Biotechnology for Health, Industry & Informatics

Biotechnology for Environment, Energy & Agribusiness Management

Poster Exhibition

IC-WEES 2021

1st International Conference on Water, Energy and Environment for Sustainability (IC-WEES)

Biotechnologies for Environment, Health and Agriculture

October 27-29, 2021

http://icwees.nust.edu.pk/

Atta-ur-Rahman School of Applied Biosciences, National University of Sciences and Technology, Islamabad, Pakistan

frontiers Event Abstracts

FIRST INTERNATIONAL CONFERENCE ON WATER, ENERGY, AND ENVIRONMENT FOR SUSTAINABILITY (IC-WEES)

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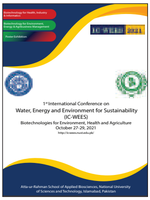

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Welcome to the First International Conference on Water, Energy, and Environment for Sustainability (IC-WEES)

The International Conference on **Water, Energy, and Environment for Sustainability (IC-WEES)** is a flagship conference of the National University of Sciences and Technology (NUST), Pakistan. This year we are organizing it at Atta-ur-Rahman School of Applied Biosciences (ASAB), with a priority theme "**Biotechnologies for Environment, Health, and Agriculture**, aiming to bring diverse research groups to exchange and share their experience and provide sustainable solutions based on biotechnological approaches in the field of environment, health, and agriculture, advances in biotechnology and its applications in environment, health and agriculture hold promises for improving human lives by providing effective diagnostics, disease prevention, and treatment measures, enhancing crop productivity, nutritional value and protecting the environment through bioremediation, waste management, and resource recovery.

IC-WEES 2021, dedicates to creating a stage for exchanging the latest research results and sharing the advanced research methods and major challenges in related fields.

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TOPICS OF INTEREST

- Bioremediation and Environmental Protection
- Biofuels and Energy
- Biocontrol and Environmental Wellbeing
- Infectious Diseases and Epidemiology
- Agribusiness Management
- Regional and Global Public Health
- Solid Waste Management & Resource Recovery
- Agricultural Biotechnology for Plant Protection
- Bioinformatics and Computational Biology

OPENING LECTURE

- Prof. Dr. Shahid Mahmood Baig

PLENARY SPEAKERS

- Prof. Moaz ur Rahman
- Prof. Thomas Pogge
- Prof. Amjad Farooq
- Prof. Imran Hashmi
- Dr. Tariq Zaman
- Prof. Dr. Safia Ahmed

KEYNOTE SPEAKERS

- Prof. Yiming Bao
- Prof. Claudia Kammann
- Prof. Khuda Bakhsh
- Prof. Tianyu Zhang
- Prof. Hans-Werner Koyro
- Prof. Jan Baumbach
- Prof. Ángel Antonio Carbonell-Barrachina
- Prof. Richard Charles Garratt
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INVITED SPEAKERS

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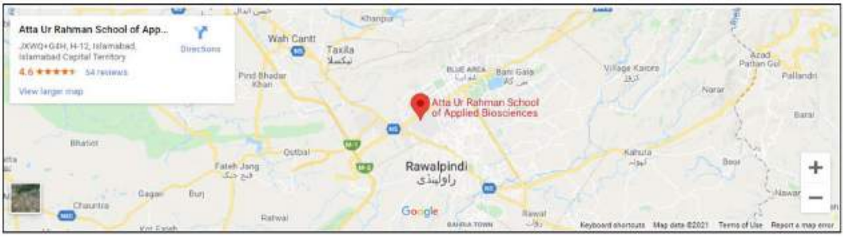
About NUST

National University of Sciences & Technology (NUST) has come a long way as a premier S&T university of Pakistan since its inception in March 1991. It has earned the infallible reputation of being a next-generation university with a progressive and innovative outlook. Comprising 19 constituent institutions sprawled over 7 campuses across 5 cities of Pakistan, NUST has secured a coveted standing amongst the World's elite Higher Education Institutions (HEIs). Today, the university proudly stands at #358 in the world, competing with the Ivy League institutions some of which are hundreds of years old, and #76 among Asian universities, making us the only university from Pakistan to stand among the top 100 in Asia. We also pride ourselves in our strong ties with international organizations and universities of repute. Over the past, nearly 3 decades, the quality of education and research at NUST has grown exponentially. It is manifest in the quality of its undergraduate and postgraduate programs in a range of disciplines, with all our 19 Engineering programs accredited under the Washington Accord. Likewise, our R&D ecosystem is completely aligned to the UN Sustainable Development Goals (SDGs) and socio-economic needs of Pakistan.

About ASAB

Atta-ur-Rahman School of Applied Biosciences (ASAB) is one of the leading schools of NUST in terms of students, Ph.D. qualified faculty, research facilities, publications, and research grants. As we know that Biotechnology is the economic exploitation of our knowledge of biological systems and their parts and this sector is fast-moving, often at the frontiers of science, thus needs imaginative and capable biotechnologists and life scientists. This school is intended for those who have a life science background and wish to develop their interest and skills to do research in a biotechnology company. This pool of expertise is an invaluable resource, enabling students to access all sorts of different biotechnological skills. As a strategic unit located within NUST, ASAB boasts state-of-the-art teaching and research. The school is unique in establishing expertise across a broad range of biotechnology, thereby encouraging innovative approaches to teaching and research. Our areas of expertise include healthcare biotechnology, industrial biotechnology, plant biotechnology, and agri-business. The institute provides excellent research and teaching facilities in the field of applied biology in Pakistan.

Venue



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Opening Lecture

Role of PSF in promotion of science in Pakistan

Shahid Mahmood Baig (Sitara-i-Imtiaz)*

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Plenary / Keynote Lectures

BIHI-KN01

Resources of China national center for bioinformation

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Genome data are increasing dramatically as a result of new technologies. Often, these data are required to be deposited into international databases such as DDBJ, EBI, and NCBI, to obtain accession numbers needed for publication. This could be challenging sometimes for researchers in China because of the large data size, slow data transfer due to limited international internet bandwidth, language barrier, and technical issues in communication. To alleviate these problems, the BIG Data Center (BIGD, https://ngdc.cncb.ac.cn/) was launched in 2016 at Beijing Institute of Genomics (BIG), Chinese Academy of Sciences (CAS). During the past few years, BIGD has grown and expanded considerably and became one of the major global centers. In 2019, the National Genomics Data Center (NGDC) was created based on BIGD. Later in the same year, BIG was given the title of China National Center for Bioinformation (CNCB). CNCB will be built on the well-established NGDC multi-omics databases such as Genome Sequence Archive (GSA), Genome Variation Map (GVM), Genome Warehouse (GWH), and 2019 Novel

Coronavirus Resource (2019nCoVR), together with specialized resources from many institutions under CAS and other ministries. CNCB is dedicated to providing freely accessible data repositories and a variety of data resources in support of worldwide research activities.

Keywords: Genome data, international databases, Data repositories

BEEA-KN02

Climate adaptation and mitigation by biochar use in agriculture

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BEEA-KN03

Pulses value chain in Pakistan: Constraints and opportunities

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The present study is designed to explore constraints and opportunities for improving the pulses value chain in Punjab, Pakistan. All stakeholders from farmers to the retailers are considered to get information on the current practices, obstacles, constraints, and opportunities for improving the pulses value chain in Pakistan. A total of 241 farmers were chosen from two tehsils of the Bhakkar district. Collectors, commission agents, processes, wholesalers, and retailers are also considered for the detailed analysis of the value chain of pulses. Findings of the study show that farm households reporting selling of the produce at the farm gate are 75-89% and the storage of the product is very negligible. Only 14% of households are of the view that they changed land use over the last 5 years, owing to the reason of improving soil productivity and relatively high profitability of sugarcane and sunflower in the region. There is no or very little value addition reported by the households (4% in the form of cleaning and drying in mung bean production at farm level). Poor agronomic practices, high transportation costs, lack of financial incentives, poor financial incentives, price fluctuation, low price of output, lack of information, and lack of skills are cited as constraints in value addition. Results reveal that size of the grain, color, packaging, cleanliness, and freshness are important attributes of pulses when the consumers decide on

purchasing pulses from the supermarkets and or super stores. Grading, sorting, and packing are done at the supermarkets and superstores whereas no or little value addition relating activities are done at grocery shops. Although wholesalers demand the quality produce of the pulses (based on the size of the grain, waste, moisture, etc.) from merchants and or farmers, they care very little during selling the produce to the daal factories or millers. This implies an absence of price incentives for selling quality products to the processors. Despite these facts, the processors deduct the amount paid to the wholesalers for waste, moisture, and damaged or broken pulses. This implies that there is a need to sensitize and build confidence among the processors and wholesalers that value addition would be beneficial to all the value chain actors. Interventions at the farm level need immediate attention to start value addition as doing this will reduce the cost of value addition at later stages of the value chain of pulses. However, this happens only if price incentives for value addition are ensured to farmers and merchants.

Keywords: Soil productivity, Bean production, Agronomic practices

BIHI-PL01

Characterization of membrane and viral proteins as targets for drug discovery, disease diagnosis, and vaccine development

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Membrane-associated and capsid proteins of human and microbial pathogens are promising drug, diagnostic and vaccine targets. In our laboratory, the research work is mainly focused on characterizing membrane proteins (human zinc transporter 8, multidrug resistance (MDR) transport proteins of *Salmonella* Typhi, and a membrane-associated protein pLPE from *Pasteurella multocida*) and viral capsid proteins (the VP2 protein of infectious bursal disease (IBD) virus, the matrix protein of Newcastle disease virus (NDV), and penton and hexon proteins of Fowl adenovirus serotype 4 (FAdV-4)) for practical purposes such as drug discovery, disease diagnosis, and vaccine development. The human zinc transporter 8 (hZnT8) is a membrane protein that plays important role in the storage of insulin in the secretory vesicles of pancreatic cells. Interestingly, the exchange of arginine to tryptophan at position 325 in the hZnT8 C-terminal domain (CTD) increases the risk of developing type 2 diabetes mellitus (T2D). Characterization of CTDs of hZnT8 (the wild-type and its disease risk variant) reveals that the CTDs form tetramers that are stabilized by zinc binding and exhibit negligible differences in their secondary structure content and zinc-binding affinities in solution. These findings provide the basis to unravel the molecular mechanism underlying the increased susceptibility to develop T2D, which is modulated by the disease risk variant. Moreover, studies were conducted on two other membrane proteins (the PlpE protein of *P. multocida* and an MDR pump (STY4874) of *S.* Typhi) as vaccine and drug targets to combat haemorrhagic septicemia in cattle and typhoid, respectively, will be discussed. To develop modern diagnostic tests and vaccines for poultry, we are targeting capsid proteins of pathogenic viruses (IBDV,

NDV, and FAdV-4). To this end, we have characterized the VP2 protein of IBDV and exploited it as a diagnostic antigen to develop a lateral flow assay for the detection of IBDV and anti-IBDV antibodies in chickens. Currently, the VP2-based adenoviral vector vaccine is being evaluated in our lab as a modern vaccine candidate against IBD. We have also characterized the matrix protein of NDV as a drug target, and penton base and hexon proteins of FAdV-4 have been investigated extensively for engineering recombinant and virus-like particle vaccines. We anticipate that the studies will contribute towards developing local solutions for the respective diseases.

Keywords: Drug discovery, Vaccine development, Drug target

BEEA-PL02

Replacing monopolies with impact rewards

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Globalized in 1995 through the TRIPs Agreement, humanity's dominant mechanism for encouraging innovations involves 20-year product patents, whose monopoly features enable innovators to reap large markups or licensing fees from early users. This way of rewarding innovations systematically hampers their diffusion. Patents do especially poorly in incentivizing the development and use of innovations that meet the specific needs of poor people and innovations whose benefits would overwhelmingly go to third parties, people other than the buyer. Governments should complement monopoly patents with domain-specific impact funds that offer to reward innovations from fixed annual reward pools, divided according to the social impact achieved with them. Innovations registered for impact rewards would have to be sold without monopoly markups and licensing fees. A Health Impact Fund in the pharmaceutical sector, for instance, would create powerful new incentives to develop remedies against diseases concentrated among the poor, rapidly to provide such remedies with ample care at very low prices, and to deploy them strategically to contain, suppress, and ideally to eradicate the target disease. A Green Impact Fund would create new incentives to develop emissions-reducing technologies in the energy, traffic, steel, cement, and agricultural sectors, vigorously promote these technologies with strong customer support at competitive prices and deploy them for optimal emissions reductions. By promoting innovations and their diffusion together, impact funds include poor people and third parties in the orientation and in the benefits of innovation and thereby massively increase its social value and cost-effectiveness.

Keywords: Monopoly, Patents, Competitive prices

BIHI-PL03

Critical assessment of ongoing pandemic with atomic insights

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Since becoming a pandemic in early-2020, the poor handling of the SARS3 coronavirus surge by the powers-that-be around the globe has left the world in tatters and nations teetering on the brink of an economic depression. In particular, the coronavirus has already become endemic to humans and the emergence of new variants suggests that it will keep us engaged in a game of whac-a-mole for many years to come. By the time all the dust has settled, the livelihoods of at least a billion people will have been wiped off the face of the planet. Yet, the coronavirus has hitherto claimed no more than one in ten deaths. In short, this talk provides a critical and blunt assessment of the ongoing pandemic with atomic insights into why certain young individuals with an excellent health profile become a statistic, all the while many elderly and sick seemingly brush off the coronavirus without breaking a sweat.

Keywords: Pandemic, SARS3 coronavirus, Economic depression

BIHI-KN04

TB47- The promising powerful drug candidate against mycobacterial diseases

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TB47, a new drug candidate targeting QcrB in the electron transport chain, has shown a unique synergistic activity with clofazimine and forms a highly sterilizing combination. It was discovered using a high throughput anti-mycobacterial drug screening platform based on the novel auto luminescent mycobacteria both in-vitro and in-vivo. Adding TB47 to amikacin + levofloxacin + ethambutol + pyrazinamide + clofazimine might shorten the drug-resistant tuberculosis treatment duration from $\geq$ 9 months to $\leq$ 5months, like five months of treatment with them achieved zero relapse rates. Furthermore, several all-oral regimens containing TB47 + clofazimine + linezolid with or without other off-patent drugs cured tuberculosis within $\leq$ 4 to 6 months. The clofazimine + TB47 combination was also very effective against *M. abscessus* both in-vitro and in-vivo in mice. The in-vivo activities of TB47 against both low-level and high-level TB47-resistant *Mycobacterium ulcerans* mutants were tested in Buruli ulcer murine model. We showed that TB47-containing oral 3-drug regimens can completely cure Buruli ulcers in $\leq$ 2 weeks for daily use or in 3 weeks given twice per week (6 doses in total) instead of the current rifampin + streptomycin for $\geq$ 2 months recommended by WHO. The promising efficacy results together with the good PK parameters and safety of TB47 warrant further studies to ascertain its clinical applicability in the treatment of DR-TB.

Keywords: Drug resistance, Mycobacterium, drug discovery, tuberculosis, animal model, high throughput

BEEA-KN05

Ecosystem services, global climatic changes and salinity dynamics. The small bridge between resilience and vulnerability

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BIHI-KN06

Privacy-preserving systems medicine

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Artificial intelligence offers game-changing opportunities to healthcare. However, it also harbors risks to patient privacy in particular when dealing with sensitive Clinical data stored in critical healthcare IT infrastructure. Specifically, data exchange over the internet is perceived insurmountable, posing a roadblock hampering big -data-based medical innovations. We created a novel AI platform, the Feature Cloud AI app store that is based on the idea of federated learning where only model parameters are communicated. To maximize privacy, sensitive datasets remain stored locally and are analyzed behind safe firewalls. We will exemplarily investigate the power of Feature Cloud apps for decentralized (1) genome-wide association studies (GWAS), (2) gene expression data mining, and (3) time-to-event data analytics to demonstrate how FeatureCloud may enhance worldwide collaboration, accelerate innovation, and democratize scientific data usage.

Keywords: Artificial intelligence, Healthcare, Medical innovations

BEEA-PL04

Treatment efficiency of integrated constructed wetland (ICW) for domestic wastewater

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Integrated constructed wetlands (ICWs) are widely employed for wastewater treatment because of their promising treatment efficiency. The objective of the current study is to monitor the efficiency of a multi-stage integrated constructed wetland located at NUST campus, sector H-12, Islamabad, Pakistan. It consists of an inlet, sedimentation tank, eight ponds of horizontal subsurface flow constructed wetland (HSSF-CW), and filtration and irrigated cropping for land treatment and effluent reuse (FILTER) technology. Specific hydrophytes such as (*Pistia stratiotes, Typha latifolia, Centella asiatica*) were used in the treatment system. Samples were collected twice for one month (i.e., April 2021) from the outlets of eleven sites including inlet, sedimentation tank, eight ponds, and collection tank to measure organic removal efficiency at each site. Different physiochemical parameters including Temperature, pH, Electrical Conductivity (EC), Turbidity, Total suspended solids (TSS), Total dissolved solids (TDS), Total solids (TS), Chemical oxygen demand (COD), Dissolved oxygen (DO), Nitrate-nitrogen (NO3-N), Nitrite-nitrogen (NO2–N), Total Kjeldahl nitrogen (TKN), and Phosphate-phosphorous (PO_4^{3-}-P) were analyzed according to American Public Health Association (APHA) standard methods. Temperature, pH and DO range between 24.7 – 25.35°C, 6.75 – 7.15, and 1.15 – 3 mg/L respectively. The results showed the removal efficiency of different parameters as EC 10.28%, Turbidity 68%, TSS 74.4%, TDS 31.98%, TS 45.41%, COD 63.67%, NO3-N 46.57%, NO2-N 40%, TKN 59.79%, and PO_4^{3-}-P 44.22%. Overall, this study shows that the integrated constructed wetland (ICW) may greatly improve the water quality and is therefore a suitable technology for wastewater treatment.

Keywords: Integrated constructed wetland, Domestic wastewater, Physicochemical parameters, Wastewater treatment

BIHI-PL05

Imagine everybody had a healthy genetic makeup!

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Neurons allow the brain and body to communicate through electrical signals. Voltage-gated ion channels like sodium, calcium, potassium and chloride channels are critical in electrical signaling. Sodium channels play an important role in the generation and propagation of the signals. Under normal conditions, these signals allow neurons to communicate, however, abnormal and excessive excitation of neurons may lead to epileptic encephalopathies. The SCN3A gene, encoding the type 3 sodium channel, Nav1.3, is highly expressed in the brain starting from 16 weeks of fetal life. We have discovered that the mutations in SCN3A result in the gain of function by altering gating properties of the channel, leaving the ion channel stuck open that in turn causes current flood leading to electric sparking, a signature of epilepsy. Magnetic resonance imaging (MRIs) and neurological evaluations further revealed that the epileptic patients carrying mutations in SCN3A also exhibit malformation of cortical folding indicating its possible role in brain development. This study reinforces the role of variants in SCN3A as a cause of neurodevelopmental disorders along a spectrum of severity that includes epilepsy and polymicrogyria and suggests that gain of channel function is an important mechanism of disease pathogenesis. Manipulating epileptic genes in utero could be used to analyze the roles of genes in embryonic development and intellectual disability. These are still early days, but precision medicine, early prenatal diagnosis, SCN3A gene manipulation during the critical window, may help prevent brain malformations in babies.

Keywords: Neurons, electrical signaling, SCN3A

BEEA-PL06

Sustainable wastewater treatment and reuse approaches for developing countries

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Wastewater treatment remains a high priority sustainability challenge. Safely reused as reclaimed water, wastewater must receive adequate treatment to meet the quality requirements for the least impact on environmental and public health. As we have technical, financial, and managerial limitations in developing countries, low-cost wastewater treatment technologies are preferred over expensive modern technologies. The treated water can effectively be used for irrigation as irrigation with untreated wastewater poses an epidemiologic risk to farms, consumers, and surrounding communities. For the development of applicable wastewater treatment options for developing countries to provide safe direct reuse of reclaimed water, low-cost treatment solutions like a constructed wetland, solar disinfection, and biofiltration are usually recommended. The decentralized system provides a long-term solution for small communities and is also more reliable and cost-effective. There are many disablements and challenges towards wastewater management in developing countries. Suitable planning and policy implementation is required especially since centralized management of the decentralized wastewater treatment systems are essential. Constructed wetlands are among the recently proven efficient technologies for wastewater treatment. Compared to conventional treatment systems, constructed wetlands are low cost, are easily operated and maintained, and have a strong potential for application in developing countries. However, these systems have not found widespread use, due to a lack of awareness, and local expertise in developing the technology on a local basis. The extremely low level of wastewater treatment reveals an urgent need for technological upgrades and safe water reuse options to support the achievement of the 2030 Agenda for Sustainable Development. (SDG Target 6.3). The paradigm of wastewater management is shifting from 'treatment and disposal' to 'reuse, recycle and resource recovery'. Wastewater can also be a cost-efficient and sustainable source of energy, nutrients, organic matter, and other useful by-products. In the context of a circular economy, wastewater represents a widely available and valuable resource. Integrated water resources management and approaches linking water, energy, food, and climate change will provide a framework for considering avenues for supporting the improved collection, transfer, treatment, and use of wastewater. By-products from domestic wastewater, such as salt, nitrogen, and phosphorus, have potential economic value that can be used to improve the livelihoods of people. Generally, the use of wastewater encounters strong public resistance due to a lack of awareness and trust regarding human health risks. Awareness-raising and education are the main tools to overcome social, cultural, and consumer barriers. Such awareness campaigns need to be tailored to consumers with different cultural and religious backgrounds. In a world where demands for freshwater are continuously growing, and where limited water resources are increasingly stressed by over-abstraction, pollution, and climate change, neglecting the opportunities arising from improved wastewater management would be great efforts in the context of a circular economy.

Keywords: Wastewater treatment, Wastewater reuse, wastewater management

BEEA-KN07

Global-Scale arsenic pollution and its potential effects on children under 3 years of age and celiac patients

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Celiac disease (CD) is a digestive illness that damages the mucous membrane of the small intestine and interferes with absorption of nutrients from food. This illness is caused by intolerance to gluten proteins from *Triticeae* cereals group: wheat (gliadine, rye (secalin), and barley (hordein). In Spain, the prevalence of CD is estimated at 1 out of 118 and 1 out of 389 in children and adults, respectively. Currently, the only effective treatment for CD is lifelong adherence to a gluten-free diet as there is no specific drug treatment. Rice is especially used due in children and celiac foods due to its blandness, material properties, low allergen potential, and nutritional value. Rice is therefore essential for the manufacturing of commodities for celiac people and reaches high percentages in their formulations. However, rice tends to accumulate arsenic (As) due to its cultivation under flooded conditions, where anaerobic soil conditions lead to the high availability of the plant. Inorganic As has been classified by the International Agency for Research on Cancer (IARC) as group 1 carcinogenic; this classification was based on the induction of primary skin cancer as well as the induction of lung and urinary bladder cancer. To summarizing, celiac foods require special attention concerning their i-As content especially those intended for children below 3 years of age. The pressure raised by researchers in the last 20 years has led to the fact for the first time in 2016, a European Union regulation by EFSA limited the maximum contents of i-As in different types of rice: i) 100 µg kg-1 of i-As in rice used to produce infants' and children's foods, and ii) 300 µg kg-1 for pancakes, wafers, biscuits, and rice cakes. In this lecture, data on the prevalence of celiac disease in Spain will be presented, a connection will be made with their diet and the levels of i-As in their urine will be discussed. Besides, data from a very recent study demonstrating that global-scale pollution of the atmosphere contributes to rice grain i-As. Data from 29 rice cultivation regions, across 6 continents, will be presented and connections with as in soil and the atmosphere will be done, including recent studies in protected areas of Spain.

Keywords: arsenic speciation, celiac disease, inorganic arsenic (i-As), i-As bioaccessibility, i-As bioavailability

BIHI-KN08

Protein crystallography off the beaten track: Septin structure, disease, and the impact of access to large experimental facilities

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Septins are GTP-binding proteins that form filaments that are considered to be part of the cytoskeleton and play fundamental roles in membrane remodeling, barrier formation, and bacterial entrapment. For the last 15 years, we have been attempting to dissect their structure and thereby shed light on their diverse physiological roles. Our crystallographic studies have been supported by a plethora of biophysical techniques using research infrastructure from around the world and culminating in the determination of the first 3D structure of a septin complex solved by cryo-electron microscopy. The termini of the complex have been described to be off-target cleavage sites for the Zika virus protease leading to anomalies in neuro progenitor cell development. Our studies have also provided insight into how nucleotide binding and hydrolysis affect filament assembly and shrinkage, how filaments might bend and thereby recognize membrane curvature, and how cross-bridges are formed during filament bundling. All of the events are important for septin function and will be described in detail during the talk.

Keywords: Septins, GTP-binding proteins, Cryo-electron microscopy

BEEA-KN09

Water, energy and sustainable development: Pakistan’s choices for survival in the 21st century

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The talk entails the speaker’s experience as an Academic staff and as a practitioner in the fields of water, energy management and linking it with Sustainable development goals. It gives an account of the water and energy woes of Pakistan in the backdrop of climate change and the possible indigenous solutions available in the realm of biosciences and allied research. It is exploring the export enhancing sectors like textile sector and leather sector along with the associated challenges it has in the realms of water and energy management and how it can further go on to link with the SDGS and the evidence-based policy mechanism to deliver benefits in the space of public policy and strengthening the Research, Innovation and Commercialization landscape of generation 3 universities and its smooth transition to generation 4.

Keywords: water management, Energy management, Sustainable development

BEEA: Biotechnology for Environment, Energy & Agribusiness Management

Abstracts of Invited Speakers

IT-01

Rice crop residue management and sustainable agriculture

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Rice is an important crop in the rice-wheat cropping system of Punjab, Pakistan. The cultivation of rice involves the generation of a massive volume of field residues. Various practices used to manage rice residues are open field burning, straw incorporation, straw removal, and surface retention. Each of these residue management practices has its own merits and demerits. This study is conducted to understand farmers' adoption of a particular rice residue management practice in the rice-wheat cropping system of Punjab, Pakistan. Data were collected from 139 respondents through a pretested structured questionnaire from various villages of Sheikhupura to estimate the ordered logit model. Farmer's age, clay soil, silt loam soil, super basmati, basmati 86, rice variety 515, the perception that incorporation improves the physical properties of soil, and perception that incorporation decreases the fertilizer requirements has a positive effect on the incorporation of rice residue. However, lack of education and livestock strength on the farm has a negative impact on the incorporation of rice residue management practice. The survey results also indicate that residue of over one-third of the rice area is managed by burning the straw completely or partially. Open field burning of rice residue is an undesirable treatment for the environment and

agricultural sustainability. Since the burning of crop residue worsens global warming besides other undesirable effects, there is a need to formulate policies, initiatives, and technologies that will help reduce the burning of residues.

Keywords: Environment management, Energy management, Agribusiness Management

IT02

Germin like protein genes battle for tomato plants against whiteflies and heat stress

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Stress resistance in plants has been a long chase for plant biologists with rising global temperatures and changing insect pests. From stress perception to the deployment of defense responses, the plants have to engage many genes. Therefore, the knowledge of stress-responsive genes and underlying mechanisms responsible for stress tolerance is of fundamental importance to use for achieving stress resistance. In this perspective, germin-like protein (GLP) genes are known for their stress responsiveness and have been investigated in many plants, however, their role in tomatoes is undefined. In this study, we transformed an important rice root-specific germin-like protein gene (*OsRGLP1*) in tomatoes and produced overexpression (O.E.) lines. The heterologous expression of the transgene was validated through *q*PCR and the enzymatic activity assays were performed for superoxide dismutase. The (O.E.) lines and control tomato plants were subjected to heat stress. Based on mortality and plant revival rates, heat exposed O.E. plants exhibited a significantly greater survival rate than control plants. To see the effect of GLP gene overexpression against whiteflies, the O.E. tomato lines, and control plants were exposed to whiteflies (*Bemisia tabaci*). Interestingly, a significant reduction in the whiteflies population and number of eggs was recorded in transgenic lines when compared with control plants. The infected control plants also showed symptoms of curling and wilting on leaves while tomato fruits exhibited necrotic lesions, whereas no such deformities were observed in transgenic plants. The study suggested a protective role of the *OsRGLP1* gene against heat stress and whiteflies infestation highlighting the potential implications of Germin like protein genes in stress adaptation in tomatoes. Further opportunities can be explored to use this important family of genes in engineering stress tolerance in tomatoes and also other crops of economic value.

Keywords: Transgenic tomato, OsRGLP1, heat stress, whitefly infestation

IT-03

Putting the knowledge of plant disease resistance into the framework of biotechnology

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Plant pathogens pose a serious threat to crop productivity. Estimates suggest that 20-30% of the global farm produce is lost to insect pests and diseases annually. A part of this lost food, if secured, could be enough to feed an additional one billion people. Plant breeding has led to the development of disease-resistant crop varieties in a sustainable and environmentally friendly manner. However, we are now at the verge of a saturation point of stacking good genes by conventional breeding methods due to the non-availability of novel resistance (R) genes in the existing germplasm. Recent advances in the understanding of host-pathogen interactions and underlying mechanisms of plant defense responses have brought us to the brink of stacking R gene(s) including pattern recognition receptors (PRRs) for durable and broad-spectrum resistance. Nevertheless, progress made in the commercialization of disease-resistant transgenic cultivars is not impressive. One reason is that disease resistance costs plant fitness and often renders a yield penalty. This was also evident in our recent experiments in which we overexpressed a highly conserved eukaryotic gene named S-NITROSOGLUTATHIONE REDUCTASE (GSNOR) in tomatoes which fine-tunes cellular nitric oxide (NO) bioavailability and signaling. Although, transgenic plants offered improved disease resistance but at the cost of in vitro regeneration inhibition and altered adult plant architecture leading to a striking plant fitness penalty. We also have established that elevated cellular NO after pathogen recognition leads to the S-nitrosylation of Cys139 within small ubiquitin-like modifier (SUMO) conjugating enzyme (SCE1) in Arabidopsis. This leads to an inhibition of SCE1 conjugation ability to promote SUMO modification of target proteins and relieves the repression of the activation of plant immunity. The knowledge of these mechanisms underpinning plant defense responses, that is, how pathogens are perceived and contained by the activation of plant immune system, and what genes and regulatory mechanisms are involved therein, seems to be the future of upcoming breeding efforts for the engineering of defense-related genes and deployment of disease resistance in crop plants.

Keywords: Disease resistance, fitness penalty, genetic transformation, R genes

IT-04

Open knowledge and new technology development - the HIF model

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The Covid-19 pandemic has provided a global challenge to the current system in place where the healthcare systems in many countries were either strained to the limits or collapsed; not just once, but many times, and in the same countries. A pandemic such as Covid-19 or worse could have been expected when in the early 2000s, we were warned by scientists that the risks of pandemics were increasing due to the continued encroachment into nature by civilization. The arrival of Covid-19 has made the warning a reality and has stimulated the rapid development of vaccines using biotechnology. Such response by the scientific community should be recognized as a major accomplishment. At the same time, both new drug discovery and access are still critical, as in general public health applications. At the international level, there are several legal obligations for countries to operate within a global normative structure for human rights, technology. Major declarations are the UN 1948 Convention on Human Rights, 2005 UNESCO Convention on Bioethics. With the various legal agreements in place, much of the work has been done to create the conditions for us to move towards a practical reality for access to what we can call qualified technology. While the conventions provide the global framework, for the conventions to have tangible meaning, there must be an application within current conditions to benefit individuals and communities. A major example of possible applied knowledge and technology framework can be found in the Health Impact Fund (HIF). The HIF creates a pool of funding from a small percentage of the GDP of each participatory country and provides rewards for innovators who will discover and bring to market new medicines for the diseases that affect most of the world such as malaria. It also provides incentives to list current medications to achieve wider distribution. After the development of new medicine, innovators agree to sell their product at a cost to participate in the rewards. Rather than funding innovation through markups, the HIF provides a novel way to reward innovators, which is to provide rewards for

the number of people who benefit from the medications. In this way, the HIF provides an analytically sound model for technology development combining incentives for production within a market system and with inclusion for access to the technology produced as a new medicine. With recent success in gaining social and political support, the HIF is moving on to prototyping in practical application; and if successful, could provide an effective model for wider technology development. Such an integral system of new drug discovery could be extrapolated to wider technology development and be a central part of the solution to the challenges we must address concerning public health and climate change. In a novel article in the Journal of Nature, an example of open knowledge or augmented reality was given for new drug development, where experts, who were not able to work in their labs, took up the challenge of discovery via digital platforms such as social media. Similar to the Linux and the Galaxy Zoo, the Covid Moonshot was developed due to the need of researchers to integrate knowledge around drug development for the treatment of Covid-19 infection in "a large, fast-moving and unscheduled experiment…probing a key protein of the coronavirus SARS-CoV-2 to find chemical starting points for drug discovery". It was a spontaneous and open "Twitter-fuelled" collaboration where scientists saw virtual collaborations spring up around the globe exactly as we saw with the production of Linux and other open-source projects in the past. A wide process of augmented deliberation and bioinformatics ensued creating the Covid Moonshot. For a world that is going digital, such examples might be worthwhile to strengthen global collaboration in scientific research.

Keywords: Covid-19 pandemic, Biotechnology, Prototyping

IT-05

WECANN project: From traditional use to genomics of wild Cannabis

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In recent years, Cannabis has become one of the most exhaustively studied plants in several scientific and biotechnological areas. The majority of research currently focuses on the chemical composition and medicinal values of high-THC and high-CBD plants. However, the diversity of Cannabis – particularly in local landraces and wild populations of the species – is much larger, with many uses and potential applications. Through centuries people have used it not only for its therapeutic properties, but also for production of fiber, textile, paper, food, as well as in social and religious rituals. In this talk we will present the project WECANN, in the frame of which we are investigating the variability of Cannabis from genomic, morphological, phytochemical and ethnobotanical points of view. We will present the first global online database of Cannabis traditional uses – http://cannusedb.csic.es – as well as other research lines that we are currently carrying out within the project.

Keywords: Biotechnological, Local landraces, Phytochemical

IT-06

Economics of precision farming: Current status and way forward

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Despite significant share in Gross Domestic Product, factor productivity in Agriculture sector is stagnant since many years. With limited scope in expansion of cultivated area, the stagnation means lack of competitiveness and the population growth outpacing the agricultural growth. As a result, the country is now net importer of many foods and agricultural commodities and is outperformed in international trade due to many factors including low productivity and resultant higher cost of production. There is a plethora of issues reported in literature ascribed to this dismal situation, but lack of modern and precise agriculture practices is discussed as a major bottleneck in agricultural growth of Pakistan. The paper discusses inefficiency of conventional modes both in terms of direct financial costs as well as social and natural resources related costs and scope for off-the-shelf solutions with potential economic gains. The paper also discusses recent initiatives in Pakistan for precision agriculture including the work of Precision Agriculture and Analytics Lab under National Centre in Big Data and Cloud Computing and identifies low hanging fruits for precision farming. The paper also analyses potential barriers and offers potential institutional solutions and opportunities under CPEC initiatives and locally available knowledge products to handle the challenges and make the national agriculture modern, competitive, sustainable, and relevant to local as well as global demand.

Keywords: Digital agriculture, Agroecological zones, Agriculture analytics, Agricultural productivity

IT-07

The impact of agriculture technologies, energy consumption on agriculture output in Pakistan

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Agriculture provides food to humans and animals. With the passage of time, modernization in agriculture also happened along with other sectors of the economy. The aim of this paper is to examine the impact of agriculture technologies and energy consumption on agriculture output in Pakistan. For this purpose, annual time series data is used for the period 1983-2019. The results of the unit root test confirmed the mix order of integration [I(0), I(1)]. To find the relationship between the variables, Autoregressive Distributed Lag (ARDL) model is employed. The results of the study showed a positive impact of energy consumption on agriculture output. As far as agriculture technologies are concerned, there are a significant positive impact of tractors and tube-wells on agriculture output, however, the insignificant impact of fertilizer on agriculture output in the long run.

Keywords: Agriculture technologies, energy consumption, Agriculture output, ARDL

IT-08

A novel transgenic resistant strategy against cotton leaf curl disease

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Cotton leaf curl disease (CLCuD) is the major limitation to cotton production in Pakistan. The disease is caused by *Begomoviruses* (family *Geminiviridae*), which contains single stranded, circular DNA genome and is transmitted by a single species of whitefly (*Bemisia tabaci* Gennadius). Approximately 5-6 species of begomoviruses are infecting cotton. Cotton leaf samples showing typical begomovirus like symptoms, vein thickening, leaf curl and enation, were collected from distinct locations of Pakistan. Full length begomoviruses, alphasatellite and betasatellite were cloned from the symptomatic samples which showed high identity to Cotton leaf curl Kokhran virus (CLCuKV), Cotton leaf curl Multan Betasatellite and Cotton leaf curl Multan Alphasatellites, respectively. The partial tandem repeat constructs of begomovirus and associated components were developed which were infectious to *Nicotiana benthamiana*. An innovative approach of program cell death was used to reduce cotton infecting begomoviral infection, by targeting the viral genomes using modified cotton leaf curl betasatellite. The *Nicotiana benthamiana* transgenes showed no symptoms compared to control plants. The expression analysis of transgenes showed high expression of *Cyt c* gene and reduced titer of CLCuKV compared to control plants. Further analyses are required to prove the concept of sustainability and durability of the technique compared to RNAi-mediated approaches to control cotton infecting begomoviruses.

Keywords: Cotton, Resistance, Apoptosis, CLCuD

IT-09

Insights into the role of nitric oxide in plant biology

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Nitric oxide (NO) is a small diatomic molecule that regulates multiple physiological processes in animals, plants and microorganisms. In animals, it is involved in vasodilation and neurotransmission and is present in exhaled breath. In plants, it regulates both defense against biotic and abiotic stresses and a plethora of developmental programs. We have performed in-depth analysis into the roles of Nitric oxide in plant biology via deep RNA sequencing, transcriptomic analysis and functional genomics of rice, tomatoes and the model plant Arabidopsis. With the help of detailed functional genomic analyses involving loss of function and gain of function mutant plants, we show a key role of nitric oxide in regulating some of the most important plant physiological processes such as plant defense against biotrophic as well as necrotrophic bacterial and fungal pathogens, responses to salt, drought, heavy metals and heat stress, regulation of plant stem cell growth, production of secondary metabolites and regulation of plant development. We also performed real time NO measurements in plant tissues at basal as well as induced levels following biotic and abiotic stresses. In addition, we have also identified key transcription factors that are required for modulation of the above-mentioned physiological processes at transcriptional level.

Keywords: Nitric Oxide, RNA-Seq, functional genomics, NO measurement

IT-10

Value addition of agricultural produce through sustainable food handling and process technologies for income generation and rural development: Opportunities and challenges

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Based on existing trends, Pakistan's food supply situation over the next decade, is not secure to meet the challenge of food security. In this regard, Pakistan was categorized in Phase 3 and Phase 4 by the Integrated Food Security Phase Classification (IPC) in 2015 which means that area under Phase 3 is highly food insecure while those under Phase 4 are severely food insecure. Having tropical climate, although 40 different kinds of vegetables and 21 types of fruits are produced in Pakistan but high post-harvest losses in the supply chain of these perishables is a major hurdle not to tap the full potential of this sector. The main reasons for such losses include non-availability of sustainable food handling, storage and processing facilities at the farms, income situation of growers, ineffective market structure and prominently energy requirement and its cost. The conventional food processing practices are uncontrollable, inefficient, energy and time consuming which provide non-homogeneous quality. In contrast, industrial scale processing offers controlled and efficient facilities which are centralized and out of approach to adopt by small to medium scale farming communities and heavily relied on depleting fossil fuels. Therefore, applications of decentralized energy efficient solutions for medium to high range temperature agricultural processing is highly needed. Pakistan is blessed with intense solar energy, 19 MJm-2 for 7.6 hours a day with an average irradiance 5 to 7 kWh m-2 d-1. Out of all available renewable energy sources, solar thermal application in agriculture possesses wide scope. The available potential of solar energy can be harvested to address the challenge of post-harvest losses through the provision of on-farm food processing facilities like solar dehydrators, solar cold storage units, solar roasting unit and solar distillation system. Promotion of such sustainable technologies in rural areas will not only upsurge the on-farm value addition services but play vital role in income generation and rural development.

Keywords: Value addition in agriculture, solar thermal technologies, rural development, Income Generation

IT-11

Development: Prosperity or disparity?

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The talk will discuss some of the factors (or forces) that are a sort of shaping the world we live in, and they are going to have a great influence on the kind of a world that we will have in the future, and therefore the ramifications or implications of these factors to the changing global economy. Analyzing the uneven growth and human migration in many regions of the world and their impacts on the emerging global economy on the one hand and highlighting some of the changes that have already been taking place in the global economy in terms of communications due to globalization on other hand, this talk will bring together aspects/forces to speculate possible scenarios like the ways for future global sustainable development.

Keywords: Ramifications, Human migration, Global economy

IT-12

Synthetic biology and biogenic nanomaterials: Advances and applications

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IT-13

Temperature and precipitation trend analysis over time series of Mangla Basin Pakistan

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Precise determination of temperature and precipitation trends is prerequisite to scientific agricultural planning, particularly in the countries where this sector is the mainstay of economy. This research investigated the temperature and precipitation variability across the 11 climatic stations of the Mangla Basin lying in Pakistani territory, over 43 years study period (1971-2013). Nonparametric Mann-Kendall test was applied to detect the variation in monthly, seasonal and annual precipitation and temperature. The results highlighted a mix of positive (increasing) and negative (decreasing) trends. Seasonal variation at Gari Dupatta and Naran exerted a significant impact on maximum temperature amounting to -5.53 °C/year and -6.09 °C/year respectively. Rawalakot also showed significant change in maximum temperature with increasing trend annually. Significantly increasing trend of precipitation was also found at Nara both annually and seasonally with highest value of precipitation 3.62

mm/year. However, at the level of entire Mangla Basin, statistically insignificant trends were found for the annual and seasonal maximum temperature. A decreasing trend was visible in seasonal maximum temperature, seasonal and annual precipitation across the basin except at Naran. The performance of Mann-Kendall test was consistent at the verified significant level.

Keywords: Precise determination, Agricultural planning, Mainstay of economy

IT-14

Use of organic waste for generation of bioenergy and compost for farm electrification

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The production of bioenergy from biomass is becoming very important in different countries due to increasing demand of energy. Pakistan generates 113.9 MT of farm residues that have a large potential to produce bioenergy and compost fertilizer. The study was planned to utilize agriculture wastes in combination of cow dung to produce bioenergy and compost fertilizer. The total weight of organic material used was 250 kg for small digester and 3048 kg for large digester. The total amount of biogas production was measured 45.73 m3 in large digester and 6.68 m3 in small digester throughout the whole time period. The parameters measured were temperature inside the digesters, canopy temperature, ambient temperature, biogas production and production of compost. The biogas production was increased with the increase in digester temperature. The production of biogas was measured from 14th day of filling of large digester and continued up to 14 weeks i.e., 96 days. The correlation relationship b/w canopy temperature and ambient temperature was higher i.e., 98%. The collected and filtered biogas was used to operate generator of 7.5 kWh. The electricity was generated to use for light and heating. Approximately 2955 W by which 1 bulb of 100 W 36 of tubes lights of 900 W and 36 LED lights of 540 W were ignited from this generated electricity. The heater of 1000 W was also used for heat energy.

Keywords: Anaerobic digestion, Biogas, Bio compost, Compost fertilizer

IT-15

Formulation and characterization of food grade O/W emulsions encapsulating quercetin and curcumin: Conventional vs microfluidic approach

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Solubility of bioactive compounds in aqueous phase is challenging while developing an emulsion-based delivery system. Therefore, this study was designed to enhance the solubility of curcumin and quercetin in oil-in-water (O/W) emulsions using modified starch as an emulsifier. The effect of different processing conditions (pH, ionic strength and temperature) was investigated on the mean droplet diameter and ζ-potential over the period of 5 months. It was found that the emulsions containing 5% (w/w) modified starch along with 10% oil (w/w) yielded the most stable formulation with a mean particle size of 175 nm. Solubility of quercetin and curcumin was found to be maximum in emulsions (2.07 and 39 times respectively) as compared to oil and water. Furthermore, stability of the emulsions under varying ionic strength (0.1-1 M NaCl) and pH (2-7) was found to be higher. Microchannel emulsification (MCE) was used to encapsulate quercetin in O/W emulsions. A silicon microchannel plate (Model WMS 1-2) comprised of 10,300 discrete 10 × 104 μm microslots, connected to a circular microhole with an inner diameter of 10 μm. 1% (w/w) Tween 20 was used as optimized emulsifier, while 0.4 mg mL-1 quercetin in different oils served as a dispersed phase. The MCE was carried by injecting the dispersed phase at 2 mL h-1. Successful emulsification was conducted below the critical dispersed phase flux, with a Sauter mean diameter of 29 μm and relative span factor below 0.25. The O/W emulsions remained stable in terms of droplet coalescence at 4 and 25°C for more than 30 days. The encapsulation efficiency of quercetin in the O/W emulsions was 80% at 4°C and 70% at 25°C during the evaluated storage period.

Keywords: O/W emulsions, Solubility, Curcumin, Quercetin, Droplet diameter, MCE

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Abstracts of Invited Speakers

IT-01

The identification and separation of specific cells from heterogeneous populations

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The identification and separation of specific cells from heterogeneous populations is an essential prerequisite for further analysis or use. Conventional passive and active separation approaches rely on fluorescent or magnetic tags introduced to the cells of interest through molecular markers. Such labeling is time- and cost-intensive, can alter cellular properties, and might be incompatible with subsequent use, for example, in transplantation. Alternative label-free approaches utilizing morphological or mechanical features are attractive but lack molecular specificity. Here we combine image-based real-time fluorescence and deformability cytometry (RT-FDC) with downstream cell sorting using standing surface acoustic waves (SSAW). We demonstrate basic sorting capabilities of the device by separating cell mimics and blood cell types based on fluorescence as well as deformability and other image parameters. The identification of blood sub-populations is enhanced by flow alignment and deformation of cells in the microfluidic channel constriction. In addition, the classification of blood cells using established fluorescence-based markers provides hundreds of thousands of labeled cell images used to train a deep neural network. The trained algorithm, with latency optimized to below 1 ms, is then used to identify and sort unlabeled blood cells at rates of 100 cells/sec. This approach transfers molecular specificity into label-free sorting and opens up new possibilities for basic biological research and clinical therapeutic applications.

Keywords: heterogeneous populations, molecular markers, deformability cytometry

IT-02

Current trends and future challenges in computational life sciences

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Computational life science is cutting-edge multidisciplinary research to decipher the structure and function of biomolecular systems by means of theoretical models, whose roots are anchored in the basic principles of chemistry and physics. It covers a broad spectrum of methodologies, from the mining of biological databases to classical molecular dynamics and quantum chemical calculations. Computational life sciences research has taken advantage of the rapid development of biological data, computer technology, especially the new algorithms, ever-increasing speed of calculations, and highly efficient memory storage devices. It aims at complete understanding of living systems across multiple levels of biological organization, from the molecule to the cell, and from there to the organism. Towards this goal, development of multi-scale simulations systems for the prediction of various pathophysiological conditions and proposed modulations could develop knowledge from the current descriptive and qualitative understanding of complex biological systems to a more rigorous and quantitative understanding. This new ability will undoubtedly increase opportunities for development of new interventions to counteract harmful biological diseases. Herein, some case studies of development of in-house multi-scale simulation systems for the prediction of metabolic stability and cardiac toxicity profiles of oral drugs by molecular dynamics simulation using Water Swap method and different data sciences approaches will be presented. Additionally, a case study of development of anti-epileptic leads by stable structural models of the hGAT1 and sequential order and role of co-transported ions (Na+, Cl-) during the translocation cycle of hGAT1 by molecular dynamics simulations (MD) will also be presented.

Keywords: Computational life sciences, Cutting-edge multidisciplinary research, biological organization

IT-03

Liquid biopsies: A non-invasive way of looking into tumor aggressiveness for dynamic personalized therapeutics

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Breast cancer is molecular and clinically heterogeneous disease and is the most common cause of cancer related death among women worldwide. The metastatic potential, treatment resistance and tumor relapse make it one of the most difficult conundrums. However, liquid biopsies led to paradigm shift in the field of translational cancer research. In recent years, small RNA regulator known as MicroRNAs, and Circulating Tumor Cells (CTCs) have been identified to participate in cancer tumorigenesis and metastatic process. CTCs provide a snapshot of tumor status over the course of time and treatment and the findings, that a patient' tumor change with time underlines a promising application of CTCs. Altering expression of MiRNAs of Let-7 family have been identified as modulators of proliferation, apoptosis and resistance treatment in breast cancer known as tumor suppressor. Objectives were to investigate the differential expression of Let-7 in breast cancer and its correlation with estrogen receptor subtype ER b, Androgen Receptors and to detect and quantify level of CTCs in parallel with the help of a panel of markers (EpCAM, KRT & MAM). 60 patients of breast cancer according to predetermined inclusion/exclusion criteria were enrolled in this cross-sectional study. Blood samples and paraffin embedded tissues samples of the patients were collected. These were subjected to immunohistochemistry and real-time quantitative reverse transcription PCR (qRT-PCR) analysis. Our results showed increase in expression of the three markers for CTCs in metastatic breast cancer patients as compared to the ones on neo adjuvant and adjuvant chemotherapeutic regimes. Moreover, the level of CTCs varied with molecular subtypes. We didn't find any association of CTCs with cancer stage and grade. Taken together, our findings indicate that mirRNA Let 7a expression and CTCs level in blood are strongly associated with tumor prognosis

and RT-qPCR may prove powerful bait in order to harness heterogeneous CTCs. The prospect of CTCs is to be provided with the platform of analysis beyond just enumeration.

Keywords: Breast Cancer, CTCs, RT-qPCR, Liquid Biopsy, MicroRNA

IT-04

Genetic toxicology (safety assessment, toxicology, mutagenesis, genetic & molecular toxicology)

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Drug development is a strictly regulated process overseen by the regulatory agencies in different geographical regions globally. In the US, any new drug has to seek approval from the US regulatory agency, Food and Drug Administration (FDA). Drug development process is divided into pre-clinical and clinical phases. Safety assessment is a major part of the pre-clinical phase. General and genetic toxicology evaluation of the drug candidate is needed to assure its safety. Pig-a is a recently developed in-vivo gene mutation assay to assess the mutagenic potential of a test compound. Phosphatidyl inositol glycan, class A (Pig-a) gene is among one of the many genes responsible for the synthesis of glycosyl phosphatidyl inositol (GPI) anchor on the cell surface to attach various kind of proteins (e.g., CD24, CD59 etc) to the cell surface. Pig-a is an X-linked gene and can be used as reporter gene for a gene mutation assay. Pig-a is a flow cytometry-based assay conducted with a small amount (~80 μL) of peripheral blood and scores >100 million RBCs in 2-3 minutes. This is a very sensitive, highly reproducible, and easily transferable assay. OECD test guidelines are in progress and are expected to get approved by 2022.

Keywords: Drug development, Geographical regions, Gene mutation

IT-05

Advances in high-throughput sequencing: Challenges and opportunities for the environmental, health and agricultural sectors

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Recent decade has witnessed tremendous growth and advancements in the next-generation or high-throughput sequencing. In the race for advancing in technology and capturing bigger market share, some NGS platforms such as SOLiD and Helicose Biosciences simply could not cope up with the challenges and hence became obsolete. Contrary to that, new platforms like MGI made their way into the market. Currently, the major market players are Illumina, Ion Torrent, Pacific Biosciences, Oxford Naopore and MGI. Not all the platforms are equally suitable for the diversity of research and applications in the fields of environmental investigations, health and diseases, and food and agriculture. In this talk, I will present some major technological differences among the extant NGS platforms, the availability of different variants of the platforms, their data output, and their suitability in different NGS applications including whole genome sequencing, human whole exome sequencing, transcriptome sequencing, metagenomics, amplicon sequencing, genotyping-by-sequencing, etc.

Keywords: high-throughput sequencing, NGS, Oxford Naopore

IT-06

Philadelphia Chromosome-positive (Ph +) leukemia; mechanism of the disease and molecular targeting

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Chronic myelogenous leukemia (CML) and Philadelphia chromosome -positive acute lymphatic leukemia (Ph+ ALL) are caused by the t (9;22) translocation which fuses the BCR gene to ABL resulting in a deregulated tyrosine kinase activity. Targeting BCR/ABL with tyrosine kinase inhibitors (TKIs) is a proven concept for the treatment of Philadelphia chromosome-positive (Ph+) leukemias. Resistance attributable to either kinase mutations in BCR/ABL or non-mutational mechanisms remains the major clinical challenge. With the exception of ponatinib, all approved TKIs are unable to inhibit the "gatekeeper" mutation T315I. However, a broad spectrum of kinase inhibition increases the off-target effects of TKIs and may be responsible for cardiovascular issues of ponatinib. Moreover, ponatinib or any other approved drug are unable to inhibit BCR/ABL compound mutations. Thus, there is a need for more selective options for the treatment of resistant Ph+ leukemias. We aimed to develop new ABL kinase inhibitors, allosteric inhibitors, oligomerization inhibitors and down-stream pathways inhibitors for the treatment of resistant Ph+ leukemia patients. We also study the mechanism of Ph+ Leukemia and focused on the main unsolved questions like disease relapse, mutational and non-mutational resistance and progression of chronic myelogenous leukemia (CML) to Philadelphia chromosome-positive acute lymphatic leukemia (Ph+ ALL). We developed novel inhibitors with the specifications of i.) targeting T315I and other resistance mutations in BCR/ABL; ii.) achieving a high selectivity to improve safety; and iii.) overcoming non-mutational resistance in Ph+ leukemias. These inhibitors inhibited native BCR/ABL and clinically important mutants including p-loop mutations (Y253F and E255K), "gatekeeper" mutation (T315I) and compound mutation, (T315I-E255K) at nano-molar concentrations. They suppressed primary Ph+ acute lymphatic leukemia derived long term cultures which displayed either non-mutational resistance or harboring

the T315I. In BCR/ABL or BCR/ABL-T315I-driven murine leukemia as well as in xenograft models of primary Ph+ leukemia harboring the T315I, they significantly prolonged survival of the mice.

In summary, our work establishes a novel approach for the molecular targeting of BCR/ABL positive leukemia and explains the clinical behavior of patients with unmutated and mutated BCR/ABL.

Keywords: Chronic myelogenous leukemia, Philadelphia chromosome, Leukemia

IT-07

Discovery and pharmacological evaluation of novel compounds as inhibitors of nucleotide metabolizing enzymes

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Members of the ectonucleoside triphosphate diphosphohydrolases (NTPDases) constitute the major family of enzymes responsible for the maintenance of extracellular levels of nucleotides and nucleosides by catalyzing the hydrolysis of nucleoside triphosphate (NTP) and nucleoside diphosphates (NDP) to nucleoside monophosphate (NMP). Although, NTPDase inhibitors can act as potential drug candidates for the treatment of various diseases, there is lack of potent as well as selective inhibitors of NTPDases. Ecto-nucleotidase enzymes catalyze the hydrolysis of extracellular nucleotides to their respective nucleosides. Here in, we place the focus on the elucidation of structural features of the cell surface located ecto-nucleoside triphosphate diphosphohydrolases (E-NTPDase1-3 and 8). The physiological role of these isozymes is crucially important as they control purinergic signaling by modulating the extracellular availability of nucleotides. Since, crystal or NMR structure of the human isozymes are not available – structures have been obtained by homology modeling. Refinement of the homology models with poor stereo-chemical quality is of utmost importance in order to derive reliable structures for subsequent studies. Therefore, the resultant models obtained by homology modelling were refined by running molecular dynamic simulation. Binding mode analysis of standard substrates and of competitive inhibitor was conducted to highlight important regions of the active site involved in hydrolysis of the substrates and possible mechanism of inhibition.

Keywords: Ectonucleoside triphosphate diphosphohydrolases (NTPDases), Nucleoside triphosphate (NTP), Homology modeling

IT-08

Assessing the role of urban ecosystem in respiratory allergies

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Respiratory allergies are the response of immune system to air borne stimuli such as dust, pollen, mold, or animal hair. These allergies are characterized as allergic respiratory disease (ARD). Generally, ARDs manifest as nasal congestion, cough, dyspnea, rhinorrhea, excess mucus production, and fever. ARDs affect persons of all ages and gender, and are more common among pregnant, asthmatic and immunocompromised patients. Children are more susceptible to ARDs such as allergic rhinitis and childhood asthma. ARDs occur when allergic stimulants, depending on their size and chemical nature, are penetrate in the lung tissues and are absorbed into the circulation reaching distal organs such as liver and heart. The circulating allergens can cause acute inflammation which is resolved in few days or weeks, such as allergic rhinitis and pollen allergy. The allergens may also cause chronic inflammation which can lead to long term disorders such as asthma, chronic obstructive pulmonary disorder (COPD), and alveolitis. While a few respiratory disorders genetically prevail in humans, most of the ARDs have anthropogenic origins. Environment plays a major role in development of ARDs by increasing the number and density of air-borne pollutants. In urban areas, the socio-ecological structures require intense human intervention to sustain. These interventions have led to a visible impairment of natural environment in terms of air pollution, land degradation, and water shortage. The potential of urban ecosystem to sustain economic well-being versus its risk on human health is the major concern of healthcare professionals globally. The prevalence of respiratory illnesses in densely populated cities is increasing at an alarming rate. The increase in air pollutants in urbanized regions has been linked with pre-term births, neonatal lung defects, and decreased lung function in growing children. We are reviewing the holistic perspective on assessing the role of urban ecosystem in respiratory allergies. The framework links prevalence

of ARDs in the urban areas with the external and internal health indicators and the dynamics of urban infrastructures.

Keywords: Allergic respiratory disease (ARD), Chronic obstructive pulmonary disorder (COPD)

IT-09

Tech-Health and future of product design in healthcare

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Healthcare technology is the biggest skyline of today's demanding era. With onset of the global pandemic, we've all witnessed what happens when demands beyond our control move the reason for adopting technology. Product design and development is the new norm of health technology, and next era is going to be embarked with such discoveries. The drive we've seen to adopt remote technologies is unprecedented, and it extends not only to the patient care but also to the clinical research. Noteworthy of them are assistive technologies, telemedicine and wearable devices. At NICHE/RCMS NUST, we are working in the areas of cutting-edge research in design and development of products in health care under Computational Biomedical Engineering research group at RCMS. Ask anybody what personal technology will look like 10 years from now, and you'll probably get a wrong answer. A decade ago, almost nobody could predict that more than a million people would buy a watch that not only tells the time, but reads your text messages, checks the weather, and tracks your workouts, too. But that's exactly what happened. Nowadays, the rise of wearable technology, from fitness trackers and the Apple Watch to Google Glass- all has been fueled by technology's tendency to get faster and smaller at the same time. Care, on the other hand is an important emotion, and the technologies enabling 'virtual care' now due to the onset of Pandemic, are expected to expand significantly. At NUST, we are enabling virtual care by numerical techniques, digital imaging, interoperability, artificial intelligence, and advanced analytics. Smart, connected devices are now on the rise, and the role of these connected devices in the healthcare industry is beyond imaginations. Services to facilitate patient can be made much easier through digital care. Have you ever imagined a normal-looking earrings will track your heart rate, body temperature and blood oxygen levels, providing you with vital health statistics? NUST is expanding, in

innovations, science, technology and research. We have designed computational devices, for Backbone health, posture mechanics, sport biomechanics, tumor detection, muscle health and disease identification. Understanding health problems is niche requirement and their dynamics is important for work efficiency, healthy life and functionality. The only possible way out is Tech-Health, and it can serve as a great platform as well as frame work to improve this picture.

Keywords: Healthcare technology, Adopting technology, Pandemic

IT-10

Development of recombinant NDV as an oncolytic agent for cancer treatment: Where are we and the way forward?

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Newcastle disease virus (NDV) has been studied extensively for its oncolytic activities since 1950s. Unlike many oncolytic viruses, NDV is an avian virus that does not cause any disease in human. Reports on the potential of wildtype NDV in treating cancer could be seen over the last decades, some of which even reporting its efficacy in phase II clinical trials. The Malaysian researchers joined this bandwagon and investigated our local NDV isolates including the velogenic strain AF2240 and vaccine lentogenic strain V4-UPM, hoping to reveal their oncolytic potential. The mechanism of NDV-mediated anticancer activities as well as their challenges have been reported, laying the foundation of developing more potent NDVs to kill the cancer cells effectively. Reverse genetics was established in the laboratory to enable genetic engineering of the RNA nature of the viral genome. Apart from modifying the viral genes to investigate the pathogenicity of the virus, several transgenes including those that express cytokines, pro-apoptotic protein, and anti-tumor antibodies have been inserted into its genome and these were expressed during virus replication. The promising results obtained *in vitro* have motivated us to progress to animal studies. A mixture of outcomes has been obtained where some recombinant NDVs successfully reduced the tumors whilst others did not show any enhanced oncolytic activities compared to that of the wildtype. Nevertheless, these findings have proven the potential of recombinant NDV to be used as an oncolytic agent for cancer treatment.

Keywords: Newcastle disease virus, reverse genetics, oncolytic virus, cancer

IT-11

Microbial pangenome and reverse vaccinology: From bench to beside

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The growing antimicrobial resistance and emergence of new resistance bacterial species are among the major challenges for the global healthcare settings. At the same time, the genome variations among several closely related genomes (species) limiting the efficacy of vaccines against a finite range of organisms. This vast genomic diversity accumulates many variable genes in the species gene pool ultimately resulting in the species' pangenome expansion. Therefore, it is very unlikely for a single representative strain (genome) to represent the whole species and is not sufficient for estimating the exact pangenome of a species, likewise, is it is not suitable for designing broad-spectrum therapeutics including the vaccine. In this context, we developed high-throughput genome analysis tools such as PanRV and VacSol for estimating the microbial genomic diversity (pangenome) and screening of potential core-vaccine candidates (PVCs).

Keywords: Pangenome, Vaccine Candidates, reverse vaccinology, PanRV, VacSol

IT-12

Current trends in immunoinformatic and vaccine development

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Vaccines are the considered as one of the greatest achievements of the modern world. It has saved several lives, reduced treatment costs and raised the quality of animal and human lives. Traditional vaccines were made with little or no knowledge of how they modulate the immune system. With advancements in sciences, there are still immune-related concerns that come up with modern vaccine deigns. These concerns are mainly related to issues like specific vulnerable populations, cases of emergence and re-emergence, pathogens with complex lifecycle and antigenic variability, need for personalized vaccinations, and vaccines' immunological safety. These concerns have paved a path for immunoinformatic to explore better understanding of infectious diseases, their pathogenesis and diagnosis, immune system response and computational vaccinology. The importance of immunoinformatic is diverse in terms of computational approaches utilized particularly related to host–pathogen relationship. Bioinformatics methods are also used to impart functions to uncharacterized genes which can then be exploited as new and improved vaccine candidates. An insight into novel computational, and experimental approaches for studying host–pathogen interactions and their role in vaccine development will be discussed.

Keywords: Immunoinformatic, computational vaccinology, vaccine design, emerging infections, immune system, vaccinology

IT-13

Value addition of apricot in Gilgit-Baltistan

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Livelihood of peoples of Gilgit-Baltistan depends upon fruits and vegetables especially for rural masses as cultivated lands are less as compared to other parts of the province. Apricot, among fruits has special importance as local people earn their livelihood at every step of value addition starting from cultivation to end product. Apricot is grown with other fruits like almond, apple, grapes, cherry, pear etc. as mixed fruit garden in Gilgit-Baltistan. Keeping in view the importance of apricot value addition in livelihood of local population, present study was conducted to see the prospects of value addition of apricot in Gilgit-Baltistan. The study focused only on district Ghizer due to limited resources. Almost 50 farmers were randomly selected for data collection regarding apricot production and value addition during year 2020. Study relies mainly on descriptive statistics to cover the objectives. Results of the study revealed that average number of trees per household was 33.6 for apricot, 24.7 for almond, 15.2 for apple, 3.9 for grapes, 6.2 for cherries and 4.34 for pear fruit. Average fresh apricot production per household was 1226.8 Kg. Out of total production, home consumption of fresh apricot was 3.06 percent (37.62 Kg) further segregating into fruit use (29.6 Kg), use in pickle (0.14 Kg), use as jam jelly (1.80 Kg) and use as fresh juice (6.08 Kg) per household. Only 107.6 Kg were marketed in local market from marketable fresh surplus of 1189.18 Kg at the rate of Rs.20/Kg while the cost of production of fresh apricot was estimated as Rs.8.09/Kg. After deducting home consumption and fresh market of apricot, the remaining production of 1081.58 Kg was dried by relying both on sun and sulphur drying keeping in view the local weather and market demand. Total achieved dried production of apricot was 313.57 Kg (28% of fresh apricot). Out of it, 41.84 Kg was used as dried home consumption and remaining quantity was marketed in two value added forms. First form as whole dried apricot (16.54 Kg) with average price of Rs.280/Kg and second form as seedless dried apricot (248.06 Kg) with average price of Rs.190/Kg. On an average, 28.6 Kg of kernel (the seed of apricot) was achieved to make it as seedless apricot. 3.40 Kg was used as domestic consumption out of total produced kernel of 28.6 Kg. Whereas 3.02 Kg was used in oil extraction and 22.14 Kg was marketed with average price of Rs.500/Kg. Average value of dried apricot increased from Rs.21631.6 to Rs.77767.8 upon incurring drying expenditures of Rs.3629.68 by the households. The net gain from value addition activities was estimated to Rs.52506 per household. The farmers reported major production issues of disease attack, alternate fruit bearing, climate changes and shortage of canal water. Non-existence and patronage of apricot cottage industry and lack of solar dryers were the major concerns of apricot processors. Patronage of cottage industry by extending soft loans to producers/processors, provision of infrastructure for easy transportation of products and strengthening of market linkages are suggested to harness the full benefits of apricot value addition in study area.

Keywords: Rural masses, Apricot production, Dried apricot

BEEA: Short Talks

ST-01

Energy generation potential from livestock waste: Case study for rural areas of Pakistan

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Energy generation through livestock waste pose significant potential particularly in rural areas that are highly dependent on livestock farming for their living. Livestock waste management system can be tapped in such areas to improve environmental quality as well as provide a means for local energy generation. This study identifies the theoretical potential of energy generation through waste from different animals based on their daily biomass production. Azad Jammu and Kashmir is dealt as a case study while Bio-IRENA simulator is used to perform waste quantification. A complete supply chain system from raw waste to end use in demand sector (Electricity and Heat) is studied. The results obtained from the model and desk review depicts that there are approximately 15 million livestock animals in AJK. These animals can further produce 4 million tons of animal waste each year. This waste can be treated through both methane engine and steam turbines to produce both heat and water. Commercial use of this waste can theoretically produce around 300 TWh of energy. Considering energy consumption per capital value of the region, 65% utilization of this waste can fulfil energy requirements of the whole region. However, this would require mobilizing the local investments for creating decentralized energy systems and creating an efficient supply chain system. Along with energy production and reducing environmental hazards, such systems also enable rural empowerment and local job creation.

Keywords: Bio-IRENA simulator, Livestock waste, Waste-to-Energy, Waste Management, Bioenergy

ST-02

Bioremediation of environmental pollution by plantation activities for clean and green Pakistan

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Quality of life is depending on quality of environment. As environment creates a favorable condition for survival and growth of living organism. All organisms are generally affected indirectly or directly due to environmental pollution. It is due to rapid increases in human population. Environmental pollution especially by anthropogenic activities in urban area is a major issue in front of the world of today, there is a rising awareness of the reality that a clean and green environment is essential for good existence of living organisms. It is our topmost priority to keep our country clean and green as cleanness is a part of our faith. Primary sources of environmental pollution are increasing by anthropogenic activities which are continuously adding different types of pollutants into environment. This environmental pollution by anthropogenic activities is causing a great hazard to plants, animals and to human. As every problem has a solution, because problem is always man made (Anthropogenic), so man needs to find the solution. In recent advances there is a need to develop clean and green spaces in and around the polluted areas for existence of improved environmental surroundings. As some plants can act as pollution sink for different pollutants, acting as natural lungs of the environment. If haphazard population growth and production of new pollution causing structures go on without realizing the importance of trees, then possibly there would be more critical changes for living organisms in near future. So, “green revolution is the best solution to arrest the pollution” in this changing climate of world.

Keywords: Anthropogenic activities, Bioremediation, Environmental pollution, green revolution, Plantation

ST-03

Functional characterization of garden pea (*Pisum Sativum*) 7s vicilin: *In-Silico* studies explains the protein binding mechanism to chitin

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Seed proteins are well known for their pharmaceutical and industrial importance. *Pisum sativum* vicilin (*Ps*V) was purified by sequential procedure of ammonium sulfate precipitation and gel filtration chromatography. Purified *Ps*V appeared as an intact 55 kDa band under both reduced and non-reduced conditions on SDS-PAGE. LC-MS/MS generated peptides showed 80% homology with *Medicago truncatula* and *Cicer arietinum* vicilins deposited in NCBI. FASTA sequence of genome based *Pisum sativum* vicilin (Accession no. P13918) from NCBI was used for the calculation of 3D model. Predicted *P. sativum* vicilin (P*Ps*V) model indicated the presence of three monomers (Chain A, B, C) that joined together through head to tail association and developed into a homotrimer. Sequence alignment of 60% showed high structural homology between predicted model and soybean β-conglycinin template (PDB ID:1IPJ) with RMSD value of 0.963. Site map analysis of P*Ps*V model showed six probable pockets, among which one pocket (Site-1) with highest drug score (0.8) and simple score (0.55) was selected for molecular docking with a chitin oligomer (GlcNAc)4. ΔG value (-6.9 kcal/mol) validated a strong binding affinity between protein and ligand molecule. On the basis of these *In-silico* studies, *In vitro* bioassays showed that *Ps*V (50 μg) significantly inhibited the growth of different fungal pathogens (*Aspergillus flavus*, *Aspergillus niger* and *Fusarium oxysporum*). Similarly, *Ps*V (3 mg) significantly reduced the mean population of all the life stages (eggs, larvae, pupae, adults, male and female ratio) of *T. castaneum*. Moreover, same concentration of *Ps*V increased the mean percent mortality of two life generations (F1 and F2) of *Sitophilus oryzae*. These findings support the pivotal importance of *in-silico* studies towards the exploration of new or more potent molecules against different pathogens.

Keywords: Pea, Vicilin, *In-silico*, Pathogen, Chitin

ST-04

Potential of simultaneous Polyhydroxy-Alkanoate production and wastewater treatment by submerged fermentation in a sequencing batch reactor

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In this work, sequencing batch reactor (SBR) has been designed and employed to produce polyhydroxyalkanoates (PHA) along with wastewater treatment. This process was designed aerobically in submerged fermentation mode. Two SBR setups were tested for PHA production. First setup (setup-1) contains the mixed microbial culture (MMC) as a biocatalyst while in the second setup (setup-II), MMC along with indigenously isolated Bacillus sp. MB353 was used. Both setups were tested for synthetic domestic wastewater having 500mg/L of chemical oxygen demand (COD) at four different hydraulic retention times i.e., 6, 12, 24, 48 hrs. In setup-I, 6 hr HRT produced maximum PHA of 3.6 g/L along with COD removal of 28 mg/L observed in treated effluent. In setup-II, maximum PHA of 6.02 g/L was reported at 12 hrs HRT with COD removal of 38.4 mg/L was observed in the effluent. These results revealed that, both setups functioned towards treatment along with valuable polymer production. In setup-I, although COD removal efficiency was high, but polymer production was low, while in setup-II with negligible decrease in COD removal efficiency almost double the quantity of the polymer was produced. Therefore, augmentation of MMC with Bacillus MB353 strain helped in increasing the levels of polymer production. Extracted polymer was characterized by HPLC and FTIR. Hence, these results indicated that SBRs are efficient systems to cater the handling of waste and reducing the contaminant load of wastewater. Valuable polymer production can also be attained simultaneously in the waste treatment process.

Keywords: Polyhydroxyalkanoates, Sequencing batch reactor, Chemical oxygen demand, Simulated wastewater, wastewater treatment

ST-05

Functional and population genetic features of copy number variations in Pakistani populations

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Copy number variations (CNVs) lately provided a vibrant dimension to the apparently static human genome. This research was carried out to analyze CNVs in 98 healthy individuals who are broadly representative of Pakistani populations (Punjabi, Sindhi and Pashtun). Common CNV regions and their frequency rates were examined in the Pakistani population to gain profound insights from CNVs. We identified 106,761 copy number variations and found 51,518 (48.2%) novel CNVs. In CNV regions, more than 4000 genes have been found. For the association of disease and drug efficacy, the variants called were then annotated by using ANNOVAR. Genes in the novel CNVRs from the Pakistani samples were enriched for genes involved in neurological, development and heart-related diseases. This study will further improve our understandings of the genetic diversity, admixture pattern of Pakistani populations and will benefit future research on disease susceptibility and will also provide a workflow example to use copy number variations for evolutionary studies and personalized medicine.

Keywords: Copy number variations, Genetic disorders, personalized medicine, Disease association

ST-06

Antimicrobial resistance profiling of biofilm forming non typhoidal *Salmonella enterica* isolates from poultry and its associated food products from Pakistan

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Salmonellosis caused by non-typhoidal *Salmonella enterica* from poultry products is a major public health concern worldwide. This study aimed at estimating the pathogenicity and antimicrobial resistance in *S. enterica* isolates, obtained from poultry birds and their food products from different areas of Pakistan. In total 95/370 (25.67%) samples from poultry droppings, organs, eggs, and meat were positive for *Salmonella*. The isolates were further identified through multiplex PCR (mPCR) as, Salmonella Typhimurium 14(14.7%), Salmonella Enteritidis 12(12.6%) and other *Salmonella spp.* 69(72.6%). Phenotypic virulence properties of 95 *Salmonella* isolates exhibited: swimming and/or swarming motility 95(100%), DNA degrading activity 93(97.8%), hemolytic activity 92(96.8%), lipase activity 87(91.6%), and protease activity 86(90.5%). The *sopE* virulence gene known for zoonotic potential was detected in S. Typhimurium (92.8*%),* S. Enteritidis (100%) and non typable *Salmonella spp.* (69.5%). The isolates were further tested against 23 antibiotics (from 10 different antimicrobial groups) and were found resistant against fifteen to twenty-one antibiotics. All isolates have shown multiple drug resistance and were found exhibiting high multiple antibiotic-resistant (MAR) index of 0.62 to 0.91. The strong biofilm formation at 37oC reflects their potential adherence to intestinal surfaces. There was a significant correlation between antimicrobial resistance and biofilm formation potential of isolates. The dominant resistance determinant genes found among the isolated strains were *bla*$_{\mathit{TEM-1}}$ (59.3%), *bla*$_{\mathit{OxA-1}}$ (18%), *bla*$_{\mathit{PSE-1}}$ (9.5%), *bla*$_{\mathit{CMY-2}}$ (43%), *ampC* (8.3%), *gyrA* (54%), *gyrB* (56%), *parC* (55%) and *parE* (37.5%). The detection of zoonotic potential MDR *Salmonella* in poultry and its associated food products carrying cephalosporin and quinolone resistance genes presents a major threat to both poultry industry and public health.

Keywords: poultry, *Salmonella enterica*, NTS, eggs, Antibiotic resistance, MAR index, Pakistan

ST-07

Current status and future prospect of agricultural biotechnology

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Agricultural biotechnology encompasses a wide range of technologies used in food and agriculture for reasons such as improving the genetics of plant types and animal populations, characterizing, and conserving genetic resources, diagnosing plant and animal illnesses, and more. The ongoing debate over genetic modification has dominated discussions concerning agricultural biotechnology. Modern biotechnology represents one-of-a-kind scientific applications that can be used to benefit society by developing crops with increased nutritional quality, pest and disease resistance, and lower production costs.

Keywords: Agricultural biotechnology, Genetic modification, Modern biotechnology

ST-08

Comprehending the efflux mediated drug resistance determinants of typhoid causing bacterium

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Infectious disease and mankind have a long history of confronting each other. This confrontation is unending despite of the 21st century's scientific and medical advancements. The emergence of novel pathogens and the existing recalcitrant bacterial/viral strains require continuous monitoring and therapeutic interventions to tackle the impending danger of epidemic or pandemic. The typhoid causing bacteria, Salmonella enterica serovar Typhi (S. Typhi), a sole human-adapted pathogen is endemic to sub-continent. The severity of the disease burden inflicted by this pathogen can be assessed by the fact that the health authorities in Pakistan have started the vaccination program for school-going children in an attempt to eradicate the typhoid in the most endemic region of urban Sindh and Punjab. To tackle this chronic disease, our group is studying the mechanism of efflux mediated drug resistance and potent inhibitor against S. Typhi for nearly a decade. The findings of our research have shown that styMdtM (STY4874), is one of the potent multidrug resistance transporters belonging to major facilitator superfamily. The clinically isolated S. Typhi strains express STY4874 at varying levels. The export of exceptionally broad substrate/ antimicrobial spectrum by STY4874 is energized by proton coupled translocation. Structural analysis reveals that among the important residues in the styMdtM, Arg at position 111 is inevitable to maintain the structural integrity of the transporter. Moreover, styMdtM is inhibited by the crude milk thistle seed extract and reserpine. However, mode

of action of this inhibition is yet not understood. AcrB is another functionally significant efflux transporter in gram negative bacteria including S. Typhi. Our research has shown that reserpine can also inhibit the AcrB pump of Salmonella Typhi (styAcrB) and hence represent an important inclusion into the existing arsenal of efflux pump inhibitors. The inhibition of styMdtM and styAcrB pumps by reserpine, which is a recommended drug for depression related ailments, is an important finding. Since, recalcitrant *S.* Typhi strains unable to be treated by the recommended therapy can be combined with reserpine to restore the efficacy of anti-typhoid drugs. These studies represent a preliminary picture of the characteristics of the efflux transporters belonging to *S.* Typhi. To understand the regulation and mode of inhibition of efflux mechanism comprehensively, further investigations are required, so that the combination therapy could be improved and morbidity as well as mortality associated with *S.* Typhi could be reduced.

Keywords: Infectious disease, medical advancements, Epidemic

BIHI: Short Talks

ST-01

The role of hypothalamic micro RNAs in the regulation of energy homeostasis

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The worldwide increasing rate of obesity and associated metabolic disorders has led to a growing demand of exploration and validation of novel causative factors, which ultimately could be manipulated to treat the pathologies with disrupted energy homeostasis. Integration of periphery signals and control of feeding behavior and weight are governed by the brain, with a number of nuclei crucial for hunger-driving and satiety-signaling responses are located within the hypothalamus. MicroRNAs (miRs) represent a well-characterized class of small non-coding RNAs that can degrade gene messages or abrogate protein translation. In our earlier studies, we showed that the selective deletion of the *Dicer1* gene in the hypothalamic arcuate nucleus (ARC) results in an increase of body weight, demonstrating that microRNAs play a critical metabolic role at the hypothalamic level. In our current study, we successfully validated microRNA candidates predicted to regulate energy homeostasis. Using cre-dependent CRISPR-Cas9 knock-out approach, we aimed to target specific satiety-mediating neurons expressing proopiomelanocortin within ARC. Our results showed that depletion of the predicted miRs in mice indeed had a drastic impact on body weight and food intake. Furthermore, the predicted target genes mediating these phenotypes were successfully validated *in vitro* and *in vivo*. To our knowledge, it is the first study delineating the metabolic roles of specific miRs in adult proopiomelanocortin neurons. These data will contribute to RNA biology field exploring neuronal control of energy homeostasis and may lead to new approaches to target metabolic disorders.

Keywords: Energy Homeostasis, Hypothalamus, MicroRNAs, CRISPR-Cas9, Obesity, Hyperphagia

ST-02

Combating superbugs with AI: System for standardized monitoring & reporting of antimicrobial resistance threats

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Antimicrobial resistance (AMR) is the ability which enables the bacterial pathogens to survive despite the antibiotic treatment. In recent years misuse and over-prescription of antibiotics have resulted in this phenomenon to become a pandemic lurking in the shadows. On the directives of WHO the Government of Pakistan adopted the National Antimicrobial Resistance Action Plan in 2017. This plan emphasizes the need for development of an integrated antimicrobial surveillance system for monitoring of AMR situation in the country. Contemporary surveillance and reporting systems which collect, analyze and report the antibiotic resistance data, these do not provide a complete picture of the spread of resistance in the developing countries. These systems lack the capabilities of real-time data collection and analysis of the resistance data from remote healthcare setups and diagnostic labs. The System for Standardized Monitoring & Reporting of Antimicrobial Resistance Threats [SMART] is a platform for collection and analysis of AMR data. It has been designed in accordance with WHO guidelines and allows integration with available global monitoring systems (WHONet & GLASS). This system is capable of issuing early warning alerts for resistance epidemics in any locality, community and/or healthcare setup(s) associated with this system. During the pilot stage the surveillance system will be subjected to healthcare requirements and needs of key public and private healthcare setups of the province in order to assess and evaluate the needs of provincial surveillance capabilities and to develop a more efficient monitoring system with capabilities of connecting all healthcare setups of the province for integrated AMR surveillance. This system will enable the researchers to not only estimate the resistance inclinations and the physicians in prescribing more effective antimicrobial treatment options but will also enable them to predict the future resistance trends.

Keywords: Infectious Diseases, Antimicrobial Resistance, Surveillance, Monitoring & Report

ST-03

Safety, efficacy, and therapeutic applications of perinatal tissue derived mesenchymal stem cells in cardiac regeneration

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Cardiovascular disease (CVD) is one of the major causes of morbidity and mortality. At present, available therapeutic options for the treatment of cardiovascular diseases are limited and provide solution only to reduce the symptoms of CVD. The indigenous capability of cardiac tissue to meet the degeneration is limited. The feasible option is stem cells based regenerative medicine to repair or regenerate the myocardial cells and restore normal cardiac function. Stem cells possess high efficiency for migration and distribution in the body, there for transplantation of stem cells through systemic circulation or at the site of injury do little homing at the target site. We aim to increase their homing and differentiation potential at the required site by pre-conditioning and forcing them to commit into specific lineage. MSCs were treated with small molecule, 2′-deoxycytidine (DC) to activate cardiac specific genes. Myocardial infarction (MI) was produced in Wistar rats by occlusion of the left anterior descending coronary artery. DC-treated MSCs were transplanted after labelling with probe to track their distribution. Cardiac function was assessed by echocardiography at 2 and 4 weeks after cell transplantation. Histological analysis was performed to observe changes at tissue level. Homing of DC-treated MSCs was significantly (***P<.001) higher as compared to normal MSCs in the infarcted hearts. This may be due to increase in the gene expression of some of the cell adhesion molecules as evident by qRT-PCR analysis. Significant (***P<.001) improvement in the restoration of heart function in terms of left ventricular diastolic and systolic internal diameters (LVIDd, LVIDs), % ejection fraction, % fraction shortening, and end-systolic and end-diastolic volumes were observed in DC-treated MSCs as compared to the MI model. Histological analyses showed significant

(***P<.001) reduction in scar, and wall thickness. Differentiation of treated MSCs into functional cardiomyocytes was evident through immunohistochemical staining. These cardiac progenitor cells exhibited increased persistence, engraftment, and homing in the infarcted region, and expressed cardiac markers within the border zone. LV wall thickness was also preserved significantly (***P<.001). Blood vessel formation was more pronounced in DC-treated group although both cell therapy groups showed significant increase as compared to MI model. Our findings showed that activation of cardiac specific genes through DC improves cardiac function through better survival, adhesion and differentiation of transplanted cells. Transplantation of these MSCs in the infarct area restored functional myocardium.

Keywords: Mesenchymal stem cells, 2-Deoxycytidine, Cardiomyocytes, Myocardial Infarction, and Regeneration

ST-04

Analysis of gut microbiome interactions in autism spectrum disorder (ASD)

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Autism spectrum disorders (ASD) is defined as a group of neurological disorders related to social behavior, issues in communication and cognitive abilities. The world- wide prevalence and financial burden of this disorder is increasing day by day. Various studies report that the gut microbiota play a significant role in aggravating the risk for developing ASD, but the underlying mechanism of its involvement is not clear yet. This study is designed to find out the mechanisms by which gut microbiota is involved in causing ASD. This study protocol focused on the metabolites that are products of gut microbiota produced as a result of food fermentation, for finding out the etiological basis of ASD. To attain this goal, an in silico methodology has been designed by exploiting physio-chemical, genetic and functional data of gut microbial metabolites in the form of protein–protein interactions, metabolic pathways and annotations. For this purpose, gut microbial metabolites were retrieved and analyzed for having some connections at both genetic and functional level. This study found 13 metabolites predicted to be associated with ASD because of having genetic connections while 7 metabolites have shown functional connections with ASD. The contribution of this study is the identification of the microbial metabolites present in gut that are playing role in ASD. This study provides the exploration of ASD etiology that will enable the researchers to find out the possible targeted treatments for this disorder.

Keywords: Autism Spectrum Disorder, Gut microbes, Gut metabolites, ASD genes

ST-05

The 150 Neuromics project

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Neurological and neuro-developmental disorders have become a major public health problem in Pakistan in recent years. Its treatment and management strategies are a daunting problem in Pakistan due to lack of funding, poorly developed primary and basic health facilities and weak political processes. These neurodegenerative disorders require special attention due to its increasing rate, poor management strategies, unaffordability of efficient treatments and illiteracy in rural areas. Identifying specific genetic markers may provide a useful explanation for disease etiology, molecular characterization and pathogenesis. We used Next generation sequencing and genome-wide studies to investigate the novel causative gene(s) in hundreds of families and understand the role in order to develop effective treatments for such devastating neurological and neuro-developmental disorders. We intend to study 150 families with neurological diseases in which 50 have already been studied thoroughly and found more than 36 (20 novel) disease associated variants, and three convincing novel genes (not published yet) are also identified. These biomarkers, along with other parameters, can be used to systematically design molecular assays and models for improving disease diagnosis. It is further expected that personal genetic profiling will also become more relevant, with implications for patient care in line with the proposed idea of personalized medicine.

Keywords: Neurological disorders, Next Generation Sequencing, Novel variants/genes, Biomarkers, Personalized medicine

ST-06

Bioinformatics based analysis of milk lactoferrin against novel coronavirus SARS-CoV-2 infection

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In the current COVID-19 pandemic, with the race of finding the specific anti-viral treatment and vaccine development, many nutritional supplements and proteins have also caught the attention to manage the disease. Therefore, the present study aimed to investigate the potential of Milk Lactoferrin LF (therapeutic nutritional protein) to prohibit the SARS-CoV-2 entry within the human body. For this purpose, molecular docking approach was utilized to evaluate the interaction of Lactoferrin (from Bovine, Camel and Yak milk) with targeted ACE2 receptor and S-protein of the virus. 3D structures of targeted proteins, Bovine and Camel milk Lactoferrin were downloaded from Protein Data Bank (PDB), whereas, owing to the unavailability of 3D structure of Yak milk Lactoferrin, its structure was predicted through I-TASSER, SWISS-MODEL and Phyre2 servers and the best predicted structure was estimated by performing SAVES analysis. Protein-protein docking was performed by utilizing HADDOCK online tool and results of docked complexes were visualized and analyzed through PyMOL and PDBsum servers. Molecular Docking results depicted that all of the studied Milk Lactoferrin proteins depicted very good binding affinity with both of the target proteins. However, the Camel milk Lactoferrin demonstrated maximum interactions with both targeted proteins followed by Bovine milk LF and Yak milk LF. Binding energy of Camel milk Lactoferrin with ACE-2 and S-protein was -120.5KJ/mol and -135.2KJ/mol respectively with 27 hydrogen bonds with ACE2 receptor and 31 Hydrogen bonds with S-protein of SARS-CoV-2. Based on the binding energy score, we suggested that further *in vitro and in vivo* studies on evaluating the pharmacological effect of Milk Lactoferrin against SARS-CoV-2 will signify its role to combat COVID-19.

Keywords: SARS-COV-2, Milk Lactoferrin, ACE2 receptor, S-protein, Molecular Docking

ST-07

A need of the hour approach to COVID-19 with clinical home monitoring services

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With Covid-19 spreading globally, into Pakistan, we started getting calls in Feb 2020 from local community with questions like, Do I have Covid? Is it real, or some conspiracy? What is the next step after a positive PCR test? Why can't I breathe? We quickly, but carefully, devised a Covid-19 home monitoring online service. Our approach being noncommercial and free of charge, serves public with limited resources. Patient education and counselling based on updated Covid-19 guidelines. Virtual monitoring for mild and moderate cases Virtual triage for severe cases requiring hospitalization. This is a retrospective observational study of de-identified Covid-19 patients' data. We are using WhatsApp audio and video calls, and a Covid electronic data repository system to monitor patients. We believe our Covid-19 services play an educational and impactful role by possibly reducing morbidity and mortality by timely hospitalizations with virtual follow-ups. We currently maintain a heterogenous, home monitored patients' database and an ICU database that can help us to understand mild to moderate disease, severe to critical, and the clinical profile of the patients' journey in between. We provide consultations to patients of different socioeconomic statuses and ages with comorbidities such as diabetes, hypertension, pregnancy, and cancers. We educate patients about infectious period, quarantine, immunity, variants, and vaccinations. We reassure mild cases for home monitoring, to reduce hospital burden and exposure, and educate them by interpreting their clinical and biochemical manifestations of Covid-19 disease. Covid is still around and not done yet, and neither are we!

Keywords: Covid-19, Corona virus, Covid Home monitoring, ICU

ST-08

Genetic elucidation of acetic acid regulatory gene network in low grade inflammation

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Obesity is the 5th major leading risk for the global deaths which causes the chronic low-grade inflammation by releasing the pro-inflammatory cytokines such as TNF-α, IL6 from the adipose tissues. This low-grade inflammation is associated with development of certain diseases such as diabetes, cardiovascular diseases stress, depression etc. To prevent this people, use different drugs and remedies, apple cider vinegar is one of them. Basically, ACV main component is acetic acid that interact with fat metabolism genes and reduce the accumulation of excess fat that release the cytokines. The aim was to explore various factors which could be associated with variation in weight loss against use of apple cider vinegar. Different tools and databases were used such as a super target database was used to retrieve the acetic acid interacted genes, validate their pathways through KEGG. Gene regulatory networks were developed in GEPHI, then identify the hub genes by apply centralities statistical analysis. Then by using the Enrichment tool, enrichment analysis of hub genes was performed and finally hub genes were validated through the literature. Out of 51 acetic acid interacted genes only 24 genes played any role in pathways. These 24 genes interaction data were retrieved and made gene regulatory networks, then by applying centralities test hub genes were identified from the networks. Hub genes enrichment analysis were performed and validated through the literature. Through literature we found that some genes induce proinflammatory and some induce anti-inflammatory activation of the pathways through disease or directly by the release of the cytokines through macrophages. Future prospects of this study will be that by taking the samples from the people that are taking the apple cider vinegar(ACV) and conduct the genetic analysis that either ACV main component acetic acid inhibit proinflammatory genes and enhance the anti-inflammatory genes to confirm that ACV help in the reduction of the inflammation and obesity that is majorly caused by the inflammation.

Keywords: Low Grade Inflammation, Apple Cider Vinegar, Pathway Analysis, acetic acid

ST-09

In Silico analysis to screen putative anti-microbial peptides and database development

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In *Acinetobacter baumannii* (*A. baumannii)*, multidrug resistance is rapidly growing, and existing therapeutic options will soon be exhausted. To improve healthcare settings and genome-based analysis, antimicrobial peptides (AMPs), for instance, are a novel approach to drug development. In the current study, Screening of antimicrobial peptides was performed against *A.baumannii* from literature and database resources. Evaluation through physicochemical properties of selected candidates was done by using peptide package in R, DNASTAR Lasergene protein, and CLC genomic workbench. Homology modeling of prioritized candidates was employed by using PEP FOLD and refined by using Galaxy refine. Sequences of pathogenic proteins Omp38 and OmpW, an important outer membrane protein of *A. baumannii* involved in virulence, were downloaded from Uniprot that was used for the homology modeling by using Phyre 2, and refinement by Galaxy refine. Eventually, each peptide sequence was docked with Omp38 and OmpW. A total of 200 sequences were selected that were fall in the category of potential antimicrobial peptides. About 60 AMPs were selected for homology modeling that had stable stereochemistry. Approximately 30 AMPs showed good interactions with Omp38, OmpW. These all-physicochemical parameters, homology modeled structures, and docking interactions were integrated into the AbAMPAb database. These characterized specific AMPs will be a part of *in-vitro* and *in-vivo* studies.

Keywords: Antibiotic resistance, multi-drug resistance *Acinetobacter baumannii*, antimicrobial peptides, protein-peptide interaction, Web database

ST-10

Genome-based analysis of multi-drug resistant *Staphylococcus aureus* reveals widespread distribution of genes associated with antimicrobial resistance and virulence

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Methicillin-resistant *Staphylococcus aureus* (MRSA) is a multi-drug resistant and opportunistic pathogen. The diversity of resistance and virulence genes in this pathogen warrants serious attention. Here, we performed a whole-genome comparative analysis of three Pakistani MRSA strains to get insight into the genetic components associated with antibiotic-resistance and virulence. The genome size of Lr2, P10, and R46 are 2 831 239 bp, 2 970 728 bp, and 2 830 137 bp, respectively with 32.7 % GC contents. These strains carry SCCmec type IV and representing two different sequence types: ST-22 (Lr2) and ST-113 (P10 and R46). The strain P10 ST113-MRSA-IV was found to carry additional resistance determinants (*mupA*, *fusA,* and *aad (6)*) compared to other studied genomes. Similarly, the strain Lr2 ST22-MRSA-IV harbors additional virulence genes, including fibronectin-binding protein (*fnbB*), collagen adhesion (*cna*), toxic shock syndrome toxin gene (*tsst-1*) and a unique cluster (GO: 0090729) involved in toxin activity. Whole-genome SNPs and MLST based phylogenetic trees grouped sequenced strains in their respective ST clades and annotation of antibiotic resistance genes showed a diverse distribution of genes associated with antibiotic resistance. These results strongly support the urgent attention to prevent the further vertical and horizontal spread of these resistance and virulent genes.

Keywords: Antibiotic-resistance, Comparative genome analysis, Multi-drug Resistant, Methicillin-resistant *Staphylococcus aureus*, Multi-locus Sequence type, whole-genome sequencing

ST-11

Osteochondral differentiation of MSCs in 3D decellularized Wharton jelly hydrogel scaffold in tissue engineering

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Extracellular matrix-derived hydrogels serve as three-dimensional scaffolds whose composition can be customized to allow attachment and proliferation of several different cell types and are considered close replica of the tissue microenvironment. The aim of the study is to analyze the culturing of MSCs on a 3D scaffold and their differentiation into Osteochondral lineage. Decellularization of Wharton jelly was evaluated by H and E, alcian blue, and Masson's trichrome staining. Scaffold was characterized by scanning electron microscopy and FT-IR spectroscopy. MSCs were isolated from human umbilical cord tissue, and were characterized by immunostaining, flow cytometry, and trilineage differentiation. The MSCs capability to differentiate into an osteochondral lineage was determined by microscopy, alizarin red, alcian blue staining, and osteochondral gene expression by quantitative PCR and by immunostaining. Decellularization was confirmed by determining DNA content and Extracellular matrix analysis. The scaffold was characterized through imaging and scanning electron microscopy for fibers formation and FT-IR analysis for cross linking. MSCs were characterized by cellular morphology, immunostaining for presence of MSCs markers Stro1, CD90, CD44, CD105, Vimentin, CD117, HLADR, and CD45. Immuno-phenotypical analysis showed positive expression for vimentin, CD73, CD90, and CD 117. Trilineage analysis showed osteogenic, adipogenic and chondrogenic differentiation. MSCs were seeded in Scaffold, and were evaluated using phase contrast microscopy, cell attachment and infiltration was observed. The viability and proliferation assays showed that hMSCs were viable and able to proliferate over time on seeded scaffold. hMSCs seeded on scaffold and cultured in stromal, osteogenic, and chondrogenic media for 28 days showed the upregulation of osteogenic and chondrogenic marker and calcium mineral deposition in scaffold.

However, the Scaffold was more efficient in inducing hMSCs osteogenic differentiation than the Chondrogenic differentiation. Immunostaining showed the expression of osteogenic markers runx2, osteopontin, and osteocalcin in MSCs seeded on 3D hydrogel. In conclusion, umbilical cord derived scaffold can be used as a 3D porous, bioactive, and biocompatible material that can effectively promote bone and cartilage tissue generation in vitro.

Keywords: Hydrogels, Scaffolds, immunostaining

Poster Abstracts

P-01

Morphological and physiological changes of *Calendula officinalis* L. (Pot Marigold) irrigated with sewage wastewater

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Sewage Wastewater is one of the best factors which affecting the growth, yield and quality of ornamental plant (Pot Marigold). The present study based on the Morph-Physio-anatomical changes of genus *Calendula*, irrigated (watered) with sewage wastewater. A different concentration of sewage wastewater (0, 20, 40, 60, 80 and 100%) was prepared with distilled water. The morphological attributes were increased throughout the experiment. The number of roots, leaves, flowers, height of roots and shoots was increased by using a SWW. The chlorophyll and minerals content were increased by using different concentrations of SWW. All Physio-chemical parameters of soil and water was observed at different concentrations of SWW e.g., including pH, EC, color, turbidity, Biological Oxygen Demand (BOD), Chemical Oxygen Demand (COD), total dissolved solid, settle able solid, total suspended solid. These parameters were increased by increasing concentrations. Most of the attributes of roots, leaves and stems of anatomy was increased by using a sewage wastewater treatment. The maximum anatomical changes observed at 100 and 60% and less shows at 20% and control treatment. It gives positive effect at 100-60 % which means wastewater increase all attributes. The study showed that wastewater is best for the ornamental plants. By use of wastewater, we don't need any fertilizers for the growth of ornamental plants.

Keywords: BOD, SSW, COD, Pot marigold, Chlorophyll

P-02

Inhibitory effect of fresh leaves of *Moringa oleifera* on Aflatoxin B1 production

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International Agency for Research on Cancer (IARC) have been classified the Aflatoxins as class IA carcinogen. According to a FAO report, about 25% of crops are contaminated by mycotoxins worldwide. Climatic conditions of Pakistan are favorable for rapid growth and proliferation of various toxigenic fungi i.e., *Aspergillus sp., Penicillium sp.* etc. Different methods (chemical, physical and biological methods) are adopted for the control of fungal growth and their toxins. Recent studies revealed the inhibitory effects of biological methods against aflatoxins. Bioactive compounds of plants are active source of antimicrobial compounds. They are safe to environment and consumer and are useful to control different diseases, being an excellent alternative source of synthetic herbicide in agriculture. In present study, fresh plant leaves were used to assess the detoxification/ inhibitory effect against Aflatoxin B1. *In-vitro* study plant leaves were used for detoxification purpose at different incubation times (0-hr, 1-hr, 3-hrs, 6-hrs and 24-hrs). Findings of present study revealed encouraging results. Ethanolic extract of *Moringa oleifera* shows 98% reduction of Aflatoxin B1 after 24-hrs of incubation time. Phytochemical analyses of selected plant revealed that saponins were absent, whereas *Moringa oleifera* contain the higher concentration of tannins, volatile oils, and phenols.

Keywords: Aflatoxins, *Moringa oleifera*, toxogenic fungi, plant leaves extract

P-03

Identification of biomarkers associated with prediabetic insulin resistance

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Prediabetes is disease state characterized by hyperglycemia that falls below the level used to define type II diabetes mellitus. The hyperglycemia in prediabetes is due to insulin resistance. Insulin resistance is a state of altered glucose uptake that is stimulated by insulin or can be defined as the decreased sensitivity of body's response to insulin. If accompanied by pancreatic beta cell dysfunction and relative insulin deficiency, insulin resistance can progress to Prediabetes and finally to Type 2 Diabetes. In Pakistan according to 2nd National Diabetes Survey of Pakistan 2016- 2017 prevalence of prediabetes is 14.4%. Prediabetes progress to diabetes if left unmanaged or untreated. This study was aimed to identify biomarkers that are associated with prediabetic insulin resistance. We used in-silico approach for identification of biomarkers associated with prediabetic insulin resistance. Associated biomarkers reported in literature was searched and interaction network were generated for those. Total 40 different genes were identified from interaction networks. Enrichment analysis was done to find biological, molecular and cellular annotation through protein-protein docking using GRAMM-X web server, all the docked proteins were checked in discovery studio. It was observed that ARG13 was most repeated amino acid in all docked proteins. It was inferred from docking that set 2 biomarkers interacts with these amino acids of set 1 biomarker, so they may be potential biomarkers for prediabetic insulin resistance. Identified biomarkers associated with prediabetes could further be confirmed or validated in our population using different wet lab technologies.

Keywords: Insulin Resistance, Prediabetes, Biomarkers, Diabetes

P-04

Screening of sunflower associated bacteria as biocontrol agents for plant growth promotion

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Deleterious effects of artificially applied chemicals have highlighted the significance of biocontrol agents as suitable substitute for sustainable agriculture. In present study, three endophytic bacterial strains SV7, SV10 and LV19 showed extensive range of antifungal as well as plant growth promoting activities signifying potential to accomplish the requirement. Phylogenetic analysis revealed 100% similarity of three strains with taxon Firmicute. However, there was division among these isolates on basis of subgroups as SV7 belonged to *Exiguobacterium auranticum*, SV10 belonged to *Paenibacillus sp*. and LV19 was best fit in subgroup *Priestia koreensis*. All strains showed antifungal activity against *Fusarium oxysporum* on three different media (PDA, NA, LA) with maximum activity (53%) of LV19 strain on NA and least activity (13%) on PDA medium as recorded by zones of inhibition. In growth promotion experiments, combination of LV19 with Fusarium significantly suppressed chances of Fusarium wilt which is commonly caused by *Fusarium oxysporum* in sunflower plants. Diverse growth parameters (seed germination percentage, lengths and fresh weights of root & shoot) were significantly increased by 34 to 909 % over pathogen infected plants only which was further proved by their root colonization analysis. Based on most efficient growth promotion by LV19 strain, expression of five plant defense related genes (SOD, PAL, NPR1, PR5, Chitinase) was evaluated revealing enhanced expression by 1.7-270 folds in consortium of LV19 and Fusarium. Thus, current study provided a scientific justification that bacterial strains in specific LV19 (*Priestia koreensis*) could be further developed as biocontrol agent with potential of plant growth promotion.

Keywords: Biological control, defense genes, *Priestia koreensis*, *Fusarium oxysporum*, antifungal activity

P-05

Disarming avian pathogenic *E.coli* (APEC) by targeting FimH, iss and hlyf genes using CRISPR-cas12a

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Infections with avian pathogenic Escherichia coli (APEC) cause colibacillosis, an acute and systemic disease resulting in significant economic losses in poultry industry worldwide. Several challenge experiments in chickens proofed the role of virulent APEC strains as the single etiological agent. Antimicrobials is the most widely used treatment strategy against APEC infections but resistance against them is a significant crisis that threatens human health and safety. There is an urgent need for new strategies to control multidrug-resistant (MDR) bacterial infections. The latest breakthrough in gene-editing tools based on CRISPR-cas systems has potential applications in combating MDR bacterial infections because of their high targeting ability to specifically disrupt the drug resistance genes that microbes use for infection or to kill the pathogen directly. Therefore, the present study is focused on the use of CRISPR-cas12a to specifically target three virulent genes to ascertain their role in pathogenicity of APEC. *FimH*, *iss* and *hlyF* encodes for the known virulent factors and therefore targeting these genes would significantly reduce the pathogenicity. Polycistronic tRNA-gRNA (PTG) expression cassette was designed using gateway cloning and employed for multiplex genome editing. *In-vitro* confirmatory tests and *in-vivo* testing on chicken models would confirm the successful knockout of the targeted genes. The findings of the study would enable the establishment of novel treatment strategy, avoiding the excessive use of antibiotics for APEC infections. The study would also provide insights to potential targets for vaccine development against APEC infections as APEC share not only identical serotypes with human pathogens but also specific virulence factors, which establishes its zoonotic potential.

Keywords: Colibacillosis, Antimicrobials, multidrug-resistant

P-06

Technological characterization of *Lactobacillus* strains for their suitability as starter or adjunct culture in dairy products

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Food fermentation by microbes is being carried out since ages due to its many benefits like improved functionality, shelf life, flavor and texture of food products. Probiotic microorganisms' act as microbial food supplements by providing prompt health benefits after consumption of probiotic enriched foods. Hence, they are an example of food fermenting microbes which can be used to improve organoleptic characteristics and to ensure long term product safety. *Lactobacillus* species such as *L. delbrueckii*, *L. rhamnosus* and *L. fermentum* are the most common starter or adjunct cultures used in the fermentation of foods such as, instant yogurt, cheese, beer, wine, cider and chocolate. The objective of the present study was to assess the technological properties of *Lactobacillus* strains by means of in vitro testing. For this purpose, strains were examined for proteolytic, lipolytic, autolytic, EPS and diacetyl production, acidifying activities, salt and heat tolerance, viability in milk acidified with lactic acid and their metabolic end product analysis was done by HPLC. The strains were tested for their suitability as adjunct culture in dairy product. *L. delbrueckii* (I-17) showed most prominent results being able to tolerate10% NaCl concentration with an OD of 0.222 ± 0.045 and an acidification rate in MRS broth of about 4.386 ± 0.05 after 8 h and 3.75 ± 0.10 after 24 h in skim milk. Followed by *L. rhamnosus* (Y-59) with an OD of 0.064 ± 0.038 in 10 % NaCl and an acidification rate in MRS broth of about 4.46 ± 0.046 after 8 h and 3.89 ± 0.215 after 24 h in skim milk. For these reasons, these strains may be suitable for use as a starter or adjunct culture for the production of probiotic dairy foods.

Keywords: Probiotics, Food fermenting microbes, *Lactobacillus* spp., Starter or adjunct culture

P-07

Genome characterization of indigenous *Lactobacillus fermentum* and evaluation of its suitability for dairy products

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Lactobacillus species are used in many fermented foods, they contribute to the flavor, texture, and shelf life of fermented foods. *Lactobacillus fermentum* strains FM6 and Y55 that were isolated previously from fermented foods with potential to reduce serum cholesterol. The DNA sequence were tested to determine the genetic basis underlying the probiotic potential of *L. fermentum* as starter culture or adjunct culture. Genes known to confer probiotic properties were identified, including genes related to stress adaptation, antibiotic resistance, biosynthesis, acidification, Exopolysaccharide production, Resistance to low pH, Hemolytic activity, cholesterol reduction and the defense machinery. The comparative genomic analysis of *L. fermentum*, encoded proteins that are putatively involved in replication, recombination and repair, defense mechanisms, transcription, amino acid transport and metabolism, and carbohydrate transport and metabolism. Finally, a procedural guideline for the safety assessment of microbial strains through whole-genome analysis was proposed.

Keywords: starter culture, Lactobacillus fermentum, probiotics, cholesterol assimilation

P-08

Evaluation of PMB and fatigue behavior of HMA containing PET

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Polyethylene Terephthalate (PET); which is globally used as Plastic Bottles for improving the pavement quality. This results in design of economical, sustainable, and eco-friendly pavements. Utilizing waste PET in crushed form in Job Mix Formula for pavement design shall prove to be a milestone in achieving national prosperity in terms of efficient road network all over the country. This study is based on Evaluating the Performance of Hot Mix Asphalt (HMA) by using Polyethylene Terephthalate (PET) as modifier in certain percentage replacement of virgin Bitumen. NHA Gradation-B, ARL Bitumen Grade 60/70 Bitumen, Margallah Aggregate, Crushed PET waste from local plastic shredder was utilized. Ductility, Penetration, Softening and Viscosity Tests were carried out on bitumen containing different percentages of PET. The results were compared with those of Virgin Bitumen. Later, Performance Testing was performed on HMA after finding Optimum Bitumen Content (OBC). Using that OBC, various mixes were prepared containing a fraction of PET as replacement of OBC. A Trend of properties was obtained for a range of PET percentage in mixes. Performance Testing which includes Indirect Tensile Fatigue Test (ITFT) was used to evaluate Fatigue behavior of HMA. Increase in PET content results in gradual decrease in Penetration and Softening Point, however, Softening Point and Viscosity increases. Study suggests significant increase in fatigue life with increase in PET content. The results of this study can be helpful to the pavement designers and staff related to construction field.

Keywords: Eco-friendly, Recycle, Plastic Bottles, Poly-Ethylene Terephthalate (PET), Hot Mix Asphalt (HMA), Fatigue Life

P-09

Effect of a novel coconut oil-based emulsion on PCR (polymerase chain reaction) efficiency

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Emulsion PCR (ePCR) is a well-known technique allowing for the creation of in-vitro compartments. This compartmentalization helps in reducing PCR biasness by making it possible for more and all kinds of DNA templates to find their way into a polymerase chain reaction. It also works to reduce intermediate product formation. The water-in-oil emulsion technique gives rise to droplets of enough stability and strength that each one of them ends up acting as a complete PCR itself. In this study, we explored the potentials of using an easy mix of emulsion for ePCR. We developed a novel formula employing Coconut Oil as an alternative to Mineral Oil in emulsions for ePCR. Our studies concluded that ePCR does result in performing the polymerase chain reaction with the Coconut Oil based emulsions. The percentage increase trends for the total amplified DNA product obtained at the end of different ePCR runs were observed quantitatively using Image J analysis and densitometry calculations.

Keywords: Emulsion PCR, Mineral Oil, Coconut Oil, Densitometry, Image J

P-10

Characterization of chromate reductase from *Bacillus* sp. strain S-9 and its role in reduction of chromium (VI)

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A chromium (Cr) resistant bacterium designated as strain S-9 was isolated from industrial sludge. Strain S-9 was identified via 16S rRNA sequencing and showed 99% similarity with *Bacillus paramycoides*. *Bacillus* sp. strain S-9 was found resistant to chromium as indicated by its significant growth up to 1400 mg/L of $K_2Cr_2O_7$ at mesophilic temperature. The enzyme chromate reductase activity was found during the experiment that causes reduction of Cr into non-toxic state. The physicochemical variables influencing chromate reductase production were identified by statistical tools, Plackette Burman Design (PBD) and Central Composite Design (CCD). The chromate reductase was purified through size exclusion column chromatography from strain S-9, exhibited specific activity of 1416.549 U/mg, 59.5% yield, and 6.6-fold increase in purity under optimum physicochemical conditions. The maximum activity chromate reductase was observed at temperature 40°C and pH 7.0. The K_m and Vmax value of bacterium were 1.36 µM and 909.09 µM respectively, using $K_2Cr_2O_7$ as a substrate. The activity of chromate reductase was strongly inhibited by Hg, SDS, and CTAB. *Bacillus* sp. strain S-9 reduced 69% of chromium at concentration up to 100 mg/L after 96 hrs. Furthermore, effluent containing 100 mg/L of $K_2Cr_2O_7$ was treated with 1-10% of both crude and purified chromate reductase. The crude and purified chromate reductase (10% v/v) showed maximum reduction of 75% and 87% after 120 hours, respectively. The result in this study indicates that this strain could effectively be utilized for remediation of metals polluted sites.

Keyword: bio reduction, Chromate reductase, industrial effluent, Statistical designs

P-11

Degradation of polyethylene terephthalate (PET) by *Pseudomonas aeruginosa* strain S4 at mesophilic temperature

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This study was conducted to evaluate *Pseudomonas aeruginosa* strain S4 from compost soil for its degradation potential against polyethylene terephthalate (PET). *P. aeruginosa* strain S4 was found to degrade PET as indicated by various experiments such as weight loss within 4 weeks, biofilm formation over PET pieces and exhibiting surface hydrophobicity. This claim was further supported by Fourier-transform infrared (FTIR) spectroscopy and scanning electron microscopy (SEM) results. *P. aeruginosa* strain S4 expressed cutinase activity during PET degradation experiment. Different physico-chemical conditions were optimized for high yield cutinase production by using one time one factor and multiple factor one-time statistical models (Placket-Burman design and Central Composite design software). Cutinase was purified to homogeneity by column chromatography technique using Sephadex G-100 gel resin and molecular weight was found to be approximately 40 kDa. The specific activity of purified cutinase was 235.89 U/mg with 13.45-fold purification and 64.01% yield. The K_m and Vmax were 2.15 mgml–1 and 769.23 µmolmg–1min–1. The enzyme was stable at wide range of temperature (20 to 40°C) and pH (8.0 to 10.0). The purified cutinase activity was significantly enhanced by surfactant (Triton X-100 and tween 40), organic solvent (Formaldehyde) and metals ($NiCl_2$ and Na_2SO_4). This study suggests that *P. aeruginosa* strain S4 possess the ability to biodegrade PET and could be further explored for hydrolysis of the various plastic waste.

Keywords: Biodegradation, PET, cutinase, *pseudomonas aeruginosa* S4, Placket-Burman design, Central Composite design

P-12

Taxonomical and phylogenetic investigations of *Carex viridula michx* and *Bolboschoenus maritimus* (L.) palla from Parachinar, Pakistan

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The family Cyperaceae, often known as sedges, has three main distinguishing features i.e., trigonous stem, terminal inflorescence, and presence of bracts. The members of this family are cosmopolitan in distribution and the plants are mostly associated with wetlands but could also be found in lakes, streams, grasslands and even sand dunes. Cypreaceae is one of the most common weeds and damages most of the country's crop plants, which attack and adversely affect the crop production because they compete with important crops for water, light, space, and nutrients, anyway the members of family also serve other economical, ecological, horticultural, and medicinal purposes. But the taxonomical study of the family is very difficult due to its complex and complicated features of morphology. So, there is a need of alternate techniques for the taxonomic study of sedges. So, the current work is focused on the taxonomical and phylogenetic investigations of Carex viridula Michx and Bolboschoenus maritimus (L.) Palla collected from Parachinar, Pakistan. This work covers the analysis of these two species based on morphological, micro-morphological, and molecular characters along with their phylogeny. Stereomicroscope was used for the morphological analysis to observe different parts of the inflorescence such as glumes, utricles, nut, anthers, and pollens. While the micromorphological characters were studied with the scanning electron microscope (SEM). For further confirmation, the molecular and phylogenetic analysis were carried out using three molecular markers: ETS, ITS, and matK, and the sequences were submitted to the GenBank database. Geneious was used to conduct the phylogenetic analysis. Three types of analysis i.e., Neighbor Joining, Maximum Likelihood, and Bayesian were done for the phylogenetic studies. The morphological and molecular

study solved the taxonomical issues of Bolboschoenus maritimus and Carex viridula species and will be used for the correct identification of these species.

Keywords: Cyperaceae, Inflorescence, nutrients

P-13

In Silico characterization of insecticide resistance in different strains of mosquito gut microbiome

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Mosquitos are medically and clinically significant arthropods they belong to the family Culicidae, order Diptera and notable genera include Aedes, Anopheles and Culex. There are 3500 species of mosquitoes. They are threatening organisms and ectoparasites which require blood to nourish their eggs and during this process transmit different infectious agents (bacteria, protists etc.) into the human host to cause different diseases such as malaria, dengue and yellow fever. To combat these diseases mosquito production, need to be controlled. There are four important stages in mosquito life cycle: egg, larvae, pupa and adult. It is easier to target mosquitoes at the early stages of their life cycle. One of the prominent methods to control them include use of insecticides (pyrenoids and organophosphates). The insecticide used may have environmental hazards that affect food chain and contaminate underground water reservoir, but they are still used at a large scale. In this study we have investigated the different bacterial strains present in mosquito gut that may render resistance against insecticides. Exploring their genomes and finding resistance gene sequences, interacting partners that participate in insecticide resistance molecular pathways. This study would pave way to understand insecticide resistance and how it can be used to counter mosquito-borne diseases.

Keywords: Mosquito, Insecticide Resistance, bacterial strains, Organophosphates, Mosquito-borne diseases

P-14

Synergistic combination of chondrogenic transcription regulators *Sox*-9 and *Six*-1 differentiated mesenchymal stem cells into chondroprogenitors, and their *in vivo* implantation regenerated the intervertebral disc degeneration

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Intervertebral disc (IVD) degeneration is a symptomatic pathophysiological condition associated with low back pain. No effective therapy to repair or restore degenerative disc disease is available. Stem cells based regenerative medicine is being considered as alternative approach to treat disc diseases. We aim to differentiate hUC-MSCs into chondrocytes by over expression of chondrogenic transcription factors, *Sox9* and *Six1,* and their combination *(Sox9+Six1), in vitro*, followed by their transplantation into rat model of degenerated intervertebral discs. MSCs isolated from umbilical cord tissue, were propagated and characterized. MSCs were transfected with transcription factors *Sox9, Six1,* and their differentiation in chondrocytes was analyzed at gene and protein level. IVD model was established in three consecutive lumber or coccygeal discs. MSCs, transfected MSCs, and induced chondroprogenitors cells were transplanted. *Sox9* and *Sox9+Six1 (*synergistic) transfected MSCs showed significant expression of chondrogenic genes and proteins *Sox9, TGFβ1, ACAN, BMP2* and *GDF5*. In *in vivo* study, transplanted cells showed better survival, homing, and distributions IVD compared to normal MSCs. The transplanted cells differentiated into functional nucleus pulposus cells evident from immunostaining of *Sox9, TGFβ1*, and *TGFβ2*. Toluidine blue and H & E staining showed better preservation of normal histological features, structure and cellularity of NP region compared to degenerated discs. Expression of pain and inflammatory genes at day 5 of treatment with MSCs and chondroprogenitors modulates the immune response and reduces the expression of inflammatory cytokines. It is concluded from this study that *in vitro* produced chondroprogenitors showed better regeneration potential

compared to normal MSCs. These findings will lead to design of better therapeutic strategy for the disc restoration.

Keywords: Disc Degeneration, Human Umbilical Cord, Transcription Factors, Mesenchymal Stem Cells, Regeneration

P-15

Development of supervised machine learning reverse vaccinology model for improved prediction of bacterial protective antigens of ESKAPE pathogens

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The identification of protective immunogens of bacteria is the most important initial step in the long-lasting and expensive process of vaccine design and development. In most of vaccine designing projects, the approach used is an innovative genome-based vaccine design approach termed reverse vaccinology (RV). Reverse vaccinology (RV) is a milestone in rational vaccine design, and machine learning (ML) is particularly effective in improving the accuracy of RV prediction, and it is a milestone in rational vaccine design. These techniques are particularly useful in data mining and the examination of large datasets, such as microbial proteomes. They've been able to drastically cut down on the amount of time it takes to find new vaccine candidates in the lab. However, prediction accuracy and program accessibility are still issues with ML-based RV.This study presents a supervised ML classification model to predict bacterial protective antigens (BPAgs). To identify the best ML method with optimized conditions, five ML methods were tested with features extracted from well-defined training data. 3 validation approaches were used to ensure unbiased performance assessment and the capability to predict vaccine candidates against a new emerging pathogen. The best performing model was compared to three publicly available programs using a high-quality benchmark dataset.

Keywords: Immunogens, Vaccine design, Machine learning

P-16

Pangenome analysis of *Acinetobacter baumannii* reveals core-drug targets, screening, and *in-vivo* bactericidal effect of promising lead compounds for drug discovery

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Acinetobacter baumannii, an ESKAPE pathogen and associated with nosocomial infections, especially in the intensive care units (ICUs) responsible for ventilator-associated pneumonia. To overcome the challenging process of developing new antibiotics and the ever growing multidrug resistance against several available antibiotics, we need to think of alterative therapeutics and drug discovery, in this context, we had a chance to explore the pangenome of this concerning pathogen and to identify the potential drug targets as alternative therapeutics for drug discovery. Employing a total of 246 complete genomes of *A.baumannii* we estimated the pangenome of the species, moreover, the core conserved proteome (984 proteins) subjected to different subsequent filters (non-human homology, essentiality, virulence, physiochemical checks, and pathways analysis) leads to the identification of nine potential broad-spectrum drug targets. Additionally, the molecular docking analysis of these drug targets with the ligands available at the Drug Bank database leads to the identification of a total of 6 promising ligands with potential inhibitory effect were shortlisted: namely Cefiderocol, 2-Hydroxyestradiol,4-chloro-N-(3-methoxypropyl)-N-[(3S)-1-(2-phenylethyl) piperidin-3-yl]benzamide,Uridine-Diphosphate-N-Acetylglucosamine, Guanosine-5′-Monophosphate, and Dalfopristin. The lead optimization and experimental validation of lead compounds in suitable animal models will provide a new insight to develop antimicrobial agents for treating *A. baumannii* infections and to combat the growing concern of antimicrobial resistance.

Keywords: Acinetobacter baumannii, lead compounds, drug targets, pangenome, drug discovery

P-17

An immuno-informatics approach for the repurposing of drugs against *Enterococcus faecium*

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Multi-drug resistant bacterial infections have presented the medical community with an increasing therapeutic dilemma. Among immunosuppressed or critically ill patients, enterococcal infections are often severe. Enterococci are long-standing members of the human microbiome, and they are also widely distributed in nature. However, with the surge of antibiotic-resistance in recent decades, two enterococcal species *(Enterococcus faecalis* and *Enterococcus faecium)* have emerged to become significant nosocomial pathogens, acquiring extensive antibiotic resistance. The intrinsic antibiotic resistance of these healthcare-associated enterococci and their capacity to rapidly acquire additional antibiotic resistance makes infections very difficult to treat and they thus pose a substantial infection control burden. Until recently, *E. faecalis* was responsible for the majority of enterococcal infections, however, infections caused by *E. faecium* have been increasing and currently account for around 40% of all enterococcal infections. It has also drawn attention of the researchers due to its evolving immune evasion strategies and increased drug resistance. The emergence of multi-drug-resistant-strains has urged the need to explore novel therapeutic options as an alternative to antibiotic. A bioinformatics framework has been employed involving, pan genomics and subtractive proteomics strategies to identify core antibiotic susceptible drug targets and has allowed to obtain repurposed drugs, respectively. The putative drug targets and the drugs will then be experimentally validated and can thus contribute to a specific drug development to combat multi drug resistance against *Enterococcus faecium*.

Keywords: Multi-drug resistant, Bacterial infections, antibiotic resistance

P-18

To investigate the effects of trace elements on the growth and proliferation of human umbilical cord mesenchymal stem cells (hUC-MSCs)

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We aim to investigate the effect of trace elements on mesenchymal stem cell growth and proliferation, their clonal expansion and cell cycle. Human Umbilical Cord Mesenchymal Stem Cells (hUC-MSCs) was scrutinized through inspecting genes and proteins involved in cell division, growth, and proliferation. Mesenchymal stem cells were isolated from human umbilical cord tissue, and were characterized by immunocytochemical staining, immunophenotyping and tri lineage differentiation. MSCs were pre-conditioned with trace elements and cytotoxicity at different concentrations was determined by MTT assay, proliferative potential was examined by alamar blue assay. Cell proliferation, clonal expansion, wound healing and migration was determined. Real-time PCR was performed to determine gene expression. Human umbilical cord derived MSCs showed fibroblast like morphology, immunostaining showed positive expression of CD90, CD44, CD117, CD105, Cd72, and vimentin expression, immunophenotyping showed the expression of CD90, CD73, CD117 and vimentin, trilineage assay showed osteogenic, adipogenic and chondrogenic differentiation. Cytotoxicity of zinc treatment showed that MSCs are non-cytotoxic at concentration lower than 100 μM. Cell proliferation showed increased proliferation in treated groups. MSCs showed increased adhesion after zinc preconditioning, wound healing and cell migration was significantly up regulated in treated group. Real time PCR showed significantly higher expression of genes involved in cell division (CDC20, CDK1, CCNA2, CDCA2), growth, and proliferation (TGFβ1, GDF5, HIF1α). The study suggests that trace elements could be utilized for *in vitro* expansion of MSCs, necessary to attain desirable quantity for *in vivo* transplantation. Currently culture media used for *in vitro* expansion are based on serum, growth factors, cytokines, and xenogeneic produce.

These products possess possibilities of adverse effects like anaphylactic shock, host versus graft disease, neoplastic transformation, and transmission of bacterial and viral infections. Their utilization could be reduced or controlled by adding trace element in culture medium.

Keywords: hUC-MSCs, Trace elements, Zinc, Proliferation, In vitro expansion, Cell division

P-19

Genome characterization of indigenous *Lactobacillus rhamnosus* and evaluation of its suitability for dairy products

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Lactobacillus species play an important role in the dairy and biotech sectors. They are utilized as starter cultures in dairy fermented foods, human and animal health products, and livestock feed. They have been classified as generally recognized as safe (GRAS) due to their general occurrence in many fermented and non-fermented food products and also being part of the human commensal micro-flora. Whole genome analysis of *Lactobacillus rhamnosus* isolated from fermented milk (lassi) was carried out for genome characterization and comparing with strains available in public database. This helped to unravel the genes involved in fermentation pathways and metabolite production. In view of this, in vitro testing like acidification, EPS production, amylase activity, etc. helped to determine the suitability of *L. rhamnosus* as a starter culture. On the basis of data from this study, the indigenous *L. rhamnosus* strain has the potential to be used as an adjunct culture in functional/probiotic/medical foods to reduce the serum cholesterol levels.

Keywords: *Lactobacillus rhamnosus,* Serum cholesterol, lactic acid bacteria

P-20

Effects of plant growth promoting rhizobacteria on sunflower irrigated with high TDS bearing water

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The present study was aimed to evaluate the bioremediation potential of PGPR (Plant growth-promoting rhizobacteria) in sunflower *(Helianthus annuus. L)* with high TDS bearing polluted water. The TDS bearing water has salinity level above sea water and also contain traces of oil. The isolated PGPR strains W1 and W2 were characterized by 16srRNA sequence analyses as ***Ralstonia pickettii*** and ***Brevibacillus invocatus*** respectively. The 48h old culture was obtained to soak the seeds of sunflower for 2-3h prior to sowing. The seeds were allowed to grow in the field. Seeds of hybrid Parsun 3 of sunflower were soaked for 3-4 hours prior to sowing in broth culture of PGPR. The contaminated high TDS water and rhizosphere soil were analyzed for EC, pH, Total dissolved solid (TDS) and organic matter. The plants were grown under natural conditions. The physiological and biochemical parameter such as shoot length, root length, shoot dry weight, root dry weight, proline content of plants and activities of antioxidant enzymes viz. superoxide dismutase and catalase were measured. There were significant increases in shoot length, shoot weight, root weight, and proline content, superoxide dismutase and catalase of inoculated plant as compared to uninoculated plants irrigated with high TDS bearing water. The EC, PH and TDS were significantly decreased due to PGPR inoculation. It is inferred from the present study that PGPR play positive role in plant growth and in alleviating the adverse effects of high TDS water. The residual effect of W1 on soil organic matter and essential nutrients Ca, Mg, K and P is noteworthy for successive plantation.

Keywords: water pollution, salinity and sodicity, sunflower, Plant growth promoting rhizobacteria (PGPR), Bioremediation

P-21

Biosurfactant production from filamentous fungus *Penicillium glabrum*

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In this study, biosurfactant production from filamentous fungus *Penicillium glabrum* was optimized. The influence of different carbon sources (orange peel, potato peel, apple peel, tomato peel and pomegranate peel) and nitrogen sources (mustard seed cake, cotton seed cake, banana peel and wheat bran) on biosurfactant production was evaluated. During initial screening, the strain produced blue halo of 4.5 cm on the 7th day of incubation. Blood hemolysis assay was also applied. But no ring formation was detected. Crude extract for biosurfactant production was tested for various surface activity assays. Among the tested nitrogen sources, such as mustard seed cake, cotton seed cake, and banana peel and wheat bran, Maximum oil spreading ability was noted 8.25 cm for crude extract obtained from mustard seed cake at 192 hours of incubation, While the highest oil spreading ability of carbon sources including orange peel, apple peel, tomato peel, potato peel and pomegranate peel was 8.1cm, as demonstrated by orange peel at 168 hours of incubation. Both values were equivalent to 16 g/l of synthetic biosurfactant CTAB but found higher in comparison with chemical surfactants SDS. For crude extract produced from the positive control of GPSY, the maximum drop-collapsing ability from nitrogen source was 2.75cm at 144 hours of incubation followed by banana peel 2.05 cm at 192 hours of incubation which found higher in comparison with synthetic surfactants (CTAB & SDS). Meanwhile, for crude extract derived from GPSY control, the highest drop-collapsing ability from carbon source was 2.1 cm at 192 hours of incubation followed by pomegranate peel 1.9 cm at 240 hours of incubation which also found higher in comparison with synthetic surfactants (CTAB & SDS). Maximum drop sliding ability from nitrogen sources 8 cm was noted for crude extract obtained from wheat bran at 192 hours of incubation, while for carbon source maximum oil spreading ability was 7.5 cm shown by orange peel at 240 hours of incubation. Both these values found greater than that of chemical surfactants. Maximum emulsification index of nitrogen sources was 54% noted for crude extract obtained from mustard seed cake and bran at 168 and 192 hours of incubation which was approximately equal to 8g/l of synthetic surfactants (SDA & CTAB), while for carbon source maximum emulsification index was 56% shown by tomato peel at 216 hours of incubation which is approximately equal to 10 g/l of synthetic surfactants (SDA & CTAB). There was a noticeable increase in fungal biomass output, maximum fresh weight was 2.88 g of cotton seed cake from nitrogen sources and 4.00 g/ 30 ml of tomato from carbon sources. Biochemical studies included assays for the detection of total sugars, reducing sugars, protein quantification and lipid estimation. Based on estimated biochemical components being larger in amounts than the total quantity of sampled biosurfactant, it has been proposed that the biosurfactant comprised of a smaller molecule than the standard used in the biochemical assay. Very little amount of protein found in crude biosurfactant, while major portion consists of sugars. Because greater surface activity was produced by using cheaper carbon and nitrogen sources, this research will aid in improving the economics of biosurfactant production. Furthermore, acceptable biosurfactant production from the *Penicillium* species EHRC4 has been reported here without the need of expensive carbon and nitrogen sources, decreasing production costs even more. Additionally, employing a locally isolated fungal strain, a biosurfactant with unique surface activity has been described, possibly extending the spectrum of biosurfactants accessible for specialized applications. Purification and chemical and biological characterization of these potentially novel biosurfactants are necessary before they can be used in higher-level applications.

Keywords: Biosurfactant production, Filamentous fungus, Penicillium glabrum

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Biosurfactant production from fungal strain from aerial parts of tomato

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Biosurfactants are surfactants of microbial origin, that are different from synthetic surfactants as these are eco-friendly and amphiphilic compound containing both hydrophilic and hydrophobic region. In this study, fungal strain from aerial parts of tomato was picked out and resulted in pure culture that was identified later by using camera microscope. These strains were identified as *aspergillus, sclerotinia, fusarium, penicillium, Rhizopus* and *Alternaria*. CTAB-MB medium was given to these strains and halo ring that formed around these strains was measured after 2-3 days. These ring zone formations confirmed the preliminary screening of biosurfactant production. Blood hemolysis assay was also performed as another part of preliminary screening, fungi grown over that media caused the breakage of sheep blood and a halo ring similar to that of CTAB ring, was formed. SYPGA media was specified for pure strains in order to preserve them in slants and arranged them in slant position. General media (glucose-peptone-starch-yeast extract) was given to strains for incubation period of 9-days, maximum biosurfactant production was achieved from day 5th to day 8th. This production was determined after performing 4 activity tests (oil displacement, drop sliding, drop collapsing and emulsification index. Phenol- sulphuric acid test was performed over the filtrate that was attained on day 5th and 6th after incubation period. Positivity rate of biosurfactant production showed when orange, dark orange and light orange was noticed. Microplate assay was performed to check out the grid view of surfactant with backing sheet of paper in 96-microwell plates little bit results was observed. Penetration assay was also performed with paste of silica gel and oil and red staining solution (safranin). 4 strains out of 11 showed high positive result.

This study will help to improve the economic condition of biosurfactant production when cheaper resources would be used. Better production of biosurfactants would be achieved when it is obtained from fungi on industrial level. Locally isolated strains like tomato may widen the range of identified biosurfactant application as these biosurfactant with exceptional surface-active properties have been reported. Because of high demand of biosurfactants now-a-days, more exploration and further biological characterization is needed.

Keywords: Biosurfactants, Surfactants, Microbial origin

P-23

Phytoremediation of heavy metal contaminated soil using four plants species: A study on green technology

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Soil contamination by heavy metals is a serious issue faced by several countries around the world, and conventional technologies to resolve this problem were expensive and caused negative impact on the environment. One solution to reduce the concentrations of heavy metals in soil is to use plants that can absorb and accumulate heavy metals into harvestable parts, a process referred as phytoremediation. To understand the plant's potential, a pot experiment was conducted with four plants species i.e., *Abelmoschus esculentus*, *Avena sativa*, *Cyamopsis tetragonoloba* and *Sesamum indicum*. The selected plants were allowed to grow in metal contaminated soil for 12 weeks. At the end of experimental period, plants were harvested and then analyzed for metal tolerance and extraction. Among the four plants investigated, the germination and growth parameters along with chlorophyll contents were significantly ($p<0.05$) higher in A. sativa followed by *C. tetragonoloba*, *S. indicum* and *A. esculentus*. Likewise, *A. sativa* exhibited highest bioconcentration factor (1.34 and 1.30), bioaccumulation coefficient (1.71 and 1.50), translocation factor (1.28 and 1.16) and phytoremediation efficiency (4.81% and 5.17%) for Cu and Zn, respectively suggested that *A. sativa* was suitable for phytoextraction. On the other hand, for Pb, the values of BCF (1.62), BAC (0.89), TF (0.55) and PR (21.74%) suggested that *A. sativa* has the great capacity to tolerate and stabilized high concentrations of Pb than other tested plants. From the experimental results, it was concluded that being non-hyperaccumulator, *A. sativa* has ability to remediate metal contaminated soil effectively up to allowable limits.

Keywords: Soil pollution, heavy metals, tolerance, accumulation, phytoremediation

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Preparation & characterization of *E. Coli* DH5α bacterial ghosts and evaluation of their loading efficacy as a delivery vehicle

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Bacterial ghosts (BGs) are Gram-negative, nonliving bacterial cell envelopes lacking cytoplasmic contents while conserving their cellular morphology and inherent external antigenic structures comprising bio-adhesive characteristics. The study focuses on development of a new delivery platform using bacterial ghosts (BGs) to combat challenges in a better way. Bacterial ghost preparation can be done using chemical or genetic methods. In the following study, BGs of *E. coli* DH5α prepared by addition of the bacterial cells to tween-80 for a long period of time tracked by an immediate decrease of pH. Scanning Electron Microscope (SEM) results showed the excellent formation of bacterial ghosts with clear holes in their outer membranes. Furthermore, Release of DNA and protein content was confirmed by agarose gel electrophoresis and Bradford assay, respectively. Evaluation of loading efficacy was done by loading Doxorubicin with different concentrations at different conditions. The main benefits of BGs are the uncomplicatedness of the preparation scheme, protection, Independency of cold chain, and adaptability as a combination vaccine. As the bacterial ghosts (BGs) are combinations of excellent natural adjuvant characteristics with adaptable carrier functions. The adjuvant characteristics of bacterial ghosts boost immune responses against envelope bound antigens, as well as mucosal immunity and T-cell activation. Therefore, it offers humoral and cell mediated immune responses. Further studies will show that the bacterial ghost can do targeted delivery of drugs and vaccines can induce a stronger immune response when delivered with BGs. Experimental validation will confirm the potential of bacterial ghost platform.

Keywords: Bacterial Ghost, Delivery Vehicle, Doxorubicin, SE

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Heavy metal removal from various wastewater samples using low cost and efficient absorbents

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The ability of wheat husk and bamboo to recover Cu, Cr, Mn, Ni and Zn from aqueous solutions was investigated on three parameters i.e., variations in pH, contact time and initial concentrations of metal. The bio-adsorbents were washed, dried and powdered up to the size of 112 µm followed by chemical activation with 0.3 M nitric acid (HNO_3) solution for 24 hours, washing with distilled water until pH became neutral and then oven drying at 75°C with constant mixing. The bio-adsorbents were applied to each metal ion solutions by preparing their 1M stock solutions made from copper (II) sulphate, potassium dichromate, manganese (II) sulphate, nickel chloride hexa-hydrate and zinc sulphate heptahydrate. The solutions were filtered and analyzed by atomic Absorption Spectrophotometer to check the efficiency of bio-adsorbents. Under optimized conditions of pH, contact time and concentration, the bio-adsorbents were allowed to react with metals in a digested industrial water samples i.e., paint. Wheat husk was found to be the most effective and low-cost bio-adsorbent which has much high potential to be used for heavy metals removal from aqueous solution.

Keywords: Wheat husk, Bamboo, Zinc sulphate heptahydrate

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COVID-19 associated mucormycosis: Emergence, linkage, factors and host defense

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Mucormycosis, also known as Black fungus, is a deadly fungal infection and has been observed in some COVID-19 patients. The type of fungi responsible for this infection includes the Rhizopus and Mucor species. The current study mainly focuses on the epidemiology and occurrence of this disease in COVID-19 patients and to highlights the source or link between these diseases. The main cause of black fungus emergence in COVID-19 patients is thought to be the immune suppression resulting from prolonged medication including steroids and serious also the cytokine storm. The brain and lungs are mainly affected by this infection. COVID or non-COVID patients both can be affected by this fungal infection by inhaling the specific fungal spores. The fungal infection in covid patients have been observed in United States, India and Pakistan. There is currently no treatment or vaccine available for this deadly fungal disease and it is also hard to identify. In this study, the root cause of co-infection and relationship between SARS-CoV-2 and Black fungus has to be established. Pathways and host proteins targeted by these pathogens can be inferred to establish the fact of pathogenesis and thus the causative factors can be highlighted. Employing computational and system biology approaches, the co-morbidity can be explored and thus may result to present a solution to combat such novel diseases.

Keywords: Mucormycosis, Black fungus, COVID-19

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Genetic and immunoinformatic mapping of SARS-COV-2 spike protein for multi-epitope vaccine design

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Global implementation of vaccine would be an effective measure to contain the ongoing COVID-19 epidemic. However, conventional vaccine development is hampered by time, cost and biosafety hurdles. It is effective against only SARS-COV-2 but showed no response against other related coronaviruses from where it has been evolved and showed higher similarity. This study aims to design a multi-epitope vaccine targeting the coronavirus spike protein. Genetic analysis revealed that the spike region is highly conserved among SARS-CoV-2, bat SL-CoV and SARS-CoV. Employing the immunoinformatic approach, we have prioritized 20 MHC I and 10 MHCII conserved epitopes among SARS-CoV-2, bat SL-CoV and SARS-CoV to design the multi-epitope vaccine. This vaccine candidate is anticipated to strongly elicit both humoral and cell-mediated immune responses against selected CoV. These results warrant further development of this vaccine into real-world application.

Keywords: COVID-19, SARS-CoV-2, bat SL-CoV, SARS-CoV, immunoinformatic approach

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