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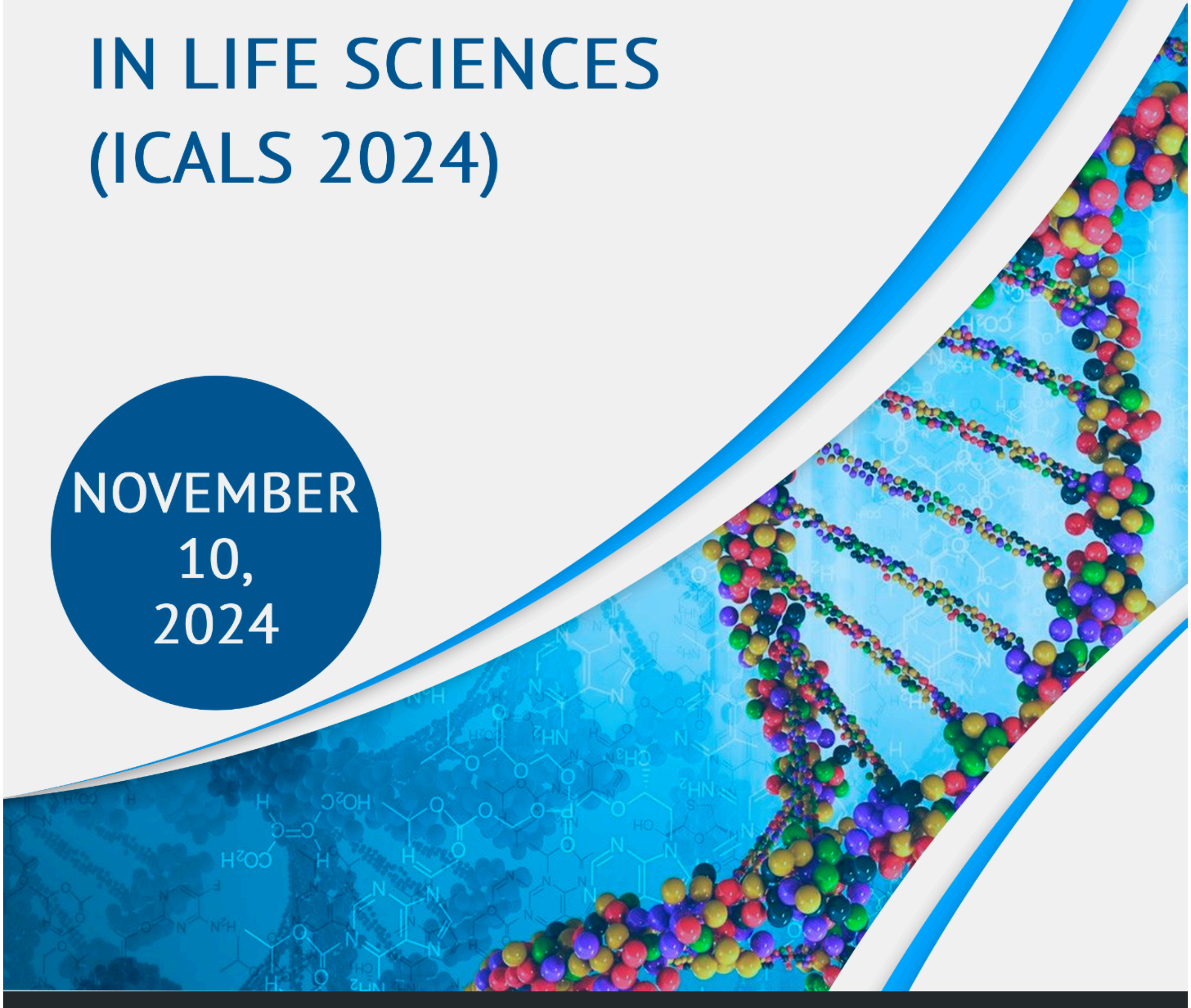

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BOOK OF ABSTRACTS

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Welcome Note

Dear Readers,

It is with immense pleasure that I welcome you to the abstract book of the *International Conference on Advances in Life Sciences (ICALS 2024)*, organized by the *World Forum for Young Scientists (WFYS)*. This conference serves as a global platform to unite scientists, researchers, and industry professionals in exploring the latest advancements in life sciences and fostering interdisciplinary collaborations.

On behalf of WFYS, I extend my heartfelt gratitude to our esteemed collaborator, the *Office of Research, Innovation, and Commercialization (ORIC)*, *The Islamia University of Bahawalpur, Pakistan*, for their invaluable support in making this event a resounding success.

I also express my deep appreciation to our distinguished speakers for sharing their expertise, the presenters for showcasing their innovative research, and the attendees for their enthusiastic participation. Your contributions are the cornerstone of this event's success and a driving force for advancing global research culture.

We hope this abstract book inspires you to push the boundaries of science and encourages meaningful collaborations. Together, let us continue to shape the future of life sciences and beyond.

Warm regards,

Muzzamil Shehzad
Founder
World Forum for Young Scientists (WFYS)

Date: November 10, 2024

ICALS 2024 Conference Schedule

Session Chair: Syeda Anza Hasnain

Time	Speaker/Presenter Name	Affiliation (Institution/Organization, Country)
6:00 PM - 6:15 PM	Dr. Hamdi Temel	Bozok University, Türkiye
6:15 PM - 6:30 PM	Dr. Malak Zirari	IBN TOFAIL University, Morocco
6:30 PM - 6:45 PM	Dr. Kamala Badalova	Azerbaijan Medical University, Azerbaijan
6:45 PM - 7:00 PM	Dr. Ammara Riaz	Khwaja Fareed University, Pakistan
7:00 PM - 7:15 PM	Dr. Samina Shabbir	The Women University, Pakistan
7:15 PM - 7:30 PM	Dr. Iram Liaqat	Government College University Lahore, Pakistan
7:30 PM - 7:45 PM	Dr. Muhammad Omar	Cairo University, Egypt
7:45 PM - 8:00 PM	Dr. Abrar Hussain	ICCBS, University of Karachi, Pakistan
7:55 PM - 8:10 PM	Dr. TAIBI Mariame	Ibn Tofail University, Morocco
8:10 PM - 8:20 PM	Joshua Sumogat	Mindanao State University, Philippines
8:20 PM - 8:30 PM	Ashiru Aliyu Zainulabidin	SR University India, Nigeria
8:30 PM - 8:40 PM	FATIMA CHARBOUB	Ibn Zohr University, Morocco
8:40 PM - 8:50 PM	Abaida Barae	Hassan 2 University, Morocco
8:50 PM - 9:00 PM	Dr. Fahmida Channa	Sindh College Education, Pakistan
9:00 PM - 9:10 PM	Dr. M Sajjad Sarwar	University of Okara, Pakistan
9:10 PM - 9:20 PM	Saif Nur Chowdhury	Applied Health and Science Hospital, Bangladesh
9:20 PM - 9:30 PM	Ramkrishna Mishra	Banaras Hindu University, India
9:30 PM - 9:40 PM	Barket Hussain	Aligarh Muslim University, India
9:40 PM - 9:50 PM	Jahan Huseynli	Azerbaijan Medical University, Azerbaijan
9:50 PM - 10:00 PM	Prof. Kiran Rafiq	Jinnah Sindh Medical University, Pakistan
10:00 PM - 10:10 PM	Hakima Farahi	Ibn Zohr University, Morocco
9:10 PM - 10:20 PM	Laiba Ashfaq	University of Agriculture Faisalabad, Pakistan
10:20 PM - 10:30 PM	Oladele Ifeoluwa Anike	Ahmadu Bello University, Nigeria
10:30 PM - 10:40 PM	Umar Ali	ABDUL WALI KHAN UNIVERSITY, Pakistan
10:40 PM - 10:50 PM	Javeria Maqbool	Government College University Faisalabad, Pakistan
10:50 PM - 11:00 PM	Sara Razzak	Ibn Tofail University, Morocco
11:00 PM - 11:10 PM	Pujita Shil	University of Science and Technology Chittagong, Bangladesh
11:10 PM - 11:20 PM	Mahnoor Shams	Federal Urdu University, Karachi, Pakistan
11:20 PM - 11:30 PM	Ishaq Yusuf	Aliko Dangote University of Science and Technology Wudil, Nigeria
11:30 PM - 11:40 PM	Muhammad Ammar	Capital University of Science and Technology, Pakistan
11:40 PM-11:50 PM	Saifullah	University of Agriculture Faisalabad, Pakistan
11:50 PM-12:00 AM	Selwyn Barreto	Nitte University, Ireland
12:00 AM- 12:15 AM	Fatima Shakeel	Government College University, Pakistan
12:15 AM- 12:30 AM	Dr. H. SHEIK JAHABAR ALI	Alagappa University, Karaikudi, Tamil Nadu.

TABLE OF CONTENTS

Nutritional composition, phytochemicals, and antioxidant activities of *Abies marocana* Trab. needles

Malak Zirari[1], Marouane Aouji[2], Sara Razzak[2], Driss Hmouni[2], and Nouredine El Mejdoub[1]

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Purpose: The search for natural sources of bioactive compounds has gained significant importance in both scientific research and industry. Abies marocana, or Moroccan fir, is particularly valued for its ecological, economic, social, and cultural significance.

Method: This study evaluated the nutritional and anti-nutritional properties, bioactive components, and antioxidant capacity of Abies marocana needles. The composition was determined using AOAC methods, while mineral content was analyzed through inductively coupled plasma optical emission spectrometry (ICP-OES). Phytochemical screening of the methanol extract followed standard procedures, and various assays assessed antioxidant activity. Gas chromatography-mass spectrometry (GC-MS) characterized the extract’s volatile profile.

Results: Proximate analysis revealed that the needles contain essential components, including carbohydrates, crude protein, crude fiber, crude fat, ash, and moisture. Anti-nutritional factors such as chlorophyll, carotenoids, and vitamin A were also confirmed. The needles were found to be a rich source of minerals, with notable levels of phenolic compounds, flavonoids, tannins, and phytosterols. GC-MS analysis identified key compounds, including palmitic acid, 17-octadecynoic acid, and (Z)-18-octadec-9-enolide. The methanolic extract displayed significant antioxidant capacity, as demonstrated by high percentage inhibition in DPPH scavenging assays.

Conclusions: Integrating Abies marocana needles into sustainable diets offers potential benefits for human health and the environment. The bioactive compounds present may have valuable applications in the pharmaceutical and food industries. This study underscores the significance of exploring natural resources like Abies marocana, which not only contribute to biodiversity but also offer promising avenues for health and nutrition.

Genome-wide identification of G-protein coupled receptors (GPCRs) and their expression profile in response to β-cypermethrin stress in *Zeugodacus cucurbitae*

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Abstract

G-protein coupled receptors (GPCRs) are the largest and most diverse transmembrane receptor family in the cell. They are involved in regulating a wide range of biological processes, including behavior, reproduction, and development. However, GPCRs have not yet been identified in *Zeugodacus cucurbitae*. The current study focuses on the GPCRs identification, classification, distribution, and their expression analysis under β-cypermethrin stress to uncover novel targets for pest management and assist in the development of effective strategies for controlling the melon fly population. We identified 80 GPCRs genes including 50 GPCRs identified in family A, 18 GPCRs identified in family B, 7 identified in family C, and 5 identified in family F. *Z. cucurbitae* GPCRs showed significant differences in both the number of genes in families or subfamilies, as well as the sequencing of the genes. Interestingly, newly identified GPCRs genes are expressed differently at various developmental stages of *Z. cucurbitae*. Further, we evaluated these 80 GPCRs using Realtime quantitative PCR (to confirm their expression between β-cypermethrin -resistant (RS) strain and susceptible strain (SS) of *Z. cucurbitae*. We identified 50 GPCR genes were highly overexpressed in a RR. Among these genes, eight genes were strongly induced by the 30% lethal concentration (LC) while two genes were significantly increased by the 50% LC of β-cypermethrin. This first genome-wide profiling and characterization of GPCRs could lay foundation for unraveling detoxification mechanism and target site modifications which may improve the insect resistance and could be effective insecticide targets for *Z. cucurbitae* management.

Keywords: Effective insecticide, G protein-coupled receptors, Pest management, Transmembrane receptor, β-cypermethrin

Probiotics as Medicine: A New Horizon in Therapeutics

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Abstract

The overwhelming applications of probiotics are extended to their therapeutic potential. Probiotics, which are live microorganisms with beneficial properties when taken in sufficient amounts, possess a huge spectrum of benefits in every sector. The probiotic health benefits are more advantageous than their other properties, as they give holistic treatment options. The debate, can we use probiotics as medicine, still remains, but currently a good number of probiotic strains are used as therapeutic agents. Contrary to traditional medicine, probiotics offer natural, safer, and vastly beneficial aspects. Literature data showed the vast benefits of probiotics for GIT-related diseases, although these are used for respiratory, infections, metabolic, and allergic diseases. The important guidelines that will follow while taking probiotics as medicine include strain level identifications, safe origin, safe nature, greater viability, and enhanced adherence potential. With the exception of immunocompromised individuals, pregnant women, and infants, probiotics showed a safer profile of usage as medicine in others. Versatility in the commercialized forms and multiple routes of administration enhance their medicinal aspects. Nevertheless, limitations are existing, including the time-consuming process, microbial diversity of the host, and strain-dependent properties. The use of advanced technologies and genetic engineering might overcome these challenges. To limit the unethical use of probiotic medicine, strict guidelines should be developed.

Keywords: probiotic, medicine, microbiome, disease, adherence

Impact of cesium and strontium contamination on Moroccan soils and wheat: A study of soil characteristics and plant responses

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Purpose: This study investigates the impact of cesium (Cs) and strontium (Sr) contamination on two wheat species, *Triticum durum* and *Triticum aestivum*. The primary objective is to assess soil properties, evaluate the toxicological effects of Sr and Cs, and analyze the physiological responses of the wheat species. The study addresses the knowledge gap concerning the influence of Cs and Sr on crop health and soil characteristics in semi-arid Moroccan regions. **Method**: Soil samples were collected from three locations in the Rabat-Sale-Kenitra region: El Koudia, Merchouch, and El Guich. The soils were analyzed for texture, pH, calcium carbonate ($CaCO_3$), organic matter (OM), cation exchange capacity (CEC), and elemental composition (Ca, K, Na, Mn, Fe). X-ray diffraction (XRD) and X-ray fluorescence (XRF) analyses identified soil mineralogy and trace element concentrations. Sr contamination levels of 0, 10, 100, and 1000 mM were tested on wheat seeds to evaluate germination rates, growth parameters, and antioxidative enzyme activity (SOD, CAT, POD). The effect of Cs exposure was also examined on biomass and root length. **Results**: Soil analysis revealed variation in texture, with clayey soils in Merchouch, sandy in El Guich, and sandy clay loam in El Koudia. Sr levels were 0.17 ppm in El Koudia and Merchouch and 0.32 ppm in El Guich, while Cs remained undetectable. Sr exposure reduced germination rates in *T. aestivum* by 18% at 10 mM, 45% at 100 mM, and 70% at 1000 mM, compared to 9%, 28%, and 52% reductions in *T. durum*, respectively. Growth parameters and enzymatic activities were similarly impacted, with *T. durum* showing better regulation of stress responses. Under Cs exposure, *T. durum* showed higher resilience, with a 22% reduction in biomass at 10 mM Cs compared to a 35% reduction in *T. aestivum*. At 100 mM Cs, biomass reductions were 40% in *T. durum* and 55% in *T. aestivum*. **Conclusions**: This study demonstrates that *T. durum* exhibits higher tolerance to both Sr and Cs contamination compared to *T. aestivum*. The findings address critical gaps in understanding the impact of Sr and Cs on wheat crops in semi-arid regions and provide valuable insights for improving agricultural practices in contaminated soils.

Establishment of *Wolbachia* infection in *Aedes aegypti* from Pakistan via embryonic microinjection and semi-field evaluation of general fitness of resultant mosquito population

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Abstract

Background: Dengue is a mosquito-borne viral disease that is mainly spread by *Aedes aegypti*. It is prevalent on five continents, predominantly in tropical and sub-tropical zones across the world. *Wolbachia* bacteria have been extensively used in vector control strategies worldwide. The focus of the current study was to obtain a natural population of *Ae. aegypti* harbouring *Wolbachia* and to determine the impact of this bacteria on the new host in a semi-field environment. **Methods**: *Wolbachia*-infected *Aedes albopictus* was collected from the city of Lahore, Punjab, Pakistan, and *Wolbachia* were successfully introduced into laboratory-reared *Ae. aegypti* via embryonic microinjection. The stable vertical transmission of *w*AlbB in the host population was observed for eight generations, and the impact of *Wolbachia* on the general fitness of the host was evaluated in semi-field conditions. **Results**: In the laboratory and semi-field experiments, *w*AlbB *Wolbachia* presented a strong cytoplasmic incompatibility (CI) effect, evidenced as zero egg hatching, in crosses between *Wolbachia*-infected males and wild (uninfected) females of *Ae. aegypti*. *Wolbachia* infection had no noticeable impact on the general fitness ($P>0.05$), fecundity, body size (females and males) and mating competitiveness of the new host, *Ae. aegypti*. However, there was a significant decrease in female fertility (egg hatch) ($P<0.001$). In addition, under starvation conditions, there was a remarkable decrease ($P<0.0001$) in the life span of *Wolbachia*-infected females compared to uninfected females (4 vs. > 5 days, respectively). **Conclusions**: *Wolbachia* strain *w*AlbB has a great potential to control the dengue vector in *Ae. aegypti* populations by producing 100% CI with a limited burden on its host in natural field conditions. This strain can be used as a biological tool against vector-borne diseases.

Keywords: *Wolbachia*, *Aedes aegypti*, *Aedes albopictus*, Embryonic microinjection, Cytoplasmic incompatibility

Exploring Heat-Resistant Genetic Traits in Maize (*Zea Mays* L.): A Pathway to Sustainable Agriculture

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Abstract

Maize (Zea mays L.) is considered the most significant cereal crop in the world. It is a dynamic cereal crop that can be grown in both the spring and autumn season. When sown in March, both the female and male flowers are subjected to high-temperature stress, often leading to poor seed development. Climate change, which introduces biotic and abiotic stresses, has been contributing to a decline in maize yields. It is crucial to identify traits that influence yield and their interrelationships to aid in the development of diverse, high-yielding germplasm. To address this, a study was conducted using a Randomized Complete Block Design (RCBD) in the research fields of the Department of Plant Breeding and Genetics at the University of Agriculture, Faisalabad. Twenty-five genetically diverse maize genotypes were planted in mid-February (as a control) and mid-March to assess their tolerance to high-temperature stress. The genotypes were evaluated for various parameters, including germination rate, leaf area, leaf temperature, plant height, pollen fresh and dry weights, anthesis-silking interval, cob length, number of grains per cob, number of cobs per plant, yield per plant, and 100-seed weight. The results indicated that genotypes such as Pbg-4, 6192, Pbg-3, 6196, 2014, Ctr3, and 6272 exhibited significant variability and performed well under heat stress. These genotypes, showing high adaptability to stress conditions, represent valuable genetic resources with a broad range of genes for heat tolerance, which could be utilized in breeding programs aimed at developing high-temperature-resistant maize varieties.

Keywords: Pollen production, High temperature, Genetic diversity, Maize, Yield

Evaluation of the adsorption characteristics of biomass produced from plant waste and its application for the removal of Lead and Cadmium

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Abstract

The biomaterial produced from plant waste was prepared and modified with low-cost H_3PO_4, which is naturally available and cost-effective in the Souss Massa region. The biomaterial was characterized using XRD, FTIR and SEM methods. The two heavy metals lead and cadmium were selected as the target pollutants, and the high-performance, environmentally-friendly 'batch adsorption' depollution technique was used. Adsorption was applied for analyzing and optimization of the experimental factors such as applied initial pH, temperature, quantity of biomaterial, contact time and initial metal concentration. Adsorption kinetics were expressed as second-order kinetics and isotherm modelling showed that the Langmuir model was adequately fitted to the experimental data with R2 (0.9994). Under optimum conditions, the maximum removal efficiency was obtained to be 87.84% for Pb and 90.2% for Cd. Furthermore, the reusability test of the biomaterial after several cycles confirmed the high adsorption activities of the adsorbent. The results of the present study revealed that the batch adsorption process was a suitable method for removing lead and cadmium from aqueous solutions.

Key Words: Biomaterial; plant waste; adsorption; cadmium; lead; desorption; kinetic model; isotherm

Harnessing Health: A Deep Dive into Antioxidants and Nutritional Profile of the Moroccan *Ulva lactuca* from the Mehdia coast

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Purpose: The investigation of seaweeds to identify their bioactive metabolites in light of their potential broader uses has gained significant relevance.

Method: This work's objective was to investigate the proximate analysis, mineral composition, fatty acid profiles, water and oil-holding capacities, and antioxidant activity of various solvent extracts of *Ulva lactuca*.

Results: The results showed that *Ulva lactuca* could be identified by its fiber content (12.68 ± 0.5%), carbohydrates (61.12 ± 1.42%), proteins (22.15 ± 1.7%), and lipids content (1.3 ± 0.1%). *Ulva lactuca* has higher quantities of unsaturated fatty acids, an excellent ω3/ω6 ratio, and a high nutritional content. It constituted a significant source of elements, especially K, Na, Mg, Ca, P. The methanolic extract showed higher phenolic (45.69 ± 3.24 mg gallic acid equivalents g^{-1} DM), flavonoid (15.49 ± 0.064 mg quercetin equivalents g^{-1} DM), and tannin (22.52 ± 8.23 mg catechin acid equivalents g^{-1} DM) content than other extracts. Using total antioxidant capacity, DPPH (2, 2-Diphenyl-1-picrylhydrazyl), and reducing power assays, the results demonstrated that the three examined extracts had antioxidant effects; however, in the three assays evaluated, the methanol extract possessed the highest antioxidant activity, with an half inihibitory concentration of 33.6 ± 1.31 µg mL^{-1} in the DPPH radical scavenging assay. The investigation demonstrated that *Ulva lactuca* water and oil holding capacities changed with temperature and were similar to those of many commercial fiber-rich goods.

Conclusions: *Ulva lactuca* from the coastal waters of Kenitra, presents a viable option for use in nutritional contexts, pharmaceuticals, and the agri-food industry because of its biochemical composition, functional characteristics, and antioxidant properties.

Keywords: *Ulva lactuca*, Proximate analysis, Biochemical composition, Nutritional profile, Antioxidant activity

Removal of 2,4,6-Tri(2-pyridyl) -s-triazine solution by Anodic Oxidation using a Boron-Doped diamond Anode

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Abstract:

This study aims to evaluate the degradation efficiency of a triazine family pesticide, a toxic herbicide released into the environment during its use in the agricultural sector, using one of the advanced oxidation processes (AOP), specifically electro-oxidation, in an open undivided electrolytic cell (BDD/carbon felt). The role of the BDD anode was crucial, as it provides a high oxygen evolution potential, promoting the efficient mineralization of organic matter. Factors such as current density, temperature, pH, and compound concentration were analyzed to assess their impact on the degradation rate. The results indicate that the removal rate reached 99.9% after 40 minutes of treatment at room temperature. The BDD electrode demonstrated the best performance in degrading this pesticide under optimal conditions: a current density of 10 mA/cm², a pH of 3, and a temperature of 25 ± 3 °C. The high efficiency of this electrochemical method can be attributed to direct electro-oxidation on the BDD surface and the involvement of hydroxyl radicals (•OH).

Keywords : Anodic oxidation, Advanced oxidation process (AOP), Degradation, Wastewater treatment. BDD/Carbon felt, Hydroxyl radicals (OH°)

Pakistan's Genetic Health Crisis: The Hidden Threat of High Consanguinity

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Purpose: Pakistan with fifth largest population globally, cousin marriages are very common because of religious, social, cultural, and economic reasons. This results in a diverse genetic landscape especially seen in first cousin marriages. Consanguinity leading to genetic disorders which is one of the greatest public health threats. This study was aimed to examine the correlation between Pakistan's rate of consanguinity and the prevalence of genetic diseases, as well as compare it to other nations.

Method: In this study, consanguinity rates and inbreeding coefficients from the most recent population surveys of Pakistan and 72 other Muslim and non-Muslim nations are compared using statistical analysis. Data on the prevalence of the 30 most prevalent genetic disorders in Pakistan was also gathered through extensive literature mining. Using Bayes' theorem, the prevalence rates of various genetic disorders were determined and compared with averages worldwide prevalence. Data visualization and analysis were performed at the end.

Results: The results highlight that Pakistan has the highest consanguinity rate in the world, but other Islamic nations also have high rates. Additionally, Pakistan has the highest inbreeding coefficient globally. By predicting, the prevalence of the 30 most common genetic disorders in Pakistan shows a direct relation between genetic disorders and consanguinity.

Conclusions: Study concludes that high consanguinity is the major factor contributing to genetic disorders in Pakistan. As a result of this profound effect, the Pakistani population shows diversity in genetic predispositions and polymorphism. To reduce this public health threat, immediate potential nationwide initiatives such as mandatory screening programs and prenatal diagnosis are required.

Keywords: Consanguinity; Genetics; Inherited Disorders; Prevalence; Public Health; Pakistan;

Nutritional composition, functional and chemical characterization of Moroccan *Opuntia ficus-indica* cladode powder

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***Purpose**: Opuntia ficus-indica*, also known as the prickly pear, is a cactus belonging to the Cactaceae family. For centuries, this remarkable plant has been valued for its medicinal, environmental, and culinary uses.

***Method**:* The primary objective of this research is to examine and contrast the chemical composition, functional attributes, and nutritional significance of *Opuntia ficus-indica* cladodes sourced from three distinct regions in Morocco: Oulad Boubker, Imzouren, and Skoura.

***Results**:* According to the results, moisture content differs significantly between the three sites, with an acid pH value. While the ash content remained consistent across all three samples. Carbohydrate content ranging from 55.40 ± 0.08% to 55.90 ± 0.60%, fat content from 2.30 ± 0.21 to 2.62 ± 0.09, protein from 7.54 ± 0.03% to 9.07 ± 0.16%, crude fibers from 20.52 ± 1.87% to 21.00 ± 0.20%, and soluble fibers from 15.08 ± 0.16% to 16.33 ± 1.25%. Additionally, total chlorophyll content varied between 102.64 ± 8.93 and 144.80 ± 3.08 mg.100 g^{-1} DM. The water holding capacity, the oil holding capacity and the solubility index as a functional properties showed considerable differences between the three samples. Mineral analysis revealed significant differences based on location. The concentrations of potassium exhibited a considerable elevation compared to those of magnesium, calcium, sodium, iron, and zinc. Moreover, the existence of diverse organic functional entities, including alcohols, ketones, and acids, was authenticated by Fourier-transform infrared spectroscopy.

***Conclusions**:* A differential distribution of the chemical composition of cladodes according to region was confirmed by nutritional, mineral and functional characterization and functional groups of cladodes.

Association Between Diabetic Nephropathy and Macrovascular Complications in Type 1 Diabetes Mellitus Patients of Nausharo Feroze and Adjoining Area

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Abstract:

Most common microvascular complication of Type 1 diabetes mellitus (T1DM), diabetic nephropathy (DN), is a strong predictor of macrovascular complications such as peripheral arterial disease (PAD), cerebrovascular disease (CVD), and coronary artery disease (CAD). The elevated morbidity and mortality seen in T1DM patients is mostly caused by these macrovascular complications. This study aims to determine the association between diabetic nephropathy (DN) and the frequency of macrovascular complications in patients with type 1 diabetes mellitus (T1DM) . In a cross-sectional study, 350 T1DM patients aged 20-25 years had an average HbA1c level of 7.5-8.5% and a diabetes duration of 10-15 years. Patients were categorized based on the presence or absence of diabetic nephropathy (DN). The results showed that DN was present in 35% of T1DM patients and that macrovascular complications were significantly more prevalent in this population. More specifically, T1DM patients with DN had significantly greater prevalences of CAD, CVD, and PAD than those without DN (25% vs. 8% for CAD, 14% vs. 4% for CVD, and 12% vs. 3% for PAD). In order to possibly decrease the risk of serious cardiovascular complications these findings highlight the vital significance of early DN identification and integrated cardiovascular risk management in T1DM patients.

Keywords: Type 1 Diabetes Mellitus, Diabetic Nephropathy, Macrovascular Complications, Coronary Artery Disease, Cerebrovascular Disease, Peripheral Arterial Disease

Phytochemical Profiling, In Vitro Antioxidant Activity, and In Silico Anti-Bacterial Analysis of Ethylacetate Leaf Extract of Daniella oliveri

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Purpose: The leaf of Daniella oliveri has been a source of traditional medicine. This study aims to determine the phytochemical constituents, evaluate the in vitro antioxidant potential, and conduct an in silico anti-bacterial analysis of the ethylacetate leaf extract of Daniella oliveri.

Method: A 50g sample of air-dried, powdered leaves was extracted using ethylacetate in a Soxhlet extractor. The crude extract was concentrated to dryness, and phytochemical screening was conducted using standard procedures. The antioxidant activities were determined in vitro at a concentration of 1000 µg/mL. An in silico analysis was performed to evaluate the antibacterial activity of the plant extract against several bacterial strains.

Results: Phytochemical analysis revealed the presence of compounds such as flavonoids (2.0103± 0.33611), phenolics (136.42±45.1616), alkaloids (8.376±0.001), tannins (0.0687±0.0003), saponins (0.0217± 0.00153), cardiac glycosides (0.0381 ±0.00016), anthraquinones, and polyphenols. The antioxidant activity assays showed: Total Antioxidant Activity (DPPH) 68.87±0.0208%, Reducing Power Assay 2.138+0.004 Absorbance, Hydroxyl Radical Scavenging Assay 74.8210+0.00%, Hydrogen Peroxide Scavenging Assay 77.3256+0.44%, and Total Antioxidant Capacity 5.5943+ 0.24 µg/mL. The in silico anti-bacterial analysis revealed inhibitory activity against Mycobacterium tuberculosis, Yersinia pestis, Staphylococcus aureus subsp. aureus MW2, Burkholderia pseudomallei, Clostridium tetani, Helicobacter pylori, Mycobacterium bovis, Streptococcus, Bacillus anthracis, and Shigella sp.

Conclusions: The presence of significant phytochemicals in the ethylacetate leaf extract of Daniella oliveri suggests its potential as a natural antioxidant and antibacterial agent. These findings support the plant's traditional use in herbal medicine and highlight its potential therapeutic applications in mitigating oxidative stress and related diseases.

Keywords: Daniella oliveri, Phytochemical analysis, Antioxidant activity, Antibacterial activity, Ethylacetate extract, Traditional medicine, In silico analysis

Genome Wide Identification of Drought Responsive, Vicinal Oxygen Chelate, a Glyoxalase 7 (*GLYI7*) in Response to Artificially Induced Drought Stress in Brassica Species.

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Abstract

Extraction of edible oil from Brassica species has been a traditional practice by humans to fulfill nutritional and therapeutic requirements. Drought stress adversely affects seed development, yield, quality, shoot elongation, germination, and seedling establishment in Brassica. The present study aimed to experimentally generate drought stress in Brassica species, specifically *B. carinata*, *B. juncea*, *B. oleracea*, *B. napus*, *B. nigra*, and *B. rapa*. This study comprehensively evaluated the genome-wide discovery of 33 *GLYI7* genes across six Brassica species. Genes were subsequently classified into five unique categories for *GLYI7* according to their evolutionary ties. The analysis of gene structures and motifs indicated that *GLYI7* genes (comprising three exons and two introns) within each group had comparable exon-intron organization and conserved motif patterns. The anticipated 33 *GLYI7* proteins varied in length from 167 to 609 amino acids, with their expected molecular weights distributed across a spectrum from 18782.64 kDa to 67800.11 kDa. The collinearity analysis indicated that *GLYI7* gene families underwent segmental duplications throughout their evolutionary history. Multiple hypothesized stress-responsive cis-acting elements were detected in the promoter region of the *GLYI7* genes. The expression profile of Bna*GLYI7* was significantly altered in various developmental tissues in reaction to drought stress. Additionally, to assess drought tolerance-related indices in six brassica species during the germination and seedling phases, treatments of 15%, 30%, and 45% Polyethylene glycol 6000 (PEG 6000) were employed to simulate artificial drought conditions, alongside a control group, in a replicated fashion. The seed, plant morphology, growth, and biomass characteristics decreased as the concentration of PEG rose. The present work elucidated that *GLYI7* gene protects plants from damage caused by environmental stresses, especially drought. This enabled the identification of Brassica species which demonstrated increased resilience to drought stress, thereby aiding in the advancement of breeding and agricultural methods aimed at improving drought tolerance.

Exploring the Morphological Diversity of Maize (*Zea Mays* L.) Genotypes in Response to Saline Condition

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Abstract

Maize is recognized as the second most important cereal crop, belonging to the Poaceae family, and is highly sensitive to salinity stress. Salinity poses a major challenge globally due to poor water management practices. It adversely impacts the growth and development of maize. This research aimed to investigate the morphological effects of different NaCl concentrations (0.0 mM, 0.3 mM, 0.6 mM, and 0.9 mM,) on various growth parameters of maize. Four maize genotypes (UAF-22, UAF-11, UAFPB-313, and UAFPB-1301) were chosen for a comparative study, with three separate trials conducted. Data on growth parameters were collected every 10 days. These parameters included root and shoot length (cm), root and shoot fresh weight (g), root and shoot fresh weight ratio (g), root and shoot dry weight (g), root and shoot dry weight ratio (g), shoot and root length (cm), number of leaves and roots per plant, and leaf area (cm^2). Statistical analyses were performed using Turkey's range test and Analysis of Variance (ANOVA). The results from Turkey's test indicated that very high (0.9 mM) and very low (0.0 mM) NaCl concentrations significantly impacted the growth of maize genotypes, whereas moderate (0.6 mM) NaCl concentrations did not affect growth and development. ANOVA results revealed significant differences among treatments and maize genotypes. Genotypes UAF-22 and UAF-11 exhibited greater salt tolerance compared to UAFPB-313 and UAFPB-1301, which were more salt-sensitive. The superior growth patterns of UAF-22 and UAF-11 under varying salinity levels suggest their higher tolerance to salinity, leading to improved growth and development under salt stress conditions.

Keywords: Salinity, maize, Genotypes, Stress, Morphological, NaCl.

Uncovering Beneath Mounds: A New Orphnaecus Species from Mimbilisan, Mindanao, Philippines

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Abstract:

Theraphosidae are ambush predators inhabiting burrows, trees, caves, or wetlands. With 1,109 total species globally, four of five *Orphnaecus* species are found in the Philippines, however, limited studies and illegal trade threaten their biodiversity. This study aims to provide a morphological description of a tarantula species collected from the Mimbilisan Protected Landscape, Misamis Oriental, and compare it with the five-known species of the genus *Orphnaecus*, a group under the family Theraphosidae. Specimens were collected from coconut husk mounds in an abandoned agricultural area at an elevation of 470 meters. The spiders' microhabitats were analyzed, and morphological traits were examined using Olympus SZ61 microscopes with digital imaging. Measurements of body parts, including legs, eyes, and copulatory organs, were taken, and taxonomic comparisons were made with descriptions from previous literature. The male holotype specimen (MPL02) measured 49.41 mm in total length, featuring distinct prosoma and opisthosoma characteristics, cheliceral dentition, and spinneret structure. Its leg measurements, body setae distribution, and pedipalp structure were analyzed in detail. The female paratype (MPL03), measuring 34.09 mm, showed notable differences in chelicerae, eye sizes, and abdomen structure. Both specimens exhibited characteristics consistent with the genus *Orphnaecus* but differed from previously described species. The collected tarantula specimens from the Mimbilisan Protected Landscape present morphological features that suggest a new species of *Orphnaecus*. This study adds to the knowledge of tarantula biodiversity in the Philippines and highlights the need for further research to document and protect the region's spider fauna amidst risks from illegal trade and habitat disturbance.

Keyword: *new species, Mindanao, endemic, spider, morphology, taxonomy*

Exploring Antimicrobial and Antioxidant Properties of Metallic Oxide Nanoparticles: ZnO and CuO

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Abstract:

Introduction: The global issue of microbial resistance against commonly used medications arises from the overuse and misuse of antibiotics, highlighting the need for the development of novel antimicrobial agents to combat this problem. As an alternative to antibiotics, nanoparticles (NPs) have become increasingly utilized to target bacteria in recent years. But metal oxide NPs are receiving more interest in this area because they have stronger antimicrobial activity. Both CuO and ZnO NPs have strong antioxidant properties. **Methodology:** Antibacterial activity has been done against four critical gram-positive bacteria and four gram-negative bacteria by the agar-well diffusion method. Likely, the antifungal activity has also been done by the same procedure of agar-well diffusion method against two different classes of fungi. While antioxidant activity was done by the DPPH method. **Result:** CuO NPs showed great efficacy against bacteria some of them are: *S.aureus* (32mm), *E.coli* (28mm). ZnO NPs also showed the zone of inhibition against bacteria some of are: *S.aureus* (24mm), *E.coli* (20mm). For fungus inhibitory zone against *Aspergillus niger* by CuO is (22mm) and against *Candidia albicans* is (16mm) and ZnO showed inhibitory zone against *Aspergillus niger* is (12mm) and against *Candidia albicans* is (17mm). While % inhibition of antioxidant activity of CuO is (92.76%) and of ZnO is (76.79%). **Conclusion:** As an outcome of microbes becoming more resistant to standard antibiotics, we believe the development of uncomplicated, inorganic antimicrobial agents, like metal oxide NPs, as a substitute for conventional antibiotics.

Keywords: CuO, Metal-Oxide, NPs, ZnO.

Role of melatonin in mitigating high-temperature stress in *Solanum lycopersicum* L.

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Abstract

High-temperature (HT) stress poses a significant challenge to tomato plants, adversely affecting growth and productivity. This study explores the innovative application of melatonin (MT) to enhance the resilience of *Solanum lycopersicum* L. under HT stress. Tomato plants were subjected to various treatments, including a control group at 25°C and elevated temperatures of 30°C, 35°C, or 40°C, at 30 days after transplant (DAT), and the plants were given 50 µM MT at 40 DAT. The elevated temperatures reduced chlorophyll content, impaired photosynthetic efficiency, diminished cell viability, stunted plant growth, and compromised fruit quality. Additionally, root morphology and stomatal physiology were negatively affected, leading to increased oxidative stress characterised by elevated reactive oxygen species (ROS), malondialdehyde (MDA), and electrolyte leakage. Conversely, the application of MT (50 µM) positively influenced plant performance by enhancing chlorophyll levels, improving photosynthetic efficiency, and increasing the activities of key antioxidant enzymes, such as catalase (CAT), peroxidase (POX), and superoxide dismutase (SOD). Remarkably, MT significantly minimised the detrimental effects of HT stress, with low levels of ROS and MDA, improved stomatal morphology, and enhanced overall plant growth and fruit quality. These results reveal the potential role of MT as a strategic tool for enhancing HT tolerance in tomato plants, providing valuable insights for improving crop resilience amid the challenges posed by climate change.

Binding affinity of Beta Vulgaris with Hb by molecular docking and evaluation of effect of its selected phytochemicals

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ABSTRACT:

Beetroot is an affiliate of the Chenopodiaceae family, especially the Amarantaceae subfamily, belonging to the Beta genus and vulgaris species. *Beta vulgaris* is a tuberous seasonal herb with long stems and is indigenous to the Mediterranean region. Beetroots are extensively cultivated in North America, Europe, Asia, and Indo-Pak. Beetroot has several advantages, such as being fat-free, high in fiber, and low in calories. This work is undertaken to explore active compounds which would contribute in the treatment of anemia. A total of 30 *beta vulgaris* plant phytochemicals and 19 phytochemicals from vulgaris species were docked to proteins involved in anemia. The compounds were docked to the active site amino acids of oxyhaemoglobin, haemoglobin and Anticalin protein as receptor proteins in order to explore their inhibiting potential. The top five compounds against each receptor protein were explored as potential drug candidates on the basis of their binding affinity and root-mean square deviation values. The top compounds against each protein were found to be betanidin (S-score -9.6 kcal/mol) and Chlorogenic acid (S-score -7.8 kcal/mol) against oxyhaemoglobin, Alpha-spinasterol glucoside (S-score -7.6 kcal/mol) and silibinin (S-score -7.8 kcal/mol) against the anticalin protein, silibinin (-9.4 Kcal/mol) and Vitamin E (-8.6 kcal/mol) against haemoglobin protein. The selected phytochemicals were further assessed through drug scanning using Lipinski's rule of five to explore their molecular properties and drugability.

Keywords: Medicinal Plant;. *Beta Vulgaris*; Betanidin; phytochemicals; Haemoglobin;

Impact of E-Sel Supplementation on Egg Production, Fertility, and Hatchability in Japanese Quail (Coturnix japonica)

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Abstract

Dietary deficiencies, particularly in vitamins and minerals, are critical issues in poultry nutrition, often leading to reduced egg production, fertility, and hatchability. This study aimed to evaluate the effects of Vitamin E, selenium, and zinc supplementation on egg production, fertility, and hatchability of Japanese Quail (Coturnix japonica). The study was conducted in a Private facility from February 2022 to May 2022 to explore the effects of supplementations (E-SEL, Albovit Selenex Plus) on egg production, fertile eggs and hatched chicks of Japanese quail kept under captivity. The birds were categorized into two groups, i.e., a control and an experimental group, each consisting of one male and three females. It was observed that the supplementations showed significant effects on fertility at $P<0.05$ with maximum egg fertility of 91%, and increased egg production and hatchability of 86% were noticed in the experimental group. It was concluded that supplementation has good impacts on egg production, fertility, and hatchability of Japanese Quail.

Keywords: Japanese Quail, Supplementation, Egg Production, Fertility, Hatchability

Role of transcription factor *Cut* in cortex glia gliopodia growth

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Abstract:

Drosophila central nervous system (CNS) mainly comprises of three types of glial cells, peripheral, cortex associated and neuropil associated glia. These are structurally and functionally different from each other. One important feature of many glial cells is their ability to extend long, thin membrane projections called gliopodia. These projections are essential for connecting glial cells to neurons and other glial cells, allowing for the formation of functional neural networks. The molecular pathways that regulate the formation and maintenance of gliopodia are still unclear. To addressing this question, we used the UAS-GAL4 binary system to drive the expression of genes of interest or knockdown specific genes thought to regulate gliopodia development in *Drosophila* glial cells. Here, we show that *Cut*, a homeodomain transcription factor regulates glial-subtype growth differentially and regulates cortex glia morphogenesis independently of PI3K-Akt-mTOR signaling. Our research finding provides knowledge of how cortex glial cells establish functional networks within the CNS. This is crucial for understanding the role of glial cells play in shaping neural connectivity and maintaining synaptic integrity, which could have broader implications for neurological disorders where glial dysfunction is implicated.

Keywords: Cortex glia, Cut, *Drosophila*, gliopodia, PI3K-Akt-mTOR

Ecological Dynamics of Hornet Predation on Honeybee Colonies Insights for Sustainable Beekeeping in Mardan, Pakistan

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Abstract:

Beekeeping is essential to agricultural and the balance of the ecosystems by the honey production and pollination.But hornet predation, particularly by Vespa orientalis,Vespa carboro and Vespa tropica poses a threat to the productivity and survival of honeybee colonies.The purpose of this study is to investigate the dynamics of these interactions in Mardan, Pakistan, in order to promote sustainable beekeeping practices and lessen the effects of predation. Between May and August, when hornet activity was at its highest point, the study has been carried out. Temperatures were constant during this time, with the majority of days being sunny and ranges between 36°C and 37.8°C.Up to 232 hornet arrivals and more than 100 bees were captured in larger honeybee colonies, including those in Umar Abad (Katlang) and Qasami (Lund Khwar). Hornets found these colonies more attractive due to their higher bee density. Predation rates varied by region as well, with smaller colonies in places like Quaied Abad (Lund Khwar) and Haithan (Sher Garh) receiving fewer visits from hornets than apiaries in Lund Khwar and Katlang. The most prevalent predator among the three hornet species under study was Vespa orientalis, which showed aggressive behaviour that resulted in a considerable loss of bees. The results show that larger colonies are more vulnerable to hornet attacks, due to its visibility.Vespa orientalis predation must be controlled with effective management strategies, demonstrating the significance of focused control measures to protect honeybee colonies in Mardan.

Keywords: Beekeeping,Ecological dynamics,Hornet predation,Honeybee colonies, Honey production, Vespa orientalis.

The Study of Phthalates in Plastic Material; A Precarious Substance for Human Health

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Abstract:

Plastic is the most commonly employed material for packaging as well as for manufacturing every day consumer goods including containers, straws, bottles etc., due to its affordability and durability. Various plasticizers, tas like phthalates, are added to soften and improve flexibility of plastic polymers. Phthalates, particularly Di-2-ethyl-hexyl phthalate (DEHP), are prevalent plasticizers used to enhance the flexibility of plastics. However, their leaching into the environment poses significant health risks, including endocrine disruption and adverse reproductive effects, impacting puberty and pregnancy. Chronic exposure to these endocrine-disrupting chemicals (EDCs) can lead to long-term health issues, particularly in vulnerable populations such as children. Regulatory measures are essential to mitigate these risks and protect public health from the harmful effects associated with phthalate exposure in everyday plastic products. DMP and DEP are two short-chained and low molecular weight phthalates that are heavily produced in diverse industries of PCPs (such as hair products), pharmaceuticals, and medical devices. Phthalates themselves are expected to be the highest selling phthalate and in 2020 a global market for all phthalates was recorded billions. Current study intends to scrutinize the occurrence of multiple phthalates in six plastic categories including water bottles, plastic straws, expanded polyester, polypropylene resins, plastic spoon,, cold drink bottle and Plastic container. Gas chromatography–mass spectroscopy was used to characterize the samples, and they identified DEHP in any of six samples that were further confirmation limit set for DEHP should be enforced to prevent related disease.

Key words: Phthalates, Plasticizers, DEHP, EDCs, Pharmaceuticals

Role of Advance technologies in precision treatment in Cancer Research

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Abstract: Cancers are a group of heterogeneous diseases characterized by the acquisition of functional capabilities during the transition from a normal to a neoplastic state. Numerous experimental and computational tools enable the discovery of mechanisms underlying cancer occurrence, progression, metastasis, and drug resistance, yet challenges remain. The growing interest and potent need for precision medicine have brought forward robust techniques, including Bulk RNA sequencing, which helps identify gene expression, perform differential expression analysis, dimensionality reduction, clustering, and enrichment analysis. Additionally, machine and deep learning models are now utilized to predict patient outcomes and treatment effects from high-dimensional data. Recently, the emergence of single-cell RNA sequencing (scRNA-seq) technologies has become widely used in cancer studies to explore tumor heterogeneity and the tumor microenvironment. This technology provides opportunities to quantify different subpopulations and characterize cellular genomics.

This study explores these advanced methodologies to understand the complexity of cancer biology. Our aim is to integrate multiple technologies to discover new biomarkers and therapeutic targets, thereby advancing personalized medicine strategies.

Keywords: Cancer, Single-cell RNA-seq, Bulk RNA-seq, genomics, Precise medicine.

Co-relation of hypomagnesemia with clinical outcomes in critically ill patients admitted to a tertiary care ICU in Bangladesh

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Background: Despite being the fourth most abundant cation in the body and second most abundant intracellular cation significance of Mg in critically ill patients is rarely considered. Mg is important in muscle contraction, enzyme activity, and many other metabolic processes. Hypomagnesemia is common with critically ill patients and strongly associated with disease severity, longer hospital stays, and increased mortality. **Aim and Objectives:** Our goal was to investigate hypomagnesemia in a tertiary care ICU in Bangladesh and observe its relationship with disease severity and patient outcome based on patient mortality and diagnosis. **Materials and Methods:** A single-center prospective observational study of patients admitted to the ICU at Bangabandhu Memorial Hospital from July 2023 to June 2024. We primarily link magnesium levels to patient outcomes including mortality, duration of ICU stays, distribution of magnesium based on diagnosis, APACHE- II, CCI and SOFA scores and associated Risk Factors.

Results: A Total of 81 critically ill patients, 40 patients (49.38%) were normomagnesemia, 32 patients (39.50%) were hypomagnesemia and nine patients were hypermagnesemia. Patients with hypomagnesemia were more likely to be associated with respiratory, septic, neurological and other diseases ($p < 0.05$). The stay of the patients in ICU ($p = 0.03$), Sequential Organ Failure Assessment (SOFA) scoring ($p = 0.017$) and Charlson Co-morbidity index ($p = 0.04$) showed a significant variation between the two groups. In hypomagnesaemia patients, the mean ICU stay was 5.531±2.3689 days, compared to 4.5 ± 2.1839 for normomagnesemia patients ($p = 0.03$). Mortality of hypomagnesemia group was 31.25% while that of normomagnesemia group was 10.1%($p = 0.024$) **Conclusion:** The effect of hypomagnesemia in critically ill patients was highlighted in our study. Hypomagnesemia was well co-related with more adverse scenarios, showing a positive relationship with mortality and longer hospital stays. A positive relation with disease severity was seen with significant APACHE-II, SOFA and Charlson Comorbidity Index in hypomagnesemia patients compared to patients with normal magnesium levels.

Keywords: Co-relation, Hypomagnesemia, Carlson-comorbidity index, APACHEII, SOFA, ICU

Immune Response and Molecular Insights of Dengue Fever: A Systematic Review

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Background: With dengue cases rising rapidly, particularly in regions like Bangladesh, there is growing concern that dengue will soon become endemic or even epidemic. The frequent travel of infected individuals across regions contributes to this spread. Dengue virus (DENV) is evolving and adapting at a rate that poses significant diagnostic challenges due to its symptom overlap with other febrile and flaviviral illnesses. This paper presents a systematic review based on the clinical and medical aspects of the complicated immune responses and the molecular insights of Dengue Fever. **Methods:** A search was conducted in the Web of Science database for original articles published in life sciences and molecular journals between 2011 and 2023. The search strategy encompassed the subjects "generalized linear mixed models," "hierarchical generalized linear models," and "multilevel generalized linear models," focusing specifically on the science and technology research domain. Papers that focused solely on methodological considerations without application or were not related to molecular studies were excluded. This review was conducted according to the PRISMA under the statement. **Results:** 410 articles were detected for the review based on our search terms, and 95 articles were suitable according to our inclusion criteria. Papers screened for information collection were based on content similarity, irrelevancy to either clinical, medical field, or unsuitable to our search category. 7.8% of articles were duplicated, 3.27% were inconsistent, and 19.50% were not found in impact factor journals. 37.04% of articles were excluded after viewing titles and abstracts and detected as non-original and the rest 66.48% did not entirely represent molecular studies of Dengue. **Conclusions:** This study provides a link to our understanding of the misalignments at the Molecular level of signaling routes due to the DENV interference leading to the severity and possible clinical manifestations.

Keywords: Replication cycle, immunopathogenesis, immune receptors, signaling pathways, viral interventions.

Comparative Analysis Of Flowers Sold In Azerbaijan Under The Name "Chamomile"

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Abstract:

Chamomile (*Matricaria recutita* L.) is one of the most popular and widely used medicinal plants due to its anti-inflammatory, analgesic, antimicrobial, antispasmodic and sedative virtues. The purpose of our work is to make a comparison between the dried flowers available on the market and the official dried chamomile flowers in order to determine a genuine plant.

Two types of raw materials were subjected to macroscopic, microscopic, phytochemical analysis, and essential oil extraction. For microscopic analysis, the "Motic" SFC-18 series microscope was used at 400X magnification. Raw material extracted with ethanol were compared by TLC analysis. For the quantitative analysis of flavonoids, spectrophotometry with aluminum chloride was applied on the Cary 60 UV-Vis, using the rutoside as a standard. To identify the presence of azulene-type sesquiterpenes, the essential oils were hydrodistilled and examined, the results were compared with the European Pharmacopoeia 7.0.

A discrepancy in morphology and anatomy of the studied inflorescences was observed. TLC profiles showed the absence of apigenin 7-O-glucoside in flowers from local market, in contrast to the ones purchased in pharmacy. The total content of flavonoids was as following: flower tops purchased on the market - 2.4%, whereas ones from the pharmacy - 2.3%. Based on the results we concluded that the flowers sold on the market under the name "chamomile" are not corresponding to *Matricaria recutita* L. , and cannot replace the officinal species.

Keywords: *Matricaria recutita* L., macroscopic and microscopic examination, thin layer chromatography, apigenin-7-O-glycoside, spectrophotometric analysis

Artificial Intelligence in Microbiology: Enhancing Diagnostic Precision and Research Efficiency

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Purpose: This study explores the growing integration of Artificial Intelligence (AI) in the field of microbiology, with a focus on its impact on diagnostics and research processes. AI technologies, particularly machine learning and deep learning, have shown the potential to improve the speed and accuracy of microbial identification, pathogen detection, and antibiotic resistance screening. The study assesses how AI-driven methodologies can transform traditional microbiological techniques and contribute to enhanced clinical outcomes. **Method:** A systematic review was conducted, analyzing recent literature on AI applications in microbiology. The review includes qualitative and quantitative studies investigating AI's role in diagnostic algorithms, automated image analysis, and genomic data interpretation. Case studies from clinical settings and laboratories employing AI-based microbiological diagnostics systems were reviewed to assess effectiveness, accuracy, and efficiency. Data was synthesized to highlight common trends, challenges, and future directions for AI in microbiology.

Results: Preliminary results suggest that AI-driven systems significantly reduce diagnostic time, especially in detecting pathogens in clinical specimens and predicting antimicrobial resistance. AI algorithms demonstrated over 90% accuracy in image-based microbial identification, and predictive models for resistance patterns were highly reliable. The use of AI in genomic analysis also showed enhanced capabilities in sequencing large datasets for pathogen detection and monitoring. **Conclusions:** AI is poised to revolutionize microbiology, substantially improving diagnostic precision and research efficiency. While challenges such as data quality and algorithm transparency remain, ongoing advancements promise to enhance clinical outcomes and open new avenues for microbial research. Future applications may include personalized treatments and real-time surveillance of emerging pathogens.

Keywords:

Artificial Intelligence, Microbiology, Diagnostics, Machine Learning, Antibiotic Resistance, Genomic Analysis, Clinical Outcomes

PHENOTYPIC DETECTION AND ANTIBIOTIC SUSCEPTIBILITY OF EXTENDED SPECTRUM BETA-LACTAMASE PRODUCING *ESCHERICHIA COLI* AND *KLEBSIELLA SPECIES* FROM URINE OF PREGNANT WOMEN ATTENDING PRIMARY HEALTH CARE CENTRE, SAMARU.

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ABSTRACT

Urinary Tract Infections (UTIs) are commonly caused by microorganisms in the urinary tract, affecting the bladder, kidney, or ureter. Pregnant women particularly susceptible to UTIs due to physiological changes. This study aimed to investigate the incidence of *Escherichia coli* and *Klebsiella* species in pregnant women attending Primary Health Care Centre, Samaru. The aim of this study was to isolate and characterize *Escherichia coli* and *Klebsiella* species from the urine of pregnant women and determine their antibiotic susceptibility patterns. A total of 100 urine samples were cultured on Eosin Methylene Blue Agar (EMB) and MacConkey Agar. Colonies with Green metallic sheen on EMB agar and pink colonies on MacConkey Agar were subjected to Gram staining and biochemical characterization. Antibiotic susceptibility testing and double disk-synergy testing were performed on isolated organisms. Out of 100 urine samples, 2% were positive for *Escherichia coli* and 5% for *Klebsiella* species, yielding a total prevalence of 7%. All isolated organisms were Gram-negative rods. Antibiotics susceptible testing revealed 100% susceptibility to Gentamicin and 57.1% susceptibility to Ofloxacin. Conversely, 100% resistant was observed against Amoxicillin, Ceftazidime, Tetracycline, Augmentin, and 71.4% against Nitrofurantoin. Double-disk synergism testing indicate no Extended Spectrum Beta-Lactamase (ESBL) production. In conclusion, *Escherichia coli* and *Klebsiella* species are significant causes of UITs in pregnant women. Gentamicin and Ofloxacin are effective treatment options, as the isolated organisms showed susceptibility to these antibiotics. Notably, none of the isolated organisms produced ESBL, suggesting that urinary antibiotics remain effective against these pathogens.

Keywords: *Escherichia coli, Klebsiella* species, Urinary Tract Infection, Pregnant women, Extended Spectrum Beta-lactamase

In Silico Prediction of Drought-Responsive Genes in Barley (*Hordeum vulgare* L.) Using Expressed Sequence Tags (ESTs)

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Abstract

In this study, a comprehensive computational approach was employed to identify drought stress-responsive genes in barley (*Hordeum vulgare L.*) using Expressed Sequence Tags (ESTs). While various barley ESTs under drought conditions are cataloged in the NCBI database, these sequences had not been previously analyzed for functional gene prediction related to drought tolerance. Recognizing the impact of drought on barley's yield, despite its general resilience to abiotic stress, this study aimed to profile drought-induced gene expression using bioinformatics tools and software. A total of 7008 ESTs were retrieved from NCBI in FASTA format, processed through EGassembler and CAP3 for cleaning and clustering, resulting in 1228 contigs and 3683 singletons. Transcription factors (TFs) were identified using PlantTFcat, which classified 71 contigs into 33 TF families. Enzyme-coding genes were predicted with Blast2GO, identifying 484 EST-contigs related to major enzyme classes. Pathway analysis via the KEGG Automatic Annotation Server (KAAS) revealed that 391 EST-contigs participated in 1103 metabolic pathways. Novel genes associated with drought tolerance were identified by mapping non-annotated contigs and those without significant GO terms onto the barley genome through the Ensemble Plants database. The top 10 EST contigs, selected for high alignment scores, were extended for positional analysis, identifying candidate genes within barley's subgenomes. Promoter analysis indicated that 29 candidate genes contained more than 10 cis-regulatory elements linked to drought response. This study highlights key drought-responsive genes and provides insights into potential targets for developing drought-resistant barley varieties through genetic enhancement.

Keywords: Prediction, Barley, Genes, Expressed Sequence Tags, Drought, NCBI

Study of genetic diversity in Maize (*Zea mays* L.) Genotypes based on yield and its associated traits

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Abstract:

Maize is considered as "Queen of Cereals" due to its major contribution to the world's food security. Globally it is ranked as 2nd important cereal crop. It supplies low-cholesterol edible oil, feed, and food for both people and animals. In the present research, 20 maize genotypes were screened using RCBD design with 3 replications to identify superior genotypes having improved yield and its related traits. The selected yield-related traits were studied in twenty different maize genotypes in field conditions. ANOVA revealed that all genotypes were significantly different from each other for cob length (cm), days to 50% tasseling, days to 50% silking, cob diameter (cm), no. of days to pollination, plant height (cm), cob height (cm), no. of grains/row, total grains cob', no. of rows per cob, 100-grain weight (g) and grain yield per plant (g). Traits the days to 50% silking ranges (79 to 64 days), days to 50% tasseling ranges (71 to 54 days), no. of days to pollination ranges (80.67 to 65.33 days), plant height (195.17cm to 124.33cm), no. of grains/row (43.00 to 14), total grains per cob (677.6 to 180.4), no. of rows/cob (15.833 to 9), cob diameter (4.52cm to 1.80cm), cob height (87.567cm to 38.2cm), cob length (22.5cm to 10.467cm), 100-grain weight (42.467g to 10.4g) and grain yield plant" (220.2g to 41.06g). The trait grain yield per plant exhibited significant positive phenotypic and genotypic correlation with total grains per cob, number of rows per cob, 100 seeds weight, and number of grains per row. Path coefficient analysis revealed the direct contribution of days for 50 % silking, days for 50% tasseling, number of days for pollination, plant height, no. of grains per row, total grains per cob, no. of rows per cob, cob diameter, cob height, cob length, 100-grain weight and grain yield per plant.

Keywords: Maize, Yield, Genotypes, Traits, Field.

Effect of biochar-based soil amendment and plant growth promoters on the Bioavailability and Phytotoxicity of Heavy Metal in Carrot (*Daucus Carota* L.) Irrigated with Wastewater

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Abstract: The study investigates the impact of heavy metal pollution on food safety and environmental sustainability, specifically focusing on its effects on agricultural soils. At the Agronomy Farm University of Agriculture Faisalabad, a field experiment was carried out using a variety of treatments to evaluate their effects on the dynamics of heavy metals in the soil-plant system by applying randomized complete block design (RCBD), to evaluate the effectiveness of various treatments aimed to mitigating Phytotoxicity and reducing the bioavailability of heavy metals in carrots (*Daucus carota* L.). The experimental setup included a control group, soil amended with biochar derived from wood, rice husk, and maize pith, application of plant growth stimulants such as melatonin, brassinosteroids, and thiourea, and combinations of these treatments. The study monitored heavy metal concentrations in both soil and carrot tissues throughout the growing period while also assessing the relevant physicochemical properties of the soil. Data analysis was performed by using Fisher's Analysis of Variance (ANOVA), with treatment means compared through Tukey's Honestly Significant Difference (HSD) test at a 5% probability level. The results indicated that incorporating biochar significantly reduced the bioavailability of heavy metals by promoting their immobilization in the soil. The results revealed that treatments involving biochar and plant growth stimulants led to notable improvements in growth metrics, including root and shoot fresh weights and root length. In contrast, plants treated with wastewater exhibited higher concentrations of heavy metals (Cu, Pb, Cr, Cd, Mg, Ni, Zn, Fe) compared to those treated with biochar or control groups. Furthermore, biochar-treated plants showed enhanced ion contents of essential nutrients such as K, Na, Ca, sulfate, phosphate, and nitrate. The findings underscore the potential of biochar as a low-cost and sustainable sorbent for water treatment applications while highlighting its role in enhancing agricultural resilience against climate change.

Keywords: Carrot, Biochar, Plant Growth Promoters, Heavy Metals, Bioavailability.

Ethnobotanical Exploration and Therapeutic Uses of Wild Plants of some Associated Villages of Dera Ghazi Khan City of Punjab Province, Pakistan

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Abstract:

Traditional herbal medicine is deeply rooted in cultural knowledge and practices, playing a vital role in maintaining human health. In economically disadvantaged regions of Pakistan, particularly in the villages surrounding Dera Ghazi Khan, many people rely on traditional remedies. However, these practices have not been extensively or systematically studied or documented. To address this gap, a quantitative ethnobotanical survey was conducted to record medicinal plants and their uses in traditional therapies. This documentation aims to contribute to socio-economic reforms in healthcare systems. The field surveys took place between February and March 2024 in the villages around Dera Ghazi Khan, Punjab, focusing on the medicinal plants used by local communities. For this purpose, interviews were conducted. A total of 42 medicinal plant species were documented and used to cure different ailments. All these recorded plant species belong to 41 families. A total of 17 species were herbs, 16 species were trees, and 8 species were shrubs. Leaves were the most frequently used plant part (35) followed by fruits (20), and seeds (4). It was found that uncostly plant parts were eaten fresh without any particular formulation. All of these indigenous plants were used as oral or topical for curing the different diseases. The study revealed that several factors have profound impacts on the existing ethnobotanical knowledge for instance urbanization, outmigration, lack of interest by new generations, allopathic drugs, and modernization. Therefore, it is necessary to preserve the valuable medicinal. Moreover; the reported medicinal plants may be screened for pharmaceutical and neutraceutical investigations respectively.

Keywords: Medicinal Plants, Ethnobotany, Diseases, Drugs, Herbal Medicine.

Regenerative Medicine for Type 1 Diabetes: Investigating the Role of INS Gene Activation in Beta Cell Recovery

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Abstract

Introduction: The **INS** gene encodes insulin, a hormone critical for glucose regulation. In Type 1 diabetes, beta-cell destruction leads to the cessation of insulin production, resulting in chronic hyperglycemia. Leveraging gene activation techniques to restore **INS** gene expression offers a promising approach to regenerate beta cells and re-establish insulin production. This study aimed to evaluate the therapeutic potential of **INS** gene activation in beta-cell recovery. **Purpose**: The research aimed to (1) explore the effectiveness of **INS** gene activation in regenerating functional beta cells, (2) assess insulin production post-treatment, and (3) evaluate the impact on glycemic control in a Type 1 diabetes model. **Methodology:** Gene activation of **INS** was performed using CRISPR-dCas9 systems with transcriptional activators in a diabetic murine model. Beta-cell function was assessed through immunohistochemistry and ELISA to quantify insulin levels. Glycemic control was evaluated using glucose tolerance tests and long-term blood glucose monitoring. **Results:** The activation of the **INS** gene successfully restored insulin production in treated mice. Histological analysis confirmed increased beta-cell numbers and reduced beta-cell apoptosis. Treated mice demonstrated improved glucose tolerance and significantly reduced fasting blood glucose levels compared to controls. **Conclusion:** The findings highlighted the potential of **INS** gene activation as an innovative strategy for beta-cell recovery and glycemic control in Type 1 diabetes. This targeted approach lays the groundwork for developing gene-based therapies to address insulin deficiency in diabetic patients.

Keywords: Type 1 diabetes, INS gene, beta-cell regeneration, gene activation, insulin production, glycemic control.

A Qualitative Analysis on the Lifestyle and Stress Management Approaches of Polycystic Ovary Syndrome (PCOS) Patients in the Philippines

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Purpose*:* The study aimed to bring to light how polycystic ovary syndrome (PCOS), which affects 5-10% of women in their reproductive years, influences the lifestyle of women diagnosed with PCOS-as an endocrine disorder, the complex presentation is noted for irregular menstruation, hyperandrogenism, alongside associated increased risks for metabolic and psychological problems. ***Method****:* The current study explored the physiological, psychological, interpersonal, and existential experiences of the Filipino women suffering from PCOS (without regard for its financial impact). The data were gleaned from the posts generated within a closed Facebook group spanning from March 2023 to May 2023. These posts included conditions such as experience, emotion, sleep-wake cycles, compromise, diet, weight, pregnancy, fertility/fertility status, workout, exercise, and food to help sampling and analysis. ***Results****:* The results showed that women expressed both active and passive coping strategies for efforts to overcome negative lifestyle changes associated with PCOS. Active coping strategies included, but are not limited to: seeking for medical help from healthcare personnel, as well as support group memberships. On the other hand, passive coping strategies included detachment and pity against oneself. The most impacted areas in lifestyle were ovulation and fertility issues, followed by those concerning diet, weight maintenance, and looks. Social interactions were the least frequently discussed, although self-image and whether or not infertility affected relationships were mentioned by some subject participants. ***Conclusions****:* The findings of this study offer an elaborate understanding of how Filipino women maneuver through the multitude of physical and emotional obstacles that are faced with PCOS. Recommendations include utilizing different methods for data collection on how culture and geography influence coping behavior in such women and expanding the search to other online groups for broader perspectives on experience with PCOS. The findings of this study offer an elaborate understanding of how Filipino women maneuver through the multitude of physical and emotional obstacles that are faced with PCOS.

Incidence, identification and antibiotic resistance of *Salmonella* spp. in the well waters of Tadla Plain, Morocco

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Abstract: Concerns about challenges with water availability in the Tadla Plain region of Morocco have grown as a result of groundwater contamination brought on by human activity, climate change, and insufficient groundwater management. The objective of the study is to measure the number of resistant bacteria in the groundwater of Beni Moussa and Beni Aamir, as well as to evaluate the level of water pollution in this area. 200 samples were therefore gathered from 43 wells over the course of four seasonal campaigns in 2017 and 2018. Additionally, the samples were examined to determine whether *Salmonella* species were present and if they were resistant to the 16 antibiotics that were tested. *Salmonella* spp. have been identified in 31 isolated strains in total, accounting for 18.02% of all isolated strains. Data on antibiotic resistance show that 58.1% of *Salmonella* spp. strains are multidrug-resistant (MDR); 38.7% of *Salmonella* strains are tolerant to at least six antibiotics, 19.4% to at least nine antibiotics, 9.7% to four to seven antibiotics, 6.5% to at least eleven antibiotics, and the remaining 3.2% to up to twelve antibiotics. A considerable level of resistance to cefepime (61.29%), imipenem (54.84%), ceftazidime (45.16%), ofloxacin (70.97%), and ertapenem (74.19%) was found in the data. Consequently, it is important to monitor and regulate the growth of MDR in order to prevent the groundwater's quality from declining.

Mitigating Abiotic Stress in Maize Using Metarhizium-Based Nanoparticles and Vermicompost

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Abstract: Maize (Zea mays L.), an important cereal crop in the Poaceae family, is extremely vulnerable to abiotic factors such as salt, drought, and heat, which can cut yields by 25-30%. Traditional reliance on fertilizers and chemicals to counteract these pressures has led to soil degradation and environmental damage. The purpose of this study was to assess the impact of organic treatments (vermicompost, nanoparticles, and Endophytic metarhizium) on maize growth and resistance under varied stress circumstances while remaining environmentally friendly. The treatments comprised three levels of vermicompost (50g, 100g, 150g), Metarhizium fungus at varying concentrations (10^4, 10^6, 10^8 conidia/mL), and nanoparticles (0.1%, 0.2%, 0.3%) applied to maize plants to assess their influence on growth metrics. Data were gathered at 7-day intervals to assess plant height, leaf area, biomass output, and root-shoot properties. Tukey's range test and Analysis of Variance (ANOVA) were used to determine the effects of the treatments. The results revealed that both high and low amounts of vermicompost and nanoparticles had a significant effect on maize growth. Moderate vermicompost (100g) and Metarhizium fungus (10^6 conidia/mL) improved nutrient absorption, drought and heat stress tolerance, and overall plant growth. The study indicated that these organic treatments not only increased maize tolerance to abiotic stress but also provided sustainable farming methods, with the potential to increase crop yields by 70%.

Keywords: Nanoparticle, Maize, Moderate, Vermicompost, Metarhizium fungus.

Obtaining and study of copolymers of vinyl ester of salicylic acid with oligoethylene macromonomers

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Abstract: One of the far reaching advances for getting antimicrobial polymer materials is the presentation of antibacterial added substances into the base polymers amid the method of arrangement ofpolymer items or the coating of the polymer item with an antibacterial layer. Another broadinnovation is the presentation of basic individuals with a organically dynamic bunch into the macrochain amid the amalgamation of polymers. The utilize of polymers containing organicallydynamic bunches as antibacterial added substances is of awesome intrigued. The aim of the presented thesis is to study the preparation of copolymers of salicylic acid vinyl ester (M1) (Vasp) with polyethylene macromonomers (M2) (PEMM) with antibacterial effects and to study some regularities. Within the IQ range of the copolymers, comparing absorption bands were recorded within the locales of 1640-1660 cm−1 (C-C), 1745 cm−1 (C=O) and 1155 cm−1 (C-O-C). Ithas been built up that vinyl ester of acetylsalicylic corrosive has tall action in copolymerizationresponses. The relative exercises of the comonomers were decided by the Mayo-Lewis strategy (r1=1.65 and r2=0.015). The values of the relative exercises and their item (r1xr2=0.024) are near to zero, showing a tall likelihood of getting measurable copolymers It is additionally watched that the properties of copolymers alter depending on their composition.

Within the copolymerization responses of vinyl ester of salicylic corrosive with PEMM, the reliance of the composition of the copolymers on the monomer composition taken for the response is due to the higher relative movement of the monomer (M1) amid the copolymerization of monomers. Typically due to the tall action of the vinyl ester of salicylic corrosive and, on the other hand, the detached nature of alpha-olefins with tall molar masses in radical polymerization. Alfrey-Price parameters were calculated for the PEMM monomer (Q=3.2 and e=0.2). The esteem of the particular movement demonstrates that PEMM may be a passive monomer. The esteem of the specific action shows that PEMM may be a passive monomer. On the other hand, the esteem of the extremity calculate (e) within the PEMM is additionally near to ero. In this case, since the polarities of both the vinyl ether and the comonomer are near to each other, the comonomers are less inclined to copolymerization responses. As a result, the alterwithin the ratio of comonomers within the response blend (an increment within the amount of PEMM) causes both the response rate and the alter within the atomic mass of the gotten copolymers. The truth that the sum of PEMM within the composition of copolymers is underneath 50 mol% demonstrates once once more that it does not experience a radical homopolymerization response. PEMM as it were enters the copolymerization reaction. Anincrement within the relative amount of PEMM within the starting monomer blend is additionally watched. It can be concluded that since PEMM effectively partakes within the chainexchange response through the monomer, the characteristic consistency of the copolymers gotten within the copolymerization responses of vinyl ester of acetylsalicylic corrosive with PEMM within the composition of the monomer blend and the reliance of the response surrender on the composition of the starting monomer blend.The values of relative exercises and their item ($r1 \cdot r2=0.024$) are near to zero, showing a tall likelihood of getting measurable co-polymers.

Keywords: salicylic acid, polymer materials, antibacterial effects, copolymers

Biological activities of stilbene derivatives obtained from Morus alba L.

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Introduction: Morus alba L. is a perennial tree plant that is widely distributed in different regions of the world, as well as in Azerbaijan, and has high medicinal and nutritional value. There are 5 types (Morus alba L., Morus bombycis Koidz., Morus multicaulis Perr., Morus Kagayamae Koidz., Morus nigra L.) and varieties of this plant in Azerbaijan. In the Republic of Azerbaijan, both the underground and above-ground parts of the this plant, as well as the plant itself, are used as a healing agent. Stilbene derivatives obtained from the roots of M. alba are constantly attracting the attention of researchers in terms of their biological activity and health benefits. Stilbenes are a group of natural chemicals and have unique properties that can affect various physiological processes. Their anti-inflammatory, antioxidant and antimicrobial effects have been confirmed by many scientific studies.

Among the stilbenes derived from M. alba, the best known is resveratrol. Resveratrol has strong antioxidant properties and prevents cell damage by reducing the effects of free radicals in the body. One of its main advantages is strengthening and increasing elasticity of vascular walls. A deeper investigation of the biological activity of stilbenes may open new opportunities to fully usage their potential.

Purpose: It is known from the scientific literature of recent years that the synthesis of chemical compounds with biological activity is one of the current directions of the modern era. Evaluation of the potential biological activity of the studied substances is a special focus in this direction. These studies are conducted using in silico methods, that is, through computer programs and algorithms. Such an approach is of great importance both in terms of providing theoretical predictions and optimizing time and resources for experiments. For this purpose, we studied the biological activity and toxicity of stilbene derivatives obtained from M. alba, including resveratrol, by modern in silico programs.

Study: In the study, several in silico programs were used to investigate the biological activity and toxicity of resveratrol, a stilbene derivative from M. alba. First, the potential effects and biological targets of resveratrol were studied with the PassOnline program (https://www.way2drug.com/passonline/). Then, the SwissTargetPrediction software (http://www.swisstargetprediction.ch/) was used to determine which proteins resveratrol binds to. Finally, the toxicity and side effects of this compound were evaluated using ProTox 3.0 (https://tox.charite.de/protox3/) software. These studies provide important information to better understand the beneficial effects and potential hazards of rez¬veratrol.

Conclusion: As a result of our studies in the PassOnline program, it was determined that the antioxidant index of resveratrol is 0.546%. However, for one of its derivatives, 3,4'-dihydroxy-3',5'-dimethoxy-trans-stilbene, this indicator has increased till 0.689%. In addition, one of the distinguishing features of this derivative from resveratrol is that it has an anti-inflammatory effect of 0.780%. By comparison, this figure is 0.554 in resveratrol. Significant differences were also found in the toxicity indices of resveratrol and its 3,4'-dihydroxy-3',5'-dimethoxy-trans-stilbene derivative. While the multi-organ dysfunction syndrome (MODS) index, one of the toxic effects of resveratrol, was 0.642%, this index was reduced to 0.476% for the same derivative.

Keywords: *Morus alba* L., stilbene derivatives, biological activity, toxicity, *in silico*