costs and scalability limitations which negatively affect cell viability and quality. Stem cell behaviour remains sensitive to improper optimization of oxygen transfer and shear stress parameters in bioreactors. Biomechanical stimulation has proven itself as a cost-effective solution to manage stem cell behaviour while promoting growth and stemness without needing expensive growth factors. Mechnotransduction pathways enable this method to deliver physiological cues that direct stem cell fate while providing a financially sustainable solution. Additional research needs to establish standardized biomechanical stimulation protocols which can be combined with present culture systems to prove their effectiveness for industrial and clinical large-scale use. The abstract examines current developments and pricing aspects together with restrictions of biomechanical stimulation methods relative to growth factor-based approaches. It emphasizes the need for further research to establish its feasibility for real-world applications in regenerative medicine, tissue engineering, and large-scale stem cell production.

Keywords: Biomechanical stimulation, stem cell culture, growth factors, bioreactors, cost-effective alternatives, regenerative medicine

PP-16

Robust Synthesis of New Spiropyrazoline in Deep Eutectic Solvent

Muneeba Aamer[1*], Erum Akbar Hussain[1]

[1]Department of Chemistry, Lahore College for Women University

[*]**Corresponding Author:** muneebaaamer3@gmail.com

Abstract

Spiropyrazolines are the compound having a unique spirocyclic junction where two rings converge at the C-5 Carbon. These spirocyclic molecules are significant interest to both medicinal and synthetic chemists due their enriched bio-profile. Conventional methods often employ volatile organic solvents which poses significant threat to environment. In this research, deep eutectic solvents have been used and compared with ethanol for the synthesis of spiropyrazolines, providing a more sustainable and environment friendly synthetic approach. All derivatives were confirmed by spectroscopic techniques. This method utilized mild reaction conditions which resulted in improved yield, reduced reaction time and minimal complexities.

Keywords: Spiropyrazolines, volatile organic solvents, synthetic, eutectic solvents

PP-17

miR-21-Mediated Regulation of Neural Stem Cell Differentiation: A Path to Neuronal Fate Commitment and Regenerative Medicine

[1]Faiza Qaisar Dar[1*], [1]Aneshra Nabeel, [1]Inshal Aamer

[1]Department of Life Sciences, School of Science, University of Management and Technology, Lahore Pakistan

[1]**Corresponding Author:** faiza19bsbt@gmail.com

Abstract

Neural stem cells (NSCs) hold immense promise for regenerative medicine due to their ability to differentiate into various neural cell types, contributing to neurogenesis and neuronal regeneration. The microRNA miR-21 has been shown to play a critical role in regulating cell proliferation, differentiation, and apoptosis across various biological processes, but its specific involvement in NSC differentiation remains poorly understood. This research aims to explore the role of miR-21 in neuronal differentiation and neuronal fate commitment by utilizing a combination of experimental and computational approaches. In the wet lab, NSCs will be isolated from adult or embryonic brain tissue and cultured under differentiation-inducing conditions to generate specific neural cell types, such as neurons and astrocytes. The role of miR-21 in neuronal differentiation will be assessed by modulating its expression through lentiviral transduction or CRISPR interference, with overexpression or knockdown of miR-21. Gene expression changes will be analyzed using quantitative PCR and RNA sequencing to examine the impact of miR-21 modulation on key neural differentiation genes, including NeuroD1, Notch1, Sox2, and GAP43. Neuronal differentiation will be confirmed by the expression of neuronal markers such as βIII-tubulin, MAP2, and Synapsin I through immunocytochemistry or Western blot analysis. In parallel, dry lab bioinformatics approaches will be employed to identify potential target genes of miR-21 involved in regulating the balance between NSC proliferation and differentiation. Pathway enrichment analysis will be conducted to uncover signalling pathways, such as PI3K/Akt, MAPK, and Wnt, which may mediate miR-21's effects on NSC fate. Computational network modeling will integrate RNA-Seq data to predict how miR-21 regulates gene networks during NSC differentiation. Additionally, computational simulations will assess the dynamic effects of miR-21 overexpression or knockdown on gene expression over time. By combining experimental data with bioinformatics and computational modeling, this study aims to provide a deeper understanding of the molecular mechanisms by which miR-21 influences NSC differentiation and neuronal fate commitment. The findings could have significant therapeutic implications for enhancing neurogenesis in brain injury and neurodegenerative diseases, such as Alzheimer's and Parkinson's, and could reveal new targets for therapeutic strategies aimed at modulating neuronal differentiation in vivo.

Keywords: Neural stem cells, Neuronal differentiation, microRNA miR-21, Gene expression, neurodegenerative diseases

PP-18

Effect of Antibiotic-Induced Gut Microbiome Dysbiosis on Constipation: An Experimental Study in Chickens

Muhammad Hasnain Sheraz[1] Urooj Fatimah[1] and Ahmad Yar[1], Qurat-ul-Ain Hanif[*1]

[1]University of Management and Technology

Corresponding Author: qurat.hanif@umt.edu.pk

Abstract

The gut microbiome plays a crucial role in regulating physiological functions, including gut motility and defecation. Probiotics, as part of the normal gut microbiota, help maintain this balance. However, antibiotic use can disrupt the gut microbiome, leading to dysbiosis and constipation. This study will investigate the impact of different antibiotic classes on gut microbiome composition and constipation in chickens. Initially, normal gut microbiota will be isolated from fecal samples before antibiotic administration. Chickens will then receive antibiotics for 4–5 days, during which signs of constipation will be observed. Following this, chickens will be slaughtered under proper SOPs to isolate intestinal microbiota for comparative analysis. This research could provide valuable insights into the role of gut microbiome dysbiosis in post-antibiotic constipation, particularly in post-surgical patients where antibiotic use is prevalent.

Keywords: Probiotics, Gut microbiome, Antibiotics, Dysbiosis, Constipation and Gut motility

PP-19

Computational Exploration of Bioactive Compounds from *Haloxylon griffithii* Reveals Promising Therapeutic Targets

Mahnoor Basit[*1], Muhammad Haroon[1], Faisal Imran[2], Rao Umair Waheed[2]

[1]School of Interdisciplinary Engineering and Sciences, National University of Science & Technology

[*]**Corresponding Author:** mahnoor98basit@gmail.com

Abstract

The therapeutic potential of *Haloxylon griffithii* found in northern region of Balochistan, has been neglected so far. There are a number of bioactive phytochemicals (18) with great therapeutic potential in *H. griffithii* which can be used for treating various diseases. To predict the binding affinity of various phytochemicals to the human proteome, the AI Bind machine learning pipeline was employed. Out of 16000 proteins, the top 20 were shortlisted in terms of their high binding probabilities and a network of nodes and edges was constructed using Network Analyst. 4-Amino-4'-methyldiphenyl ether, Piperidine, 1- (5-trifluoromethyl-2-pyridyl)-4-(1H-pyrrol-1-yl) and 2(4H) Benzofuranone-5,6,7,7a-tetrahydro-4,4,7a-trimethyl had the highest scores against FANCB, AGRE3, CCNB3, TRPV1, HRH1, ACM5, SCNBA, SCN4A as well as GSTCD. Protein-ligand docking studies were conducted by using Auto Dock Vina to determine the binding affinities. The findings concluded that Piperidine, 1-(5-trifluoromethyl-2-pyridyl)-4-(1H-pyrrol-1-yl) had a broad activity against cancer cell relevant targets (FANCB, CCNB3 and GSTCD) and pain/inflammatory-related targets. 2(4H) Benzofuranone-5,6,7,7a-tetrahydro-4,4,7a-trimethyl had a relatively good binding to CCNB3 and it could be explored for cancer-related applications. The ADME properties were calculated by using Swiss ADME and the findings concluded that 2(4H) Benzofuranone-5,6,7,7a-tetrahydro-4,4,7a-trimethyl appears to be the best candidate due to its high solubility, high GI absorption, BBB permeation, and lack of significant CYP inhibition. In addition to this, Piperidine has good absorption and BBB permeation but is a Pgp substrate and inhibits multiple CYP enzymes. Furthermore, 4-Amino-4'-methyldiphenyl ether has a moderate solubility and a good bioavailability score. To validate these findings, in vitro-experimentation should be carried out to know about the binding of these compounds. Measuring the IC50 values would be beneficial for quantifying the potency of inhibition.

Keywords: Phytochemicals, Protein-ligand Interaction, ADME, AIBind, *Haloxylon griffithii*

PP-20

The Interplay Between Physical Activity, Body Composition, HDL, and LDL in Prehypertensive Individuals

Dr. Imran Tipu[1] and Huzaifa Binte Rashid*[1]

Department of Life Science, School of Science, University of Management and Technology, Lahore, Pakistan

Corresponding Author: zafu012@gmail.com

ABSTRACT

This study investigates that how physical activity as well as body composition affect the HDL and LDL levels in people who has prehypertension. There is a condition where blood pressure is little higher than normal but not too much as in the hypertensive range. Prehypertension is an important risk factor for heart disease and they also understanding that how lifestyle factors like exercise and body weight manage the HDL and LDL levels that can help to prevent the prehypertension to hypertension. The goal of this study is to identify the different ways to improve the HDL and LDL levels and reduce heart disease risks. This study included n=100 adults both male and female aged 20-25 years old to investigate prehypertensive individuals. Out of n=100 participants, n=39 participants were prehypertensive. All participants were assessed for body composition by using measurements like body mass index, waist-to-hip ratio, visceral fat and body fat percentage and then measured HDL and LDL level by using bioscience kit and then measured physical activity by using a standard IPAQ questionnaire. Blood pressure readings were also taken by using digital sphygmomanometer to confirm their prehypertensive status. The data were analysed to determine how physical activity and body composition relate with HDL and LDL levels while accounting for factors like age, gender, blood pressure and physical activity. The findings of this study showed that people who engaged in more moderate to vigorous physical activity had higher levels of HDL and lower levels of LDL. Specifically, those participants who exercised more than average and they have increase in HDL and a decrease in LDL levels but some have slightly increase LDL. So, they are suggesting that regular physical activity can improve cholesterol profiles. Additionally, those participants have low body fat percentages, normal visceral fat and normal BMI also had higher HDL and lower LDL. These results indicate that maintaining a healthy body weight and shape is important for heart health especially in prehypertensive individuals. The benefits of physical activity on HDL and LDL levels were more noticeable in people with normal Body Mass Index. This study suggests that regular exercise and weight management may have a good impact on improving HDL and LDL levels in the participants. These results show the importance of lifestyle changes such as increasing physical activity and maintaining a healthy weight for managing prehypertension and reducing the risk of heart disease. Doctors can use these findings to encourage patients with prehypertension to maintain body weight and perform physical activity. In conclusion, this research shows the strong connection between physical activity, body composition, and HDL and LDL levels in prehypertensive individuals. These findings support the early interventions as well as lifestyle modifications to manage prehypertension. Future studies could explore that how these factors work over time and investigate other ways to support heart health in this population. Overall, this

study provides valuable results and show how simple and everyday activity can make a big difference in preventing serious health problems.

Keywords: HDL, LDL, physical activity, body composition, prehypertension, cardiovascular disease, blood pressure, lifestyle interventions, early modification

---

PP-21

Maternal genetic diversity, differentiation and phylogeny of three white yak breeds/populations in China

Muhammad Awais Hussain[1], Amna Mazhar[1], Hania Ishtiaq[1], Nimra Hameed[1], Quratulain Hanif[1*]

University of Management and Technology, Lahore, Pakistan

Corresponding Author: qurat.hanif@umt.edu.pk

Abstract

White yak is a unique economic livestock animal on the Qilian Mountains of Qinghai-Tibet Plateau (QTP). Here, 369 mitochondrial D-loop sequences from three Chinese white yak breeds/populations (Tianzhu, Menyuan and Huzhu) were comprehensively analyzed to indicate their maternal genetic diversity, differentiation and phylogenetic relationship. Our results showed that the haplotype diversity (Hd) was found to be highest in Tianzhu white yak (Hd ± SD ¼ 0.9501 ± 0.0058), while the lowest was recorded in Huzhu white yak (Hd ± SD ¼ 0.7178 ± 0.0474). Totally, the haplotype and nucleotide diversities of white yak were 0.9407 ± 0.0069 and 0.0187 ± 0.0094, respectively, indicating an abundant maternal genetic diversity in white yak. Estimates of FST (Fixation Index) values showed a high genetic differentiation between Tianzhu and Menyuan populations (FST¼ 0.2928, $p < 0.05$) as well as that between Tianzhu and Huzhu populations (FST¼ 0.2721, $p < 0.05$), but a moderate genetic differentiation between Menyuan and Huzhu populations (FST¼ 0.1352, $p > 0.05$) was observed. Cluster analysis based on FST values among populations indicated that the genetic relationship between Menyuan and Huzhu white yak was closer, but they had a far genetic relationship with Tianzhu white yak. Maternal phylogenetic analysis revealed that white yak represented two maternal lineages (I and II), suggesting two maternal origins. In addition, it is notable that taurine mtDNA haplotypes were detected in Tianzhu and Huzhu white yak populations, indicating taurine genetic introgression to some extent. Our study would provide useful information for the conservation and utilization of white yak.

Keywords: White yak; mitochondrial D-loop; genetic diversity; differentiation; phylogenetic relationship

PP-22

Bacterial Cellulose Biocomposites from Fruit Waste: A Transparent, Flexible Alternative to Single-Use Plastics

Arqam Tahir*[1], Muhammad Bilal Arshad[1], Mudassir Anayat[1], Sadaqat Hussain[1]

[1]Department of Life Sciences, University of Management and Technology, Lahore

***Corresponding Author:** arqamtahir@yahoo.com

Abstract

The global reliance on petroleum-based cling films demands urgent innovation in sustainable packaging. This study proposes a novel method to synthesize biodegradable, transparent films using bacterial cellulose (BC) fermented from banana peel waste—a resource often discarded in agricultural industries. *Komagataeibacter xylinus* was cultured in a nutrient medium enriched with hydrolyzed banana peel extract, yielding high-purity cellulose nanofibers. To enhance flexibility and water resistance, the BC matrix was blended with citrus pectin (from orange rind waste) and glycerol, then cast into thin films. The resulting material demonstrated exceptional mechanical properties (tensile strength: ~18 MPa; elongation: 35%) comparable to low-density polyethylene, while maintaining full biodegradability in compost (100% degradation within 21 days). Spectroscopic analysis confirmed the films' UV-blocking capabilities, adding value for food preservation. Crucially, the process avoids toxic solvents and utilizes dual waste streams (banana peels, citrus rinds), reducing production costs by ~40% compared to existing BC film methods. Prototype testing showed the films effectively preserved avocado freshness for 10 days, outperforming commercial cling wraps in moisture retention. This approach not only addresses plastic pollution but also valorizes food waste, aligning with circular economy goals. Future work will optimize scalability and industrial compatibility. By merging microbial synthesis with agro-waste valorization, this research offers a viable, eco-conscious alternative to single-use plastics for packaging and beyond.

Keywords: Bacterial cellulose, Banana peel waste, Citrus pectin, *Komagataeibacter xylinus*, Biodegradable films, Circular economy

PP-23

Modulating the Genetic Trajectory of Huntington's Disease through RNA-Based Therapeutic Strategies

Hanan Mirza*[1], Nabeeha Hassan[1]
[1]Department of Life Sciences, School of Science, University of Management & Technology

Corresponding author email: hanan1mirza@gmail.com

Abstract

Huntington's disease (HD) is an autosomal dominant neurodegenerative disorder marked by progressive motor, cognitive, and psychiatric deterioration, resulting from an expanded CAG trinucleotide repeat in the *HTT* gene. The resultant mutant huntington protein induces neuronal degeneration, particularly in the striatum and cortex. Current treatments predominantly focus on symptomatic relief rather than modifying disease progression, with limitations such as adverse effects and inability to reverse neuronal damage. This review discusses RNA-based therapeutic approaches for HD, including small interfering RNAs (siRNAs), short hairpin RNAs (shRNAs), antisense oligonucleotides (ASOs), and microRNAs (miRNAs). These strategies aim to selectively target mutant *HTT* mRNA, thereby reducing toxic protein synthesis. While siRNAs and shRNAs have demonstrated efficacy in animal models, ASOs offer transient yet reversible suppression of mutant huntington, showing promise in clinical trials. Moreover, miRNA-based therapies, particularly those employing artificial miRNAs delivered via adeno-associated viral vectors, represent a novel avenue with potential for sustained therapeutic effects. Compared to traditional treatments, RNA-based approaches address the underlying genetic cause of HD, offering targeted intervention. However, challenges such as efficient delivery across the blood-brain barrier, allele selectivity, and potential immune responses persist. This review comprehensively examines each RNA-based strategy, comparing their mechanisms, efficacy, delivery systems, and limitations. Additionally, we highlight current advancements, ongoing clinical trials, and potential improvements required to enhance the therapeutic utility of RNA-based interventions for HD. Future research must focus on optimizing delivery methods, enhancing specificity, and ensuring long-term safety to fully harness the potential of these therapies in altering the genetic trajectory of Huntington's disease.

Keywords: siRNA, shRNA, antisense oligonucleotides, microRNA, gene silencing

PP-24

In-Silico Drug Designing Against Protein Causing Colorectal Cancer

Laraib[1], Laiqa Sajjad[1], Rana Muhammad Mateen[*1]

[1]Department of Life Sciences, School of Science, University of Management & Technology

Corresponding author email: muhammad.mateen@umt.edu.pk

Abstract

Colorectal cancer (CRC) is the second deadliest cancer after lung cancer, primarily due to late-stage diagnoses, tumor heterogeneity, and treatment resistance. The disease progresses through complex genetic and epigenetic alterations affecting key regulatory genes such as APC, TP53, KRAS, BRAF, and CDK2, leading to uncontrolled cell division, tumor growth, and metastasis. Among these, BRAF V600E mutations drive aggressive tumor behavior and confer resistance to standard therapies. Additionally, CDK2 dysregulation is linked to increased tumor aggressiveness and chemotherapy resistance, highlighting the urgent need for novel therapeutic strategies. This study employs an in-silico drug discovery approach to identify potential BRAF inhibitors and overcome CRC treatment challenges. AutoDock Vina will be used for molecular docking, targeting B-Raf kinase (PDB ID: 8QQG) with a docking grid focused on key active site residues (Asp594, Phe595, Gly596, Lys483, Glu501, Asp576, Val600). Discovery Studio Visualizer will analyze the top-binding ligands, followed by molecular dynamics (MD) simulations and density functional theory (DFT) analysis to assess ligand stability and reactivity. Additionally, this study will explore drug repurposing strategies and resistance circumvention techniques, such as PI3K inhibition and epigenetic modifications, to enhance treatment efficacy. Traditional CRC drug development is slow, expensive, and labor-intensive, necessitating the adoption of computational methods to accelerate research. In silico approaches provide a cost-effective and efficient alternative by enabling the prediction of drug interactions, analysis of biological data, and simulation of molecular behavior. This research aims to contribute to the development of targeted therapies for BRAF-mutant CRC, ultimately improving treatment outcomes and addressing drug resistance challenges.

Key words: BRAF V600E mutation, In silico drug discovery, Molecular docking, AutoDock Vina, B-Raf kinase (PDB ID: 8QQG), CDK2 dysregulation, G1/S phase transition, Drug repurposing

PP-25

Bioremediation of Textile Disperse Dyes using White-Rot Fungi *Trametes gibbose* and *Trametes versicolor*

Tooba Ffiaz[1], Amina Bibi[1], Fatima Naeem[1], Dr. Muhammad Akram[*1]
[1]Department of Life Sciences University of Management and Technology

Corresponding Author: muhammad_akram@umt.edu.pk

Abstract

Due to their discharge into aquatic environments, the growing industrial usage of dyes and pigments has sparked environmental concerns. The resistant character of disperse dyes, which are frequently employed in textile dyeing, presents a considerable issue. The bioremediation capability of the white-rot fungi *Trametes* versicolor and *Trametes gibbosa* for the breakdown of dispersion dyes is investigated in this work. These fungi create ligninolytic enzymes, which aid in the breakdown of dyes, through redox reactions and the generation of radicals. PDA, YBD, and nutritional agar/broth media were used to cultivate both fungi, and the ideal growth conditions were 28–30°C and pH 6. While *T. gibbosa* flourished with beef extract alone, *T. versicolor* grew best when given both yeast extract and beef extract as nitrogen sources. Under ideal circumstances, *T. gibbosa's* biomass increased more quickly than *T. versicolor's.* Visual observation and UV-visual spectrophotometry were used to evaluate the effectiveness of dye degradation. While *T. gibbosa* shown reduced efficiency (0.02% DR1 solution, 1.56 to 2.98 absorbance in 6 days), T. versicolor demonstrated improved dye degradation, breaking down 0.05% DR1 solution (0.02 to -0.11 absorbance in 3 days). For both fungi, the breakdown efficiency in wastewater was above 80%, with the greatest decline taking place in six days. At greater dye concentrations, *T. gibbosa*, however, demonstrated a decrease in efficiency. According to these results, *T. versicolor* is a more potent disperse dye degrading agent, which makes it a viable option for wastewater treatment applications. Its efficiency can be increased further, lessening the negative effects of dye pollution on the environment.

Key words: Bioremediation, white-Rot fungi, disperse dyes, ligninolytic enzymes

PP-26

Breast Cancer Biology & Behaviour: A Comparative analysis of Cancer Characteristics in Diverse Age-Groups

Sameen Masroor[1], Muhammad Khurram[1], Muhammad Sohail Afzal*[1]

[1]Department of Life Sciences, School of Science, University of Management & Technology

***Corresponding Author:** f2023253003@umt.edu.pk

Abstract

Breast cancer is the most common malignancy or cancer among all cancers in Pakistani women. Studies reported that Pakistan is the top most country among the whole Asian countries having the highest breast cancer incidence rates. Almost 90,000 new cases diagnose in each year with annual deaths of 40,000. The highest proportion of breast cancer cases, approximately 67.6%, is reported from the province of Punjab. The risk rate increases with the factors like early menarche, delayed menopause, lack of breast feeding and of course the obesity. Child bearing reduces risk and breast feeding somehow have a protective effect. The mortality rate in Pakistan is high due to late-stage diagnosis also. This study aims to analyse the patient data to determine the most At-risk age group and to understand the relationship between age and the other key characteristics of cancer which include staging, tumor grading, TNM (Tumor, Node, Metastasis) status and the major molecular markers that are the key factors for the treatment plan. A retrospective analysis of patients who are diagnosed with breast cancer from late 2023 to early 2025 from a tertiary care hospital in Punjab, Pakistan was conducted to evaluate demographic and clinical parameters of breast cancer, using some statistical tools. Preliminary findings suggest that the age group of women between 41 to 50 have the highest incidence rate of breast cancer. Among all women, 2 of the men also developed breast cancer later in their age. Younger patients with age 35 ≤ have been found with more aggressive stages and grades and lowest positivity of markers. These findings will provide better understanding and highlights the importance of age-specific diagnostic approaches and treatment plans so that ultimately the patient's outcome should increase.

Keywords: Breast Cancer, Age, Stage, Grade, Age-specific analysis, TNM status, Diagnosis, Pakistan, statistical evaluation, late-stage diagnosis

PP-27

Effect of Iron Overload on LFT, RFT And CBC of Beta-Thalassemia Patients

Laiba Irfan*[1], Muhammad Irfan Fareed[1], Muhammad Mateen[1]

[1]Department of Life Sciences, University of Management and Technology, Lahore

Corresponding author: S2023254009@umt.edu.pk

Abstract

Beta thalassemia is a hereditary blood disorder characterized by the reduced production of hemoglobin, leading to anemia and the need for frequent blood transfusions. While transfusions are essential for managing the condition, they also result in the accumulation of excess iron in the body, as the body has limited mechanisms to excrete iron. This iron overload can cause damage to vital organs, particularly the liver, heart, and kidneys. This study aims to evaluate the effects of iron overload on liver function tests (LFT), renal function tests (RFT), and complete blood count (CBC) in beta thalassemia patients. Iron overload is a common complication in beta thalassemia due to the repeated transfusions required for managing anemia. Elevated serum ferritin levels, an indicator of iron overload, are often observed, and iron deposits in the liver and kidneys may lead to organ dysfunction. Alterations in LFTs, such as increased levels of serum bilirubin, alanine aminotransferase (ALT), and aspartate aminotransferase (AST), suggest liver damage, ranging from mild elevations to more severe conditions like cirrhosis. Similarly, RFTs, including serum creatinine and blood urea nitrogen (BUN), may show elevated levels, signaling potential kidney dysfunction. CBC parameters, such as hemoglobin levels, mean corpuscular volume (MCV), and reticulocyte count, are also important indicators of the hematological status in beta thalassemia patients. Changes in these parameters can occur due to the effects of iron overload on erythropoiesis. In conclusion, iron overload significantly impacts LFT, RFT, and CBC in beta thalassemia patients, underlining the importance of regular monitoring to prevent complications. Early detection and management of iron overload can help improve both the quality of life and long-term outcomes for these individuals.

Key words: LFT, RFT, CBC, Liver, Iron, Health, Blood

PP-28

In-Silico Analysis of Functional SNPs of ARID1A Gene Associated with Liver Cancer

Fatima Arshad*[1], Iftikhar Ali[1]

[1]School of Science, Life Sciences Department, University of Management and Technology (UMT) Lahore

***Corresponding Author:** tanzeelafatima33@gmail.com

Abstract

Cancer remains a global health issue, with liver cancer being one of the causes of cancer related deaths worldwide. The global age-standardized incidence rate and mortality rate for liver cancer stands at 9.5% per 100,000. The highest incidence of liver cancer was observed in Eastern Asia with a rate of 17.8% followed by North Africa 15.2% per 100,000 respectively. Pakistan faces its own significant challenges with hepatocellular carcinoma incidence at 7.6% for males and 2.8% for females. The Tumor Protein ARID1A belongs to a class of chromatin regulatory proteins that function by maintaining accessibility at most promoters and enhancers, thereby regulating gene expression. The high frequency of ARID1A alterations in human cancers has highlighted its significance in tumorigenesis. ARID1A (also known as BAF250a, p270 or SMARCF1) is a key component of the mammalian SWI/SNF protein complex. The gain of ARID1A function triggers tumor initiation by enhancing CYP450-mediated oxidative stress, while the loss of ARID1A during the later phases of tumor growth decreases the DNA accessibility and inhibits the transcription of genes associated with migration, invasion, and metastasis. ARID1A genetic variations and their functional impact was analyzed using in-silico approach combining with homology-based, supervised learning and structural based methods. Out of 222 SNPs analyzed, eight missense mutations rs756839728, rs757045273, 1057520664, 1(205536026, 1404019220, s1029852196, rs1064793282, rs1057517985 were found to significantly impair protein structure and function. potentially disrupting signaling pathways and leading to DNA damage. (T281A) Threonine at 281 was changed into Alanine, (P289S) Proline at 289 into Serine, (C312Y) Cysteine at 312 into Tyrosine, (R318C) Arginine at 318 into Cysteine, (R338C). Arginine at 338 into Cysteine, (R338H) Arginine at 338 into Histidine, (C347F) Cysteine at 347 into Phenylalanine and (R350G) Arginine at 350 into Glycine. Primary, secondary and Tertiary structures were analyzed by Protoparam, GOR4 and I-TASSER. By advancing the understanding of ARID1A mutations, this study lays the groundwork for targeted therapeutic strategies, improved prevention measures, and a better grasp of the regional and global burden of liver cancer.

Keywords: ARID1A, mutations, computational tools, liver cancer

PP-29

Genome Wide Analysis of Aquaporin Protein Family in Land Plants

Hajra Murtaza[1], Sibgha Butt [1], Razia Anwar[1], and Aquib Nazar*[1]
[1]Department of Life Sciences, University of Management and Technology

***Corresponding Author:** aquib.nazar@umt.edu.pk

Abstract

Aquaporins (AQPs), pivotal members of the Major Intrinsic Protein (MIP) superfamily, facilitate the transport of water and solutes through plant membranes and are thus vital for abiotic stress resilience. This study presents a comprehensive genome-wide analysis of AQP families from 34 higher plant species, ranging from mosses and gymnosperms to monocots and dicots, to understand their evolutionary diversification and functional adaptation to salinity stress. By using comparative genomics, transcriptomics, and bioinformatics approaches, we will identify and group AQP genes, search for conserved domains, and reconstruct phylogenetic relationships to follow their evolutionary path. With cotton *Gossypium hirsutum* as model system, the present study explores the stress-regulated salinity differential expression of different AQP subtypes (PIPs, TIPs, SIPs) in contrasting tolerant and susceptible cultivars. The investigation would test the hypothesis that GhPIP1;1 and GhTIP2;1 play central roles as regulators of osmotic balance in that their downregulation due to salinity stress would contribute to reduced root hydraulic conductance—an adaptive mechanism to limit water loss. The functions of AQPs in ion homeostasis and stress signaling, including post-translational modifications like phosphorylation, will be assessed by molecular docking, protein interaction networks, and gene ontology analyses. The study will integrate multi-omics approaches to propose AQPs as breeding stress-resistant crop biomarkers. Cis-regulatory element analysis will identify stress-responsive motifs, and 3D protein modeling will reveal structural adaptations. This study will connect evolutionary genomics and functional biology, offering a platform for crop improvement strategies against AQP-mediated stress tolerance. Such discoveries will be of significance to sustainable agriculture, particularly in saline-prone regions, and will provide an avenue for future genetic modification of cotton and other economically valuable crops.

Keywords: Aquaporins, Salt stress, *Gossypium*, Genome-wide analysis, Protein-protein interaction, Evolutionary adaptation, Osmotic Stress Tolerance, Stress-Resilient Varieties

PP-30

Synthesis of anti-IL-6 Polyclonal Antibody and its Characteristics

Laraib Tabassum*[1], Kalsoom Ijaz[1], Areeha Alyas[1], Maryam Zarif[1], Mehreen Fatima[1]

[1]Department of Life Sciences, School of Science, University of Management and Technology, Lahore, Pakistan

Corresponding: F2021231041@umt.edu.pk

Abstract

For regulation of various biological processes such as immune response and inflammation, a pleiotropic cytokine interleukin-6 plays a crucial role. Dysregulation of IL-6 signaling is associated with certain types of cancers, autoimmune disorders, and inflammatory diseases. The development of polyclonal antibodies is a valuable tool against IL-6 for studying its biology, detecting its presence, and to evaluate therapeutic strategies. This study involves the synthesis of novel polyclonal antibody and to evaluate it subsequently in murine models. The primary aim of this study was to synthesize a reliable and specific antibody targeting IL-6, which is essential for the understanding of various pathological and physiological processes. Synthesis of the anti-IL-6 polyclonal antibody included mice immunization with recombinant IL-6, which was followed by serum collection and ultimately antibody purification. Characterization of the resulting antibodies was done via immuno dot blot and Enzyme-Linked Immunosorbent Assay (ELISA) which revealed that it exhibits high specificity and affinity against IL-6, with no cross-reactivity to other cytokines, where the antibody demonstrated a high degree of sensitivity in detecting IL-6. Synthesis and characterization were essential to generate a robust immune response in animal models. Findings revealed that synthesis of polyclonal antibody effectively recognizes and binds to IL-6 in murine samples, demonstrating its significance in research, therapeutics, and diagnosis. The results suggest that the synthesized polyclonal antibody has a potential as a valuable tool for IL-6 signaling and its related mechanisms in various biological contexts, making it suitable for both research and clinical settings. Furthermore, the methodologies and results provide basis for future research focused on IL-6 and other related cytokines.

Keywords: Interleukin-6, Polyclonal antibody, Immune response, Immunization, Clinical settings

PP-31

Silica-Acid Catalyzed Synthesis of O-Alkyl Glycosides: A Green Approach for Drug Delivery

Mishal Shahzad[1], Saliha Nazir[1], Erum Akbar Hussain*[1]
[1]Department of Chemistry, Lahore College for Women University, Lahore, Pakistan.

Corresponding author: erum.hussain@gmail.com

Abstract

The biological profile of Alkyl glycosides makes them a potential candidate for drug delivery system. In this study, a biodegradable drug carrier system was developed through the chemical modification of naturally occurring monosaccharides with aliphatic alcohols, leading to the formation of alkyl O-glycosides. The structure confirmation was achieved by Fourier-transform infrared spectroscopy (FTIR), nuclear magnetic resonance (^{1}H NMR), and X-ray diffraction (XRD) techniques. The thermotropic and lyotropic behavior of these glycosides was evaluated via differential scanning calorimetry (DSC), thermogravimetric analysis (TGA), and optical microscopy. The drug delivery potential of the formulations was assessed *in vitro* using aspirin as a model drug, with release profiles monitored by UV–visible spectrophotometry. The results demonstrated effective and sustained drug release of the entrapped drug, indicating that alkyl *O*-glycosides are potential and cost-effective drug delivery systems with enhanced therapeutic efficacy. This work aligns with SDG 3: Good Health and Well-Being, by improving therapeutic outcomes, enabling sustained drug release, and minimizing side effects.

Keywords: Alkyl O-glycosides, Mesogens, Biocompatible, Drug carrier, Sustained release

PP-32

Synergistic Adsorption of Heavy metals using Bentonite Guaran Composites

Hadia Haq*[1]

[1]Lahore College for Women University, Lahore

Corresponding Author: Hadiahaq54@gmail.com

Abstract

Clean water scarcity and the environmental impact of industrial effluents on water bodies have become critical global concerns. Thus, polymer clay composites have been emerged as adsorbents due to their biodegradability and non-toxicity. This study focuses on preparing composites by blending bentonite clay with chitosan and guar gum. The synthesized composites were characterized using FT-IR, SEM, and XRD analyses. These composites functioned as an efficient adsorbent for removing heavy metals, particularly nickel, from wastewater, through a chelation mechanism, forming stable complexes that enhance their adsorption capacity.

Keywords: XRD, FTIR, Polymer, Wastewater, SEM, Environment

PP-33

Hybrid Pollution Control Systems: Integrating CCU, Scrubbers, and Catalytic Converters for Comprehensive Smog Reduction

Rabiha Bakhtiar*[1], Fiza Naeem[1], Atiqa Mushtaq[1], Madiha[1], Abeeha[1]

[1]Department of Life Sciences University of management & Technology

***Corresponding Author:** rabihabakhtiar@gmail.com

Abstract

Smog remains a critical environmental and public health challenge, particularly in urban and industrial regions. Smog—a toxic blend of ground-level ozone (O_3), particulate matter (PM), NOx, SO_2, and VOCs—causes millions of premature deaths annually. Traditional mitigation strategies often address single pollutants, leaving gaps in comprehensive smog control. While individual technologies like Carbon Capture and Utilization (CCU), scrubbers, and catalytic converters have shown promise in reducing specific pollutants, none alone can fully mitigate smog's complex composition. This paper explores hybrid systems that integrate these technologies to simultaneously target CO_2, NOx, SO_2, PM2.5, and VOCs—key contributors to smog formation. We review recent advancements (2022–2024), analyze system synergies, and evaluate real-world applications in industrial and vehicular emissions control. Findings indicate that hybrid systems can achieve >90% reduction in major smog precursors while enabling resource recovery (e.g., converting NOx into fertilizers). Challenges such as energy demands and scalability are discussed, along with emerging solutions like AI-optimized capture and plasma-assisted catalysis. Hybrid CCU-scrubber-catalyst systems represent a paradigm shift in smog mitigation, offering holistic pollution control while enabling resource recovery. While challenges remain, technological advancements and policy support could make these systems mainstream within 5–10 years. Future work should focus on scaling pilots and reducing costs through material innovations. The study concludes that policy support and cross-industry collaboration are essential to accelerate deployment.

Keywords: Carbon Capture and Utilization (CCU), smog reduction, hybrid pollution control, Scrubbers

PP-34

Computational Analysis of Variants of Uncertain Significance in *ALDOA* Gene

Anaya Manzoor[*1], Manahil Hussain[1], Sundas Saif[1], Tahreem Bibi[1], Tahseen Amin[1], Dr. Mureed Hussain[1]

[1]Department of Life Sciences University of management & Technology

***Corresponding Author:** F2024254001@umt.edu.pk

Abstract

Glycogen Storage Disease Type XII (GSD12) is an extremely rare autosomal recessive metabolic disorder characterized by hemolytic anemia, mental retardation, episodic rhabdomyolysis, exercise intolerance and muscle weakness with or without intellectual deficit or myopathy. GSD12 is triggered by mutations in *ALDOA* gene which is present on chromosome 16 of human genome having 8 coding exon that is involve in encoding a tetramer of 364 amino acids protein aldolase A. Aldolase A enzyme catalyzes the reversible conversion of FBP (fructose-1,6-bisphophate) into two thiophosphates G3P (glyceraldehyde 3-phosphate) and DHAP (dihydroxyacetone phosphate) in fourth step of glycolysis or in reversible pathway of gluconeogenesis. In this study, we are applying in-silico analysis to predict the most deleterious missense and splice site mutations in *ALDOA* gene and their impact on stability, function, post translational modification and ligand interactions of aldolase A protein. For that purpose, variety of bioinformatics tools based on different algorithms were utilized. In missense analysis, 22 variants were predicted as deleterious as well as were declared as pathogenic by functional analysis, 3 were destabilizing, only a single variant was found to be lying in PTM site ranges but was not disturbing the motif, and 24% of whole ALDOA protein was predicted as conserved through conservation analysis. However, in splice site analysis, 4 variants were found to be disturbing the splice site of *ALDOA* gene. These finding can be very helpful for scientists in future as they can directly target these mutations in order to produce certain medications and drugs related to GSD12 disorder.

Keywords: *InSilico*, Computational Biology, Gene, Health, Prevalence

PP-35

Role of VPg in Viral Life Cycle and a Potential Antiviral Drug Target

Hafsa Naeem[1], Muhammad Awais Saleem[1], Muhammad Ali*[1]

[1]Department of Life Sciences, University of Management and Technology

*Corresponding Author: Muhammad_ali@umt.edu.pk

Abstract

Positive-sense single-stranded RNA (ss(+) RNA) viruses have a variety of mechanisms of genome replication and protein synthesis. It is a characteristic of some viruses to have a 5’ cap structure, whereas others, viz., Secoviridae, Potyviridae, Luteoviridae, and Picornaviridae, including Poliovirus, have a viral protein genome-linked (VPg) at the 5’ terminus. VPg plays a central role in viral RNA replication and acts as a primer for RNA-dependent RNA polymerase (RdRP) by uridylation, which aids in RNA synthesis. VPg is also involved in host translation hijacking machinery and thus aids viral protein synthesis. Although VPg plays a critical role, it is structurally diverse among viral families and shows different interactions with host factors. Future studies of VPg inhibitors hold promising antiviral application. Small compounds, peptides, and RNA medicines can interfere with VPg-RdRP complexes, inhibiting uridylation and viral RNA replication. Inhibitors of VPg-host protein interactions can inhibit viral replication and translation. Structure-based strategies of drug discovery, leveraging VPg’s conformational properties, can produce highly specific medicine. As an essential component in viral genome replication, VPg is a target for drug discovery in the therapy of VPg-related RNA viruses. Further investigations of VPg structure, interaction dynamics, and resistance mechanisms are necessary for antiviral therapies to be made effective.

Keywords: VPg, RNA viruses, Poliovirus, uridylation, antiviral targets, RdRP, inhibitors

PP-36

The Interplay Between Physical Activity, Diet, Cholesterol, and Triglycerides in Prehypertensive Individuals

Warda Razzaq Cheema*[1]

[1]Department of Life Sciences University of Management & Technology

***Corresponding Author:** wardarazzaq678@gmail.com

Abstract

NCDs account for 41 million deaths around the globe every year, which is equal to 71% of all deaths. Hypertension and hypercholesterolemia are among the primary risk factors for heart diseases. People with prehypertension have a greater chance of developing hypertension. Exercise is a natural remedy for NCDs. This research determined the association between lifestyle variables, anthropometric parameters, and cardiometabolic risk indicators among young university students aged 20-25 years. The study involved 100 participants, with a slightly higher proportion of females (55%) than males (45%). All the participants were unmarried students with no major medical, drug, or smoking history. The mean BMI was 22.02 kg/m², where 64% of the volunteers were within normal range, 16% underweight, 17% overweight, and 3% obese. Blood pressure studies revealed 49% of subjects had normal readings, 39% prehypertensive, and 12% hypertensive, where a higher incidence was seen among the males with regard to prehypertension and hypertension. Fat percentage range differed between men and women, with men having a broader range that included high and very high fat percentages and women having a considerable number of participants with normal fat percentages. The level of visceral fat was normal in 92% of the participants, but 8% had increased levels. Nutritional habits showed below-optimal consumption of fruits and vegetables, with a high proportion consuming only 1-2 servings a day or nothing. Fast food consumption was prevalent, with 41% consuming it 1-2 times weekly, and sugary beverages were frequently consumed by many. Physical activity levels were concerning, with 58% minimally active, 29% inactive, and only 13% highly active. The correlational tests noted significant associations that included moderate positive correlation of blood pressure and BMI, weak negative correlation between BMI and MET value (exercise level), and also moderate positive correlation of cholesterol with blood pressure. Moreover, with increased exercise was noted lesser BMI, blood pressure, and also triglycerides. Dietary habits played a role as well, with fast food consumption linked to higher blood pressure, cholesterol, and triglyceride levels, while an increase in fruit and vegetable intake was associated with better cholesterol and triglyceride levels.

Keywords: Prehypertension, Body Mass Index, Blood Pressure, Cholesterol, Triglycerides, Cardiovascular diseases, lifestyle interventions

PP-37

Genome-Wide Identification and Expression Analysis of Kinase Proteins in Land Plants, with a Focus on *Gossypium hirsutum* under Abiotic Stress

Sania Munir[1], Aquib Nazar[1], Zomah Malik[1], Ayesha Murad[1], Athar Hussain[2,3]*
[1]Department of Life Sciences, School of Science, University of Management and Technology (UMT), Lahore, 54000, Pakistan
[2]School of Food and Agricultural Sciences (SFAS), University of Management and Technology (UMT), Lahore, 54000, Pakistan
[3]Genomics & Informatics Lab (GIL), Lahore, 54000, Pakistan

***Corresponding author:** atharmutahari@gmail.com

Abstract

The kinase proteins are a superfamily in plants and are involved in diverse biological and molecular functions for better adaptation of land plants. The current study aims to identify the kinase superfamily in land plants, covering from mosses to angiosperm. We have identified 49,611 genes in 32 land plants across mosses, bryophytes, lycophytes, gymnosperms, and angiosperms. All identified genes were classified into 26 major classes (I-XXVI) based on domain architectures e.g., Proline kinase like Tyrosine (PkT), Leucine Rich Repeat Receptor Kinases (LRR), Leucine Rich Repeat Receptor-Proline like Kinases (LRR-Pk), Leucine Rich Repeat Receptor-Proline like Tyrosine Kinases (LRR-PkT), and Proline kinase (PK) and "X" represents other than listed domains. Comparative genomics revealed evolutionary history, duplication, divergence, gene gain/loss, species relationships, and structural diversity of kinases in land plants, highlighting their molecular complexity and adaptive significance. Molecular docking analysis demonstrated the preferential binding of ATP to *Gossypium hirsutum* (*G. hirsutum*) kinase proteins, indicating their conserved phosphorylation mechanisms. Furthermore, SNP and Indel analyses in salt-resistant (*Mac7*) and salt-susceptible (*Coker 312*) cotton genotypes revealed genetic variations potentially linked to differential stress responses. Expression profiling highlighted strong upregulation of *OG12_LR_GhPk08* in *G. hirsutum* under both biotic, (e.g., *Xanthomonas citri*) and abiotic (e.g., salt, heat, and cold) stress, as well as in specific tissues like roots and seedlings. Conversely, consistently downregulated genes include *OG7_LRR_GhPk11*, which remained unresponsive across all biotic and abiotic conditions despite its presence in the genome, suggesting a limited role in stress responses. Moreover, the qRT-PCR based expression analysis of three genes (*OG12_LR_GhPk08*: *Gohir.D08G10000*, and *OG35_Pk_GhPk02*: *Gohir.D05G155340*) of *Mac7* and *Coker312* under salt stress demonstrated that these genes were highly expressed in both accessions under salt stress while *OG44_PkT_GhPk09*: *Gohir.A03G148700* expression was decreased in both varieties under the same condition. The study provides a deep insight into diversity and function of kinase genes in land plants, particularly, cotton and can be helpful in future research on kinome related studies.

Keywords: Kinase, Cotton, Abiotic Stress, Evolution, Expression, Domain, Molecular Docking

PP-38

Genome-Wide Association Study Reveals that the IBSP Locus Affects Ear Size In Cattle

Usman Ali*[1], Musab Rasool[1], Quratulain Hanif [1]
[1]Department of Life Sciences School of Science, UMT

*Corresponding Author: usmanali06177@gmail.com

Abstract

Background Ear size is a classical model for hot climate adaptation following evolution, however, the genetic basis of the traits associated with the ear size remains to be elucidated. Results In the current study, we performed GWAS on 158 cattle individuals to explain the genetic mechanism of ear size. The results suggested significant association of IBSP locus with ear size. A missense mutation (Threonine-250→Isoleucine) on the seventh exon of IBSP was observed, which occurred at a quite conserved site and changed the three-dimensional (3D) structure simulations. In addition to GWAS, 14 cattle breeds were screened for the selection signals associating with the ear size using Fst and SweepD. The selective sweep analysis also suggested that IBSP was under positive selection amongst 4 breeds with relatively large ear size. The allele distribution of this mutation was validated among 394 samples from 21 worldwide cattle breeds, which strongly implied the origin of the A allele mutation to be from the Bos taurus. Conclusions These findings not only have important theoretical significance for the exploration of major genes associated with the ear size but also provide important molecular markers for the identification of cattle germplasm resources.

Keywords: Cattle, Ear size, GWAS, IBSP

PP-39

Characterization and Synergistic Antibacterial Effects of Phytogenic Silver Nanoparticles Synthesized from Garlic, Black Pepper and Fig Extracts

Amal Wahid[1], Muneeba Mushtaq[1], Zomah Malik[1], Maheen Latif[1], Ghadir Ali*[1]

[1]Department of Life Sciences, University of Management & Technology

*** Corresponding Author:** Ghadir.ali@umt.edu.pk

Abstract

The synthesis of silver nanoparticles (AgNPs) using plant extracts has gained significant attention due to its eco-friendly and cost-effective approach. This study focuses on the characterization and synergistic antibacterial effects of phytogenic silver nanoparticles synthesized using garlic, black pepper, and fig extracts. These plant-based extracts contain bioactive compounds that facilitate the reduction of silver ions and enhance the antimicrobial properties of the resulting nanoparticles. The synthesized AgNPs are characterized using various analytical techniques to determine their size, morphology, and stability. Their antibacterial efficacy is evaluated against pathogenic bacterial strains, both individually and in combination, to assess their synergistic effects. The study aims to compare the antimicrobial potential of these nanoparticles against conventional antibiotics and explore their possible applications in biomedical and food preservation fields. The results are expected to provide insights into the enhanced antibacterial activity of phytogenic silver nanoparticles, highlighting their potential as natural and sustainable antimicrobial agents. By leveraging the synergistic properties of garlic, black pepper, and fig extracts, this research contributes to the advancement of nanotechnology in combating bacterial infections while minimizing environmental impact.

Keywords: Phytogenic Silver Nanoparticles, Garlic Black Pepper and Fig Extracts, Antibacterial Synergy, Green Synthesis, Nanotechnology in Medicine, Biomedical Applications

PP-40

Deciphering Rheumatoid Arthritis: Candidate Gene Discovery via Machine Learning and WGCNA

Hamna Habib[1], Haseeb Nisar[*2]
[1]Department of Life Science, University of Management and Technology, Lahore
[2]King Fahd University of Petroleum & Minerals, KSA
***Corresponding Author**: haseebnisar@kfupm.edu.sa

Abstract

Rheumatoid arthritis is a complex systemic autoimmune disorder that significantly impacts morbidity, mortality, and overall quality of life. This study utilizes gene expression data from the GEO database. We applied weighted gene co-expression network analysis (WGCNA) to identify key genes within significant modules, constructed a PPI network, and then leveraged machine learning algorithms to pinpoint feature genes. Various bioinformatics tools were employed, including *clusterProfiler* for functional enrichment analysis, gene set enrichment analysis for identifying biologically significant functions, *CIBERSORT* for immune infiltration analysis, and *DEGGs* to detect differentially expressed gene-gene interactions. Finally, FDA-approved anti-rheumatic drugs were docked against selected target regions. Our study identified IFIT3 and IFIT2 as two potential intersecting biomarkers through MLSeq and WGCNA analysis. These biomarkers were closely associated with elevated levels of specific immune cells, particularly neutrophils, in rheumatoid arthritis patients. Gene set enrichment analysis (GSEA) revealed significant downregulation of the oxidative phosphorylation pathway. Additionally, molecular docking results highlighted Anakinra and Methotrexate as the most promising drug candidates for suppressing the expression of RA-associated proteins. Our findings suggest that these biomarkers hold potential for clinical validation and could serve as a foundation for further investigation into RA-related pathways. This research may also contribute to identifying novel therapeutic targets that could influence disease onset and progression.

Keywords: Machine Learning, WGCNA, gene expression, Rheumatoid Arthritis, Molecular docking

PP-41

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

Tehreem Sajjad[1*], Muhammad Khurram[1*], Mureed Hussain[1], Koukab Imran[1], Mohammad Perwaiz Iqbal[1]

1Department of Life Sciences, University of Management and Technology, Lahore

***Corresponding Author**: F2022253017@umt.edu.pk/muhammad.khurram@umt.edu.pk

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-42

In-Silico Drug Discovery Targeting Glycogen Phosphorylase in *Echinococcus granulosus*: A Novel Approach for Therapeutic Development

Ahmed Ghulam Nabi [1], Muhammad Mateen[1]

[1]Department of Bioinformatics and Biosciences Capital University of Science & Technology

*__Corresponding Author:__ muhammadmateen@umt.edu.pk

Abstract

Echinococcus granulosus, a parasitic tapeworm responsible for echinococcosis, presents a major public health challenge due to its ability to cause hydatid cysts in various organs, often leading to life-threatening complications. Despite its high morbidity and zoonotic potential, effective therapeutic options remain limited, with existing treatments carrying considerable side effects. In this concept article, we propose an innovative in-silico drug discovery strategy targeting the glycogen phosphorylase (GP) protein of *Echinococcus granulosus*. This enzyme plays a crucial role in glycogen metabolism, and its inhibition could potentially disrupt the parasite's energy homeostasis, offering a novel therapeutic avenue. The study focuses on the GP protein, a validated drug target, using a curated phytochemical library of 17,967 ADMET-compliant compounds for screening. The compounds will undergo molecular docking, density functional theory (DFT) analysis, and molecular dynamics (MD) simulations to identify stable, high-affinity ligands. Albendazole, a commonly used anti-helminthic drug, will serve as a benchmark. This in-silico approach aims to uncover novel chemical scaffolds and functional groups that could inhibit GP activity, thereby disrupting parasite survival and development. By exploring previously unaddressed aspects of the parasite's biochemistry, this model aims to stimulate further research into first-in-class therapeutics for Echinococcus granulosus.

Keywords: In-silico study; *Echinococcus granulosus*; Glycogen phosphorylase; Molecular docking; Density functional theory (DFT); Molecular dynamics (MD) simulation; Drug discovery.

PP-43

Computational Analysis for Potential Drug Targets Against Selected Proteins Involved in Glioma

Syeda Sheher Bano[1], Muhammad Mateen[1*]
Department of Life Sciences University of Management and Technology
Corresponding Author: muhammad.mateen@umt.edu.pk

Abstract

Glioma, a prevalent and aggressive form of brain tumor, necessitates the identification of novel therapeutic targets for effective treatment. This study employs a comprehensive computational approach to identify potential drug targets among selected proteins implicated in glioma pathogenesis. Initially, the three-dimensional structures of these proteins are predicted using advanced modeling techniques, ensuring accurate representations for subsequent analyses. A diverse compound library is then curated and subjected to molecular docking studies to assess the binding affinities and interactions between the compounds and target proteins. Promising protein-ligand complexes are further evaluated through Density Functional Theory (DFT) calculations, providing insights into their electronic properties and stability. To simulate the dynamic behavior of these complexes within a biological environment, Molecular Dynamics (MD) simulations are conducted, analyzing their stability and conformational changes over time. This integrative in silico methodology aims to elucidate potential drug candidates and therapeutic targets for glioma, offering a foundation for future experimental validations and contributing to the advancement of targeted glioma therapies.

Keywords: DFT; MD; I-TASSER; Alphafold; Protein-ligand Interactions; Targeted Therapy; Electronic Structure Analysis

PP-44

Extraction of Cyanidin-3-Glucoside from *Litchi chinensis* and its Biochemical Characterization

Tehreem Hamid[1*], Amina Nasir[1*], Emaan Babar[1], Faiza Aziz[1], Muhammad Akram[1]

[1]Department of Life Sciences, School of Science, University of Management and Technology

Corresponding Author(s): tehreemhamid22@gmail.com , aminanasir921@gmail.com

Abstract

Litchi chinensis is a tropical fruit which has been used in ancient Chinese herbal medications due to its medicinal properties. It holds a great potential for various biological activities as it contains a variety of phytochemicals, particularly, terpenoids, saponins, tannins, steroids, resins and flavonoids. The stability of the phytochemicals differs in various solvents. Phytochemicals, particularly, flavonoids have shown efficient anti-microbial, anti-oxidant and anti-inflammatory activities. This study was particularly focused on extraction of flavonoid (cyanidin-3-O-glucoside) from *L. chinensis* fruits, peels and leaves using different solvents, quantification of total phenolic compounds, flavonoids and C-3-G from leaves, fruits and peels of *L. chinensis* and anti-microbial activity of *L. chinensis* extracts against diverse pathogenic bacterial strains. *L. chinensis* is a regional fruit in many South Asian countries, including Pakistan. It can be found in abundance in the peak summer season and due to its local availability, the extracts from its various components can be used to create medications in a more economical manner. Although, there are some limitations, the purification of cyanidin-3-glucoside was not carried out but the results of this study are promising. The research aims to exploit extracts of various *L. chinensis* components in the health industry and it can be used to treat a variety of bacterial infections.

Keywords: *L. chinensis*, Phytochemicals, Flavonoids, Cyanidin-3-Glucoside, Antimicrobial activity

PP-45

Chitosan Hydrogels for Sustained Vitamin D3 Release

Manahal Furqan[1*], Amna Ashfaq[1], Erum Akbar Hussain[1]

[1]Department of Chemistry, Lahore College for Women University

Corresponding Author: manahalshah462@gmail.com

Abstract

The low bioavailability and potential loss of bioactivity during oral delivery exacerbate Vitamin D3 deficiency which emphasizes the need for the development of a sustained release system. In this study cost-effective, and eco-friendly polymeric blends of chitosan and sago starch as sustainable nutraceutical carriers (CS 1-4) of Vitamin D3 has been synthesized. All prepared hydrogels were confirmed by FTIR, XRD and SEM analysis. The swelling studies reveal the pH-responsive behavior of these blends, affirming their potential for sustainable release. Furthermore, it's release predominantly follows zero-order kinetics, indicating a controlled release mechanism significantly influenced by the concentration of chitosan. These prepared samples were biocompatible and biodegradable and provide sustainable material for good health and wellbeing.

Keywords: Vitamin D3, Chitosan, nutraceutical carrier, FTIR, XRD, SEM

PP-46

Microwave-Assisted Synthesis of Anti-inflammatory Oxazoles

Kainat Ibrahim[1*]

[1]Lahore College for Women University, Lahore

Corresponding Author: ibrahimkainat50@gmail.com

Abstract

Inflammatory disorders cause to severe health complications, often leading to chronic diseases that significantly reduces the quality of life. This study focuses on the green synthesis of anti-inflammatory oxazole derivatives employing microwave radiations via a Schiff base of coumarin. The hetroannulation achieved with acetyl coumarin catalyzed by iodine under the influence of microwaves. The synthesized oxazole derivatives were characterized using spectroscopic techniques, including FTIR, ^{1}HNMR, and EIMS. Their pharmacological potential was assessed, revealing notable antioxidant by DPPH assay and anti-inflammatory studies by HRBC membrane stabilization method. These findings highlighted the efficient and practical approach adopted for synthesis of targeted bioactive oxazoles that can be utilized to reduce the inflammation.

Keywords: FTIR, HNMR, EIMS, HRBC, DPPH, Health, Inflammation

PP-47

Neem-Derived Graphene Quantum Dots for Sustainable Nanotechnology

Khadija Aqeel[1*]

[1]Lahore College for Women University, Lahore

Corresponding Author: khadijaaqeel27@gmail.com

Abstract

Graphene Quantum Dots (GQDs) are valuable in bioimaging and drug delivery due to their unique properties. Traditional synthesis methods often employ toxic chemicals and non-renewable resources, creating environmental hazards. This research utilizes a simple, environment-friendly method to synthesize GQDs from neem tree leaves using a water-based heating process at 200 °C, seeking a cleaner, more sustainable approach. Readily available neem leaves were hydrothermally treated to afford GQDs, and doped with Boron to enhance their properties. The prepared GQDs were confirmed by UV and FTIR spectroscopic techniques. The abundant, renewable precursor avoids toxic chemicals, making it a "green" alternative to traditional methods and demonstrates utilization of natural sources for nanomaterial synthesis. This method offers a sustainable route for GQD preparation. This research approach promotes a benign method and highlights the potential of plant-based materials for future innovations.

Keywords: FTIR, GQD, DPPH, Health, Inflammation

PP-48

Unlocking Nanoparticle Potential: A Machine Learning Approach to Predict and Optimize Band Gaps of ZnS

Eman Naseer[1*], Fizzah Zafar[1], Rabia Raza[*, 1]

[1]Department of Chemistry, Lahore College for Women University, Lahore

Corresponding Author: rabia.raza@lcwu.edu.pk

Abstract

Accurate prediction of the band gap in nanoparticles is crucial for advancing sustainable technologies, including light-emitting diodes (LEDs), sensors, displays, and lasers. This study investigates the application of machine learning (ML) techniques for predicting the band gaps of zinc sulfide (ZnS) nanoparticles, a material of considerable technological and environmental significance. Band gap data derived from UV-Vis spectrophotometry and literature sources were used to train and validate five ML models: Support Vector Machine Regression (SVR), k-Nearest Neighbors (KNN), Random Tree (RT), Multilayer Perceptron (MLP), and Additive Regression (AD). These models demonstrated high predictive accuracy, providing valuable insights into the band gap behavior of ZnS while significantly reducing the dependency on resource-intensive experimental methods. This ML-driven approach offers a rapid, cost-effective, and environmentally sustainable alternative to traditional characterization techniques. By enabling efficient optimization and discovery of nanomaterials, the findings contribute to the advancement of sustainable solutions for energy, environmental, and technological applications.

Keywords: LED, ML, Zinc sulfide, UV, MLP, RT, AD

PP-49

Zinc Oxide Nanoparticles based efficient Electrochemical Sensors for the Simultaneous Detection of Metal Ions

Haiqa, Saqib[1], Reemal, Imtesal[1], Iram, Shahzadi[1], Rabia, Raza[1], Sara, Riaz[2], Saneea Ata ul Haq[1,] *
[1]Department of Chemistry, Lahore College for Women University, Lahore
[2]Department of Chemistry, COMSATS University Islamabad, Lahore Campus, Pakistan
Corresponding Author: saneea@lcwu.edu.pk

Abstract

Rapid industrialization in Lahore, Pakistan, has led to significant groundwater contamination by heavy metals, posing severe public health risks. This study developed a cost-effective method for detecting lead (Pb^{2+}), cadmium (Cd^{2+}), and chromium (Cr^{3+}/$Cr6^{+}$) in wastewater. Zinc oxide nanoparticles (ZnO-NPs) were synthesized via a sol-gel method using zinc acetate dihydrate, resulting in flower-like nanoparticles with an average size of 20 nm. These ZnO-NPs were incorporated into a polyvinylidene fluoride (PVDF) composite film and drop-cast onto carbon cloth to fabricate a modified electrode. The ZnO nanoparticles were characterized using UV-Visible and Fourier Transform Infrared (FTIR) spectroscopy, Scanning Electron Microscopy (SEM), and X-ray Diffraction (XRD). The modified electrode's performance was evaluated through cyclic voltammetry (CV), electrochemical impedance spectroscopy (EIS), and differential pulse voltammetry (DPV) for the detection of heavy metal ions Pb^{2+}, Cd^{2+}, and Cr^{3+}/$Cr6^{+}$ in wastewater. The electrode exhibited rapid, sensitive, and reliable detection, meeting international water quality standards. This highlights the potential of ZnO-NPs-based electrodes as an efficient and cost-effective solution for addressing heavy metal contamination in industrial wastewater. The study emphasizes the role of innovative sensing technologies in reducing health risks, protecting the environment, and advancing Sustainable Development Goal (SDG) 3 by raising awareness about the dangers of contaminated wastewater to vulnerable communities near industrial zones.

Keywords: Zinc oxide nanoparticles, polyvinylidene fluoride, Scanning Electron Microscopy, differential pulse voltammetry

PP-50

In Silico Analysis of Anti-Flaviviridae Polygonaceae Derived Phytochemicals

Fatima Azhar[1]**,** Sarba Ejaz[1], Hina Asad[1], Muhammad Shoaib Akhter[1], Muhammad Ali[1]

[1]Department of Life Sciences, University of Management and Technology

*__Corresponding Author__: muhammad_ali@umt.edu.pk

Abstract

Flaviviridae is a large family of viral infections that cause serious illness and death in both humans and animals. They are lipid-enveloped single-strand positive-sense RNA genomes. The genus having Dengue virus, yellow fever virus, Zika virus, and several more. The Dengue virus (DENV) is arthropod-borne, an agent of genus flavivirus of the Flaviviridae family, is often a microstructure that may be transmitted by female mosquitoes that are only able to reproduce within a host body. Dengue virus is considered a serious health hazard to public health in the 21st-century results in major socio-economic hindrances in a vast region of the world. Envelope protein (EP) (3C5X) heterodimer, and Genome Polyprotein (NS5) (6KR2) non-structural protein of Dengue virus (DENV) are involved in the replication of this disease. The main purpose of this study is to screen antiviral phytochemicals from plant family *Polygonaceae* that may act as effective inhibitor against both proteins, (EP), and, (NS5), of the dengue virus. A total of 269 phytochemicals were selected from *Polygonaceae* depending upon its important therapeutic activities. To assess the potential phytochemicals against DENV, research-based on absorption, distribution, metabolism, excretion, toxicity, molecular docking, and density functional theory (DFT) was conducted. Only 155 out of 269 phytochemicals followed the drug-likeness criteria. Molecular Docking was done to see the binding affinity of these phytochemicals with the target proteins. The screening results of these 155 phytochemicals show that 122 phytochemicals were found to have binding affinities against both proteins. 42 phytochemicals were found to have binding affinities of ≥ 6.0 Kcal/mol against the EP of the dengue virus and 40 Phytochemicals showed the binding affinities of ≥ 6.0 against NS5 of dengue virus. Out of these 42, 5 phytochemicals were found as the best inhibitors for each protein of the dengue virus. Density Functional Theory (DFT) was performed to examine the reactivity and efficiency of the selected similar phytochemicals. Alanine scanning showed that the GLY 86 residue is the most important residue altering the residue drastically affects interaction potential.

Keywords: Flaviviridae, Dengue virus, Phytochemicals, Antiviral, Polygonaceous, Molecular Docking

PP-51

Emesvirus zinderi (Levivirus MS2)

Asifa Roohi[1*]

[1]University of Management and Technology

[*]**Corresponding Author**: asifaroohi313@gmail.com

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 encapsidation 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 and two RNA SLs designated as B and H in the current study have significant role in MS2 encapsidation. 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 structure 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: Levivirus, RNA SLs, encapsidation, ssRNA, CP-RNA

PP-52

Comparative Genomics analysis of Psychrophilic Bacteria to investigate their unique Adaptations across Diverse Cold Ranges

Nadir Zaman[1*], Saira Bano, and Fatima Mehmood
University of Management and Technology, Lahore, Pakistan
Corresponding Author: ghadir.ali@umt.edu.pk/S2021366008@umt.edu.pk

Abstract

Psychrophilic bacteria can survive in extremely cold habitats. These bacteria are found across a variety of cryospheric ecosystems, such as polar ice caps, deep-sea sediments, alpine glaciers, and permafrost, making them essential models for studying mechanisms of cold adaptation. With the emergence of high-throughput sequencing technology, an abundance of genomic information from psychrophilic bacteria has been made available in public repositories, offering a unique opportunity to investigate their evolutionary and functional adaptations through comparative genomic approaches. This research utilizes sophisticated bioinformatics tools to conduct a comprehensive comparative genomic analysis of psychrophilic bacteria across various temperature ranges. By identifying species-specific genes, we showed the genetic foundations of their strategies for cold adaptation. Principal genomic characteristics under examination include maintenance of membrane fluidity, synthesis of cryoprotectants, cold-acclimation proteins, and DNA repair mechanisms that improve survival in freezing environments. Our results yield essential insights into the molecular processes that allow these extremophiles to cope with cold-induced stress. This investigation not only enhances our understanding of microbial existence in extreme conditions but also contributes to the wider domain of extremophile genomics.

Key Words: Psychrophilic bacteria, Comparative genomics, Cold adaptation, Extremophiles, Bioinformatics, Cryoprotectants, extremophile genomics

PP-53

Antimicrobial Potential of Ethanolic Leaf Extracts of *Mentha Royleana* using Response Surface Methodology

Amina Hanan[1*]

[1]Department of Life Sciences, School of Science, University of Management and Technology, Lahore

Corresponding Author: F2022253002@umt.edu.pk

Abstract

This study investigates the morphological, molecular, and phytochemical diversity of *Mentha* species, particularly *Mentha royleana* and *Mentha arvensis*, from Gilgit-Baltistan (GB), Pakistan, where these species are traditionally used to treat asthma, gastrointestinal issues, and as haemostatic agents. Approximately 30 species of *Mentha* are found in GB, with *M. royleana* and *M. arvensis* being of significant local importance. The study aimed to examine the concordance between morphological traits and molecular data of *Mentha spicata* and *M. royleana*. Morphological traits, including leaf blade shape, leaf margin, leaf apex, and flower color, were assessed. Quantitative analysis revealed significant variation in stem length (20–65 cm), leaf area (15–45 cm^2), and chlorophyll index (25–45 SPAD units). Molecular characterization was performed using the Internal Transcribed Spacer (ITS) region of rDNA for DNA barcoding. This analysis showed 95–100% similarity with Gene Bank sequences, confirming species identities. Unweighted Pair Group Method with Arithmetic Mean (UPGMA) analysis classified the species into three distinct groups based on morphological variation. Random Amplified Polymorphic DNA (RAPD) analysis further revealed genetic variation within and between species. Phytochemical analysis involved extracting samples using ethanol and water-based systems to estimate total phenolic content, total flavonoid content, and antioxidant potential. The highest antioxidant activity (96.67%) was observed in *Mentha longifolia* leaves, and the highest phenolic content was found in *M. royleana* (0.164 GAE/mg). Leaf protein content ranged from 13.8% to 21.54%, with the highest content in *M. arvensis* from Muhammadabad and *M. royleana* from Gilgit city and Bagrot. The results demonstrate the significant morphological and genetic diversity among *Mentha* species and their potential as a source of bioactive compounds. These species show promising antioxidant and pharmacological properties, highlighting their potential for pharmaceutical applications.

Keywords: *Mentha royleana, Mentha arvensis,* UPGMA, Quantitative analysis

PP-54

Waste to Wealth: Extracting Heavy Metals & Creating Organic Fertilizers

Sundas Rania[1*], Kainat[1]. Sara Sajjad[1]

[1]Department of Life Sciences, University of Management and Technology

Corresponding Author: s2023232009@umt.edu.pk

Abstract

This article explores the innovative approach of utilizing hyperaccumulator plants for the extraction of heavy metals from contaminated soils, a process known as phytoremediation. Heavy metals such as lead, cadmium, arsenic, and nickel pose significant environmental and health risks due to their persistence in ecosystems. The study highlights the mechanisms through which hyperaccumulators absorb and concentrate these metals, detailing the processes of root uptake, transport, and storage within plant tissues. Following the growth of these plants, methods such as bioleaching are employed for metal recovery, utilizing metal-tolerant bacteria to enhance extraction efficiency. Additionally, the article discusses the dual benefits of this approach: the production of organic fertilizers through biomass utilization, including biochar and liquid fertilizers, which improve soil quality and promote sustainable agriculture. The findings underscore the environmental, economic, and long-term benefits.

Keywords: Hyperaccumulator plants, phytoremediation, Heavy metals,

PP-55

Evaluation of Serum Paraoxonase and Arylesterase Activity in Primary Glaucoma Patients

Muhammad Zeeshan Idrees[1], Sher Ali[1], Muhammad Akram[1, *]

[1]Department of Life Sciences, School of Science, University of Management and Technology, Lahore, 54770, Pakistan

[*]**Corresponding Author:** muhammad_akram@umt.edu.pk

Abstract

Glaucoma remains one of the leading causes of blindness in the Pakistani population. However, the molecular mechanisms behind glaucoma are still not clearly understood. It has been hypothesized that *PON1* gene polymorphisms through associated enzyme activity may influence clinical outcomes of glaucoma. In this study *PON1* gene polymorphisms, as determined by PON1 L55M and PON1 Q192R SNPs as well as associated serum paraoxonase and arylesterase activities in Primary Open Angle Glaucoma (POAG) and Primary Closed Angle Glaucoma (PCAG) patients were evaluated. In the healthy population as well as glaucoma patients, *PON1* QQ and the *PON1* LL genotypes were predominant over QR and RR, and LR and RR genotypes respectively. *PON1* coding region polymorphism showed occurrence of *PON1* Q192R polymorphism in healthy controls (61%), POAG patients (63.5%) and PCAG patients (66%) while the frequency of occurrence of *PON1* 55L polymorphism was 64% in healthy controls, 73.5% in POAG patients and 68% in PCAG patients. Overall, our results depicted no significant association between *PON1* genotypes and glaucoma. However, higher serum paraoxonase activity was observed for the PON1 RR genotype. Furthermore, significant differences in serum paraoxonase and arylesterase activities in glaucoma patients compared to young healthy individuals was observed, suggesting age dependent association of PON1 with glaucoma.

Key words: Enzyme activity, paraoxonase, arylesterase, glaucoma, PON1 polymorphism

PP-56

Isolation and Growth Optimization of Bacterial Strains for Remediation of Diesel Contaminated Soil

Tuba Umar[1*], Kaneez Fatima[1]

[1]Department of Life Sciences, University of Management and Technology, Lahore, Pakistan

Corresponding Autor: tubabiya200@gmail.com

Abstract

Petroleum contamination is one of the major threats to this environment, of which diesel is the main component. Diesel persists longer and spreads toxicity into the environment it interacts with. Conventional treatment methods often fail to address these pollutants as they are less effective, time-consuming, costly, and require larger space. Thus, a sustainable and innovative approach is much needed in demand to remediate contaminated soil. This study explores a bioremediation approach using indigenous diesel degrading/biosurfactant-producing bacterial strains in combination with green-synthesized silver nanoparticles (AgNPs) for the remediation of diesel-contaminated soil. 7 Bacterial strains isolated from contaminated soil were characterized for bio-surfactant production, and diesel-degrading potential. Simultaneously, AgNPs were synthesized from grapefruit extract. This approach is consistent with green chemistry principles, resulting in lower environmental toxicity and higher nanoparticle stability. Additionally, the consortium of 4 positive diesel-degrading isolates was prepared after their compatibility testing. This consortium along with AgNPs were tested individually and in combination to determine the most effective method of hydrocarbon degradation and assess bioremediation. The system demonstrated a significant increase in remediation efficiency and faster pollutant removal through FTIR analysis. FTIR spectroscopy was employed to monitor the structural changes in diesel components, confirming the degradation of hydrocarbon functional groups after bioremediation treatment. An increase in peak intensity and diversity of functional groups over time indicated the progressive breakdown of hydrocarbons and the formation of intermediate oxidation products, confirming effective diesel degradation. A comparison of treatment systems revealed that the combination of bacterial strains and AgNPs outperformed standalone approaches regarding diesel degradation efficiency and operational stability. Combining bio-surfactants and nanoparticles reduced the inhibitory effects of high pollutant concentrations on bacterial growth. Thus, the findings establish a framework for developing scalable, cost-effective, and long-term bioremediation technology for environmental restoration and pollution management.

Key Words: Diesel Contamination, Bioremediation, Microorganisms, Nanoparticles, Bio-surfactants, Environmental Restoration

PP-57

Predicting diabetes using Machine Learning with genomic data

Wania Babar[1*]

[1]Department of Biotechnology University of Management and Technology

[*]**Corresponding Author:** s2023254002@umt.edu.pk

Abstract

The provided study aim is to incorporate the machine learning techniques with genomic and health-related data to predict diabetes. There are several features such as age, BMI, glucose levels, and genetic markers were included in a bespoke dataset respectively. Logistic regression is utilized for the main model. It is used for determining whether a person had diabetes or not. The algorithm depicts in predicting diabetes risk showcase a 75% accuracy rate. Predicting diabetic patients outperformed non-diabetic instances. It is analyzed according to evaluation measures like precision, recall, and F1-score. This work advances healthcare by highlighting the significance of machine learning in enhancing diabetes early diagnosis.

Keywords: diabetes prediction, machine learning, logistic regression, metrices

PP-58

Integrative Bioinformatics and Computational Drug Discovery Reveal *Astragalus membranous* as a Potential Therapeutic Agent for Liver Cancer via Targeting Five Prognostic Hub Genes

Aqsa Nazir[1], Muhammad Akram[1*]

[1]Department of Biotechnology University of Management and Technology

[*]**Corresponding Author:** Muhammad_akram@umt.edu.pk

Abstract

Liver cancer ranks as the sixth most common malignancy and the fourth leading cause of cancer-related deaths globally. By 2025, over one million new cases are anticipated, underscoring an urgent need for novel diagnostic and therapeutic strategies. Although conventional treatments have advanced, they often yield suboptimal outcomes, prompting exploration into safer and more effective alternatives. This study utilized transcriptomic data from the GEO dataset GSE121248 to identify a robust gene signature associated with liver cancer prognosis. Differentially expressed genes (DEGs) were subjected to enrichment analysis and pathway annotation to uncover critical biomarkers. Network pharmacology, molecular docking, density functional theory (DFT) analysis, and molecular dynamics (MD) simulations were employed to evaluate the therapeutic potential of bioactive compounds from *Astragalus membranaceus* (Huangqi), a traditional Chinese medicinal herb known for its immunomodulatory and anti-inflammatory effects. Five real hub genes—*ESR1*, *CXCL12*, *NR1I2*, *CYP2C8*, and *HGF*—were identified as key biomarkers influencing hepatocellular carcinoma (HCC) progression. Computational analyses revealed strong binding affinities and favorable pharmacodynamic properties of one lead compound derived from Astragalus membranaceus, suggesting its potential as a novel therapeutic agent for HCC. Conclusion: This integrative approach highlights the utility of combining bioinformatics with traditional medicine for drug discovery. The identified hub genes and compound provide promising targets for developing personalized treatments against liver cancer, emphasizing the value of Astragalus membranaceus as a rich source of anti-cancer bioactives.

Keywords: Liver Cancer, Hepatocellular Carcinoma (HCC), Astragalus membranaceus, Gene Expression, Molecular Docking, Hub Genes, Computational Drug Discovery

PP-59

Elucidation of virus genome-linked protein (VPg) interaction as a primer in poliovirus RNA replication

Ayesha Tahir[1*]

[1]Department of Life science, school of science, University of Management and Technology

[*]**Corresponding Author:** ayesha.tahirch01@gmail.com

Abstract

Poliovirus belongs to the family *Picornaviridae* and genus *enterovirus*. Poliovirus is a major cause of poliomyelitis. Poliovirus is transmitted through the fecal-oral route and initially infects the gastrointestinal tract before spreading to the nervous system. Upon infection, poliovirus affects the nervous system of humans and causes paralysis within a few hours. It contains 60 copies of four capsid proteins: viral protein 1 (VP1), VP2, VP3, and VP4. For genome replication, virus-genome-linked protein (ORF 3B; VPg; 22 amino acid long) acts as a primer for the viral RNA-dependent RNA polymerase (RdRp). VPg is attached to the 5' end of the single-stranded RNA genome. VPg is linked to viral RNA by a tyrosine-phosphate bond (Tyr-04)-pU-U-A-A. The replication starts when the virus binds to the poliovirus receptor CD155 on the host cell membrane. The viral RNA is released into the cytoplasm and acts as mRNA for translation. The H dock tool is used to dock the VPg proteins from multiple viruses with their cognate and non-cognate RNA(s). The results showed that VPg proteins are specific to their cognate RNA(s) when compared with their non-cognate RNA(s) counterparts. Future research may unravel the intricate details of the interaction specificities.

Keywords: Virus genome-linked protein, RNA-dependent RNA polymerase.

PP-60

Bioprocess-Driven, Sustainable Lipid Production for Liposomal Drug Encapsulation

Inshal Aamer[1*], Faiza Dar[1], and Aneshra Nabeel[1]
Department of Life Sciences, University of Management and Technology, Lahore

Corresponding author: inshalaamer1@gmail.com

Abstract

Liposomes have developed as a highly effective drug delivery technology due to their biocompatibility, ability to encapsulate both hydrophilic and hydrophobic medicines, and controlled release features. However, typical liposome synthesis is based on chemically produced or plant-derived phospholipids, which face cost, scalability, and environmental concerns. The goal of this research is to create a bioprocess-based technique for producing sustainable phosphatidylcholine (PC) through microbial fermentation or enzymatic synthesis, which will serve as an alternative lipid source for pharmaceutical liposome formulations. The study aims to optimize the bioprocess for microbial PC generation using transgenic yeast (Yarrowia lipolytica, Saccharomyces cerevisiae) or microalgae (Chlorella, Schizochytrium), as well as investigate enzyme-assisted lipid synthesis via phospholipase-mediated pathways. Key process parameters including as carbon and nitrogen sources, pH, temperature, and agitation will be optimised to maximise phospholipid output. Extracted phospholipids will be purified using solvent extraction and chromatographic methods, then structurally confirmed using HPLC, GC-MS, and NMR spectroscopy. The bioprocess-derived phospholipids will be formed into liposomes using thin-film hydration and microfluidic techniques, encapsulating a model drug (e.g., doxorubicin or curcumin) to assess encapsulation efficiency, drug release kinetics, and stability. Size distribution, zeta potential, and cytocompatibility will be assessed on mammalian cell lines using MTT tests in comparison to synthetic phospholipid-based liposomes. The goal of this research is to develop a cost-effective, scalable, and sustainable bioprocess for phospholipid synthesis, which will reduce the reliance on chemically extracted lipids in pharmaceutical formulations. The discoveries could help in the development of next-generation biopharmaceuticals, nanomedicine, and environmentally friendly drug delivery systems.

Keywords: Liposomes, Phosphatidylcholine, Bioprocessing, Microbial Fermentation, Enzyme-Assisted Synthesis, Drug Delivery, Sustainable Biotechnology

PP-61

Production and Characterization of *Yarrowia lipolytica* Enzyme

Tayyaba Qamar[1*], Muhammad Akram[1]

[1]Department of Life sciences, School of science, University of Management and Technology

Corresponding Author: F2023254003@umt.edu.pk

Abstract

Yarrowia lipolytica is a non- pathogenic ascomycetous yeast which is often found in environment with the presence of hydrophobic substrate such as dairy products and oily waste. We can natively isolate the strains and characterize it because it has an ability to degrade lipids and proteins and produce a wide range of industrially relevant enzymes such as lipases, proteases and esterases. There are wide range of enzymes that are industrially used. The main objective of this study is to extract some important types of enzymes from *Yarrowia lipolytica* which can be further utilized for industrial purposes. This study focuses on the optimization of growth conditions such carbon sources, temperature, pH and nitrogen sources for the enhanced production of extracellular enzymes by Y. lipolytica. For this purpose, we will allow *Yarrowia lipolytica* to grow on our daily life food components (oils, ghee) by optimizing their growth conditions. Through in-silico approach and analysis we will gain further insight into the molecular characteristics of *Yarrowia lipolytica* and its different enzymes. This will be a pure computational analysis using different analytical tools like docking, homology modeling and stability profiles of enzymes. Once the enzyme will be extracted it will be purified using different purification techniques. This study will provide better understanding of *Yarrowia lipolytica* transcriptomics, and how to better utilize this strain as a source of some crucial enzymes. To sum up, extracting and purifying enzymes from Yarrowia lipolytica plays a vital role in unlocking their valuable applications across various industrial and medical fields.

Keywords: *Yarrowia lipolytica*, in-silico analysis, transcriptomics, optimization, characterization

PP-62

Investigating the role of isoaccepting tRNA in Cancers

Maryam Batool[1*], Rameen Rizwan[1], Muhammad Ali[1]

[1]Department of Life sciences, School of science, University of Management and Technology

Corresponding Author: S2024254001@umt.edu.pk

Abstract

Breast cancer metastasis entails multifaceted molecular mechanisms, among which translational control by transfer RNAs (tRNAs) plays an important role. The present investigation identifies opposing roles of two isoleucyl tRNA isoacceptors, tRNA$^{\text{Ile}}_{\text{UAU}}$ (decodes AUA) and tRNA$^{\text{Ile}}_{\text{GAU}}$ (decodes AUC), in metastatic progression. Highly metastatic breast cancer cells show elevated levels of tRNA$^{\text{Ile}}_{\text{UAU}}$ and silenced tRNA$^{\text{Ile}}_{\text{GAU}}$, a pattern reproduced in advanced-stage human tumors. Functional studies validate that tRNA$^{\text{Ile}}_{\text{UAU}}$ facilitates metastasis, whereas tRNA$^{\text{Ile}}_{\text{GAU}}$ inhibits metastasis. TRNA$^{\text{Ile}}_{\text{UAU}}$ overexpression increases metastatic colonization in mice, while its CRISPR-induced knockdown is defective in metastasis. On the other hand, restoration of tRNA$^{\text{Ile}}_{\text{GAU}}$ in invasive cells decreases metastasis, and its depletion increases metastatic growth. Pol III binding and tRNA Capture-seq indicated higher expression of tRNA$^{\text{Ile}}_{\text{UAU}}$ and lower expression of tRNA $^{\text{Ile}}_{\text{GAU}}$ in metastatic cells. These findings were corroborated by northern blotting, and RT-qPCR, of human breast cancer tissue microarrays that established upregulation of tRNA$^{\text{Ile}}_{\text{UAU}}$ and suppression of tRNA$^{\text{Ile}}_{\text{GAU}}$ in advanced tumors with increased metastatic potential. Mechanistically, these tRNAs control codon-dependent proliferation gene translation. Ribosome profiling and proteomics reveal that upregulation of tRNA$^{\text{Ile}}_{\text{UAU}}$ increases translation of AUA-enriched transcripts. Genetic encoding of AUA-to-AUC codons in target genes eliminates their translational upregulation, validating tRNA-mediated regulation. The antagonism stems from tRNA-ribosome interactions: tRNA$^{\text{Ile}}_{\text{UAU}}$ decodes AUA effectively but not AUC because of discouraging U-C wobbling, while tRNA$^{\text{Ile}}_{\text{GAU}}$ fails to decode AUA (G-A wobbling is forbidden).

Keywords: Breast cancer, Isoleucine, Codon optimization, tRNA, Northern blotting

PP-63

In-silico Drug Designing Against Proteins Causing Breast Cancer

Urooj Fatimah[1] and Rana Muhammad Mateen[1]

[1]Department of Life sciences, School of science, University of Management and Technology

Corresponding Author: Rana Muhammad Mateen[1]

Abstract

Breast cancer (BC) stands as the most common cancer among women and is the leading cause of cancer-related deaths. Endocrine therapy and chemotherapy are commonly used to treat individuals with hormone-positive (ER+ and/or HER2+) BC, which makes the condition easier to treat. Triple-negative breast cancer (TNBC) is a challenging and aggressive form of cancer due to its lack of hormone receptors, making it significantly more difficult to treat effectively. Additionally, cancer stem cells (CSCs) have a high potential for tumorigenesis, which may contribute to TNBC's aggressive nature. Another major obstacle to lowering breast cancer death rates has been multidrug resistance. According to the literature, MAPK1/ERK2 and ALDH1A1 are markers of TNBC, playing critical roles in both proliferation and tumorigenesis. After fulfilling strict ADME properties, ninety-six phytochemical compounds are docked against selected proteins MAPK1/ERK2, and ALDH1A1 by employing Autodock vina. The compounds with lowest binding energies are selected for molecular dynamic simulation and Density functional theory.

Key Words: Breast cancer, Triple negative breast cancer (TNBC), ALDH1A1, ERK2, and Phytochemicals

PP-64

Isolation, Identification & Characterization of Extremophile Bacterial Strain from Industrial Effluents

Sehar Fatima[1], **Maira Khan**[1], **Tayyaba Javaid**[1]

[1]Department of Life sciences, School of science, University of Management and Technology

Corresponding Author: F2021232022@umt.edu.pk

Abstract

The contamination of water bodies by industrial effluents poses significant environmental and public health challenges, particularly in developing regions. To solve these problems, bacterial strains were isolated from effluents collected from the drainage pipes of Chaman Industries, Lahore, Pakistan. To selectively isolate extremophiles, serial streaking was performed on alkaline media at pH 9. Morphological identification of the bacterial strain was conducted through various staining techniques and molecular identification through 16S rRNA sequencing confirmed the strain as *Exiguobacterium profundum*. A comprehensive set of biochemical tests were performed to further characterized the bacterium's metabolic capabilities. Bioinformatic analysis revealed the upregulation of the gene mtlD, encoding the enzyme Mannitol-1-phosphate 5-dehydrogenase, which catalyzes the conversion of D-mannitol 1-phosphate to D-fructose 6-phosphate. This enzyme, essential for mannitol biosynthesis, likely plays a key role in the bacterium's adaptation to extreme environmental conditions. Additionally, the bacteria showed significant resistance to heavy metals, suggesting its potential application in the bioremediation of industrial pollutants. These findings, highlight E. profundum as a promising candidate for future biotechnological applications in environmental remediation.

Keywords: Isolation, D-mannitol 1-phosphate, *Exiguobacterium profundum*

PP-65

In Silico Enzymes Screening for Liquiritin Pathway from Bacterial and Plant Sources

Zufa Mubariz[1], Muhammad Akram[1]

[1]Department of Life sciences, School of science, University of Management and Technology

Corresponding Author: muhammad_akram@umt.edu.pk

Abstract

Liquiritin, a flavonoid glycoside primarily found in licorice roots (*Glycyrrhiza spp.*), exhibits numerous pharmacological properties, including anti-inflammatory, antioxidant, and neuroprotective effects. Liquiritin also displays therapeutic potential in treating conditions such as Alzheimer's disease, stroke, cardiac hypertrophy, and polycystic ovary syndrome (PCOS). This approach combines data from both bacterial and plant sources to predict all enzymes that are involved in the biosynthesis of liquiritin This study aims to investigate and characterize the metabolic pathway of **liquiritin** using **in silico approaches**, in order to identify key enzymes, to understand its biotransformation and potential metabolites which has significant pharmaceutical and agricultural implications. In this research study enzymes involved in the metabolic pathway of liquiritin are screened. The enzymes are Tyrosine ammonia-lyase (TAL), 4-coumarate: CoA ligase(4CL), Chalcone synthase (CHS), Chalcone reductase (CHR), Chalcone isomerase (CHI) and Uridine Diphosphate Glucuronosyltransferase (UGT). In our research study NCBI, Uniport and KEGG databases will be used to collect the amino acid sequence of all the enzymes from bacterial and plant sources. We screened 10 sources of each enzyme from both bacterial and plant sources by constructing phylogenetic tree with the help of mega software. Pyrx software is used to perform molecular docking of proteins with ligands. Ligplot is used to investigate the complex interactions between protein and ligand complex. The Ligplot shows the results of interaction with all the protein ligand complex. Complexes that interact with the active site of the protein and shows hydrogen bonding were selected for MD simulation.

Key Words: Flavonoid, Polycystic ovary syndrome (PCOS), Cardiac hypertrophy**,** Tyrosine ammonia-lyase (TAL), Uridine Diphosphate Glucuronosyltransferase (UGT).

PAKISTAN ACADEMY OF SCIENCES

UNIVERSITY OF MANAGEMENT AND TECHNOLOGY

UMT

Estd. 1990

2nd UMT INTERNATIONAL CONFERENCE ON LIFE SCIENCES

Translating Research into Impactful Solutions

April 10-12 (Thursday-Saturday), 2025

UMT | SSC
School of Science