Pak. J. Biochem. Mol. Biol., 2022, 55(1):53-57

Conference Proceedings

Abstracts of Plenary lectures delivered during 2nd International Conference on Applied Biosciences (ICAB2021) held in Mohammad Ali Jinnah University, Karachi, Pakistan during December 30-31, 2021.

Preface

Department of Biosciences, Mohammad Ali Jinnah University, Karachi, Pakistan organized 2nd International Conference on Applied Biosciences (ICAB2021) during December 30-31, 2021. Hundreds of scientists, post-doctoral fellows and graduate students from Pakistan and other countries attended this conference. In this conference, an array of topics related to applied biosciences including Biochemistry, Molecular Biology, Bioinformatics, Metabolomics, Biotechnology, Cancer Biology, Genomics, Metagenomics, Proteomics, Health Biotechnology, Immunology, Infectious Diseases, Microbiology, Genetic Engineering, Molecular Medicine, Neurosciences, Virology were discussed.

In this issue of PJBMB, we are publishing abstracts of plenary lectures delivered during ICAB2021 conference. All abstracts submitted to ICAB2021 for presentations in technical sessions were peer reviewed. Editorial board of PJBMB is grateful to the organizing committee of ICAB2021 for providing abstracts of plenary presentations for publication in PJBMB.

Editorial Board

Pakistan Journal of Biochemistry and Molecular Biology

PLENARY LECTURES IN ICAB2021

DESIGING PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC APPLICATIONS

M. Waheed Akhtar

School of Biological Sciences, University of the Punjab, Lahore, Pakistan.

ABSTRACT

In biological systems regulatory and other functional proteins are synthesized according to the demand of the biochemical processes in the cells in a healthy state. However, if these proteins are required to be produced on a large scale for specific applications, the factors like biological activity, stability, specific activity, specificity, etc., in addition to economic consideration become highly relevant. A rapid expansion in the application of enzymes and regulatory, immunological and other proteins have led to the development of a large variety of strategies, largely based on E. coli expression system, for their production. Techniques including site-directed mutagenesis, error prone PCR, in vitro recombination, truncation of molecules, fusion of selected protein segments, supported by in silico tools and high-throughput screening allow unlimited possibilities. An important area for application of these strategies is development of a reliable serodiagnosis and an effective vaccine for tuberculosis (TB), which is caused by Mycobacterium tuberculosis (Mtb) and takes over one million lives every year. Mtb antigens with their immunodominant epitopes have a crucial role in the development of vaccine as well as a sensitive serodiagnostic procedure. The varied response against different Mtb antigens between individuals according to the stage of microbial growth and the disease, make serodiagnosis or vaccine development rather complex. One approach for developing a

sensitive serodiagnosis procedure and an effective multistage vaccine would be to produce molecules of the required sensitivity based on B- and T-lymphocyte specific epitopes from multiple Mtb antigens. We have constructed, produced and evaluated a series of such fusion molecules towards achieving these desired goals. Using the same strategies we have made advances towards developing sensitive serodiagnosis procedure for Covid19. Some of the recent work of our laboratory in these connections shall be discussed.

AMAZING MEDICINAL PROPERTIES OF NATURAL HONEY AND ITS GLYCOPROTEINS

Muhammad Kamran Azim

Department of Biosciences, Mohammad Ali

Jinnah University, Karachi, Pakistan.

ABSTRACT

Recent evidences suggest an important role(s) for natural honey and honey glycoproteins in modulating immune response. Honey proteins/peptides were separated by size exclusion chromatography into fractions with molecular masses in the range of 2−450 kDa. High molecular mass fractions of honey proteins contained major royal jelly protein-1 (MRJP1); the predominant honey glycoprotein. We showed that honey MRJP1 predominantly occurs in dimeric and tetrameric forms. The oligomeric MRJP1 might be comprised of glycosylated MRJP1 as well as 'arabinogalactan-MRJP1'. Moreover, MALDI-ToF provided evidence of complexation of a 5.5 kDa molecule with different quaternary structures of MRJP1. The honey proteins exhibited potent inhibition of ROS production in zymosan-activated human neutrophils (IC50 = 6−14 ng/mL) and murine macrophages (IC50 = 2−9 ng/mL). The production of pro-inflammatory cytokines IL-1β and TNF-α by human monocytic cell line in the presence of honey proteins was analyzed. Honey proteins did not affect the production of IL-1β; however, TNF-α production was significantly suppressed. These findings indicated that honey glycoproteins and glycopeptides significantly interfere with molecules of the innate immune system.

UPREGULATED TYPE I INTERFERON RESPONSES IN ASYMPTOMATIC COVID-19 INFECTION ARE ASSOCIATED WITH IMPROVED CLINICAL OUTCOME

Kiran Iqbal Masood, Maliha Yameen, Javeria Ashraf, Saba Shahid, Syed Faisal Mahmood, Asghar Nasir, Nosheen Nasir, Bushra Jamil, Najia Karim Ghanchi, Iffat Khanum, Safina Abdul Razzak, Akbar Kanji, Rabia Hussain, Martin Rottenberg, and Zahra Hasan*

Department of Pathology and Laboratory

Medicine, The Aga Khan University,

Karachi, Pakistan

ABSTRACT

Understanding key host protective mechanisms against SARS-CoV-2 infection can help improve treatment modalities for COVID-19. We used a blood transcriptome approach to study biomarkers associated with differing severity of COVID-19, comparing cases with severe and mild Symptomatic disease with Asymptomatic COVID-19 and uninfected Controls. There was a suppression of antigen presentation but upregulation of inflammatory and viral mRNA translation associated pathways in Symptomatic as compared with Asymptomatic cases. In severe COVID-19, CD177 a neutrophil marker, was upregulated while interferon stimulated genes (ISGs) were downregulated.

In Asymptomatic COVID-19 cases there was a strong upregulation of ISGs and humoral response genes with downregulation of ICAM3 and TLR8. Compared across the COVID-19 disease spectrum, we found type I interferon (IFN) responses to be significantly upregulated (IFNAR2, IRF2BP1, IRF4, MAVS, SAMHD1, TRIM1), or downregulated (SOCS3, IRF2BP2, IRF2BPL) in Asymptomatic as compared with mild and severe COVID-19 with the dysregulation of an increasing number of ISGs associated with progressive disease. These data suggest that initial early responses against SARS-CoV-2 may be effectively controlled by ISGs. Therefore, we hypothesize that treatment with type I interferons in the early stage of COVID-19 may limit disease progression by limiting SARS-CoV-2 in the host.

INTERDISCIPLINARY RESEARCH AT A CROSSROADS: SNAKE VENOM PROTEOMICS - ANTIVENOMICS AND THE SYNTHESIS OF SILVER-ANTIDOTE

Syed Abid Ali

Third World Center for Science and Technology, H.E.J. Research Institute of Chemistry, University of Karachi, Karachi-75270, Pakistan.

ABSTRACT

Pakistan is a very large country with various ecological niche since inhabiting highly biodiverse, venoumous snakes and the snakebite cases are on rise. Poor access to healthcare, lack of basic knowledge about snakes and their venom composition, and non-availability of antivenoms mainly contribute to higher mortality and morbidity in most cases. Fuel in fire, in absence or insufficient amount of indigenously produced antivenoms (i.e., IgG or F(ab')2 isolated from serum of hyperimmunized horses), Pakistan is solely reliant on polyvalent antivenins imported from other countries, like India and Saudi Arabia. Thus, the need for high throughput venomics and antivenomics studies (to generate baseline data), preparation of geographically specific, and/or monovalent antivenoms with improved efficacies are the dire need to save precious lives. Despite sporadic reports, venomous fauna of Pakistan even the common 'Big-4 snakes' (i.e., Cobra, Krait, Russell's and Saw-scaled vipers) responsible for major fatalities is among the most neglected issue. Metallic nanoparticles (like silver and gold) have been extensively utilized in medicines and biomaterials as a drug carrier, diagnostic and/or therapeutics - mainly because of their smaller size, large surface area, unique spectroscopic properties and cell penetration ability . In the current research, one-pot synthesis of silver nanoparticles (AgNPs) functionalized with polyvalent antivenom was conducted using silver nitrate and sodium borohydride as green chemistry. State-of-the-art methodologies including; separation (SEC-FPLC and 1D SDS-PAGE), spectroscopy (Uv/Vis, FTIR and CD), microscopy (AFM, and SEM/SEM-EDX), hydrodynamics (DLS and Zeta-potential), and the complementary immunoturbidity and double immune-diffusion neutralization techniques were utilized. Despite, polyspecific nature of antivenom used, obtain data demonstrated quite encouraging results with reference to

size, shape, polydispersity and surface charges (RH = 53.3±8 nm; PDI = 22.7%; Z-average = -15.9), intrinsic antimicrobial potential, cellular uptake and toxicity as well as neutralization and/or interaction studies with Big-4 snake venoms.

Key Words: Antivenom, Silver nanoparticles, Snake, Toxins, Venom.

§ This project is financially supported by the Higher Education Commission of Pakistan to SA Ali (HEC NRPU No. 20-3891).

OMICS TECHNOLOGIES ENCOMPASSING BIOINFORMATICS APPROACHES FOR AGROBIOTECHNOLOGY AND BIOLOGICAL CONTROL OF PLANT DISEASES

Ömür BAYSAL

Molecular Microbiology Unit, Department of Molecular Biology & Genetics, Faculty of Science, Mugla Sitki Kocman University, Mugla, Turkey

ABSTRACT

The omics-approaches help for investigating microbial diversity and plant-microbe interactions across diverse ecological communities. The holistic approach to understand how and why pathogenesis occurs, and to effective management for the disease development considering a multi-omics approach by bioinformatics tools allow us to provide a detailed picture of plant-microbial interactions involving the control of biological control and induction of plant growth using effective biological agents with the promising genes cloned from selected microorganisms by recombinant DNA technology. The data obtained with whole-genome sequence analysis and RNA seq data and their evaluations by bioinformatics tools can also ultimately provide us with the background to build predictive models for how microbes and plants respond to biotic/ abiotic stress. In this presentation, a piece of brief information on integrating-omic approaches related to our ongoing lab studies involving genomics, metagenomics, metabolomics where multi-omics have been successfully used for plant disease management as well as providing information about promising future studies.

STATUS OF CANDIDA AND CANDIDIASIS IN PAKISTAN

Muhammad Mushtaq

Department of Biotechnology, Faculty of Life Sciences & Informatics Balochistan, University of Information Technology, Engineering & Management Sciences (BUITEMS), Quetta, Pakistan.

ABSTRACT

Candidiasis is an infection caused by Candida species which rank 4th among systemic microbial human infections. Candida albicans, C. tropicalis, C. parapsilosis, C. glabrata and C. krusei are among the most frequent cause of systemic and opportunistic mucosal infections especially in patients with organ transplantation, immunocompromised, intensive immunosuppressive treatment, cancer and in patients using broad spectrum antibiotics. A very recent epidemiological alert has been released by WHO (2021) indicating the outbreaks and greatest risk of another Candida species as emerging pathogen the “Candida auris” in healthcare

services during Covid-19 pandemic particularly in ICU patients. C. auris is a multidrug resistant pathogen causing nosocomial transmission among hospitals globally. Identification of human pathogenic Candida species from clinical specimens is important not only from the view of epidemiology, but also for selecting the antifungal treatment. Various serological and/ or biochemical as well as molecular biology techniques have been extensively used for Candida species identification. Unfortunately, very less research work has been done in Pakistan. In the current talk, therefore, a review of research work which has been done in Pakistan and contribution of BUITEMS Quetta regarding Candida species prevalence will be discussed.