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EURO-GLOBAL SUMMIT ON ADVANCES IN CLINICAL AND CELLULAR IMMUNOLOGY

September 11-12, 2023 | London, UK

Adv. Immunology 2023

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A CONFLUENCE OF ERUDITE & KNOWLEDGE-SEEKER

PROGRAM-AT-A-GLANCE

ADV. IMMUNOLOGY 2023

DAY 1
SEPTEMBER 11, 2023

Scientific Program

Moderator: Jocelyn Yelle, *Antiviral InteliStrat, Canada*

Chair: Huan Ren, *Southern University of Science and Technology, China*

07:45-08:15	**Registrations**
08:15-08:30	**Opening Ceremony**

Topics: Immunology | Immunology Education | Autoimmunity | Epidemiology | Immunogenetics | Cancer Immunology and Immunotherapy | Immunotherapy | Translational Immunology | Vaccines and Immunotherapy | Cytokines and Chemokines | Transplantation Immunology | Inflammation | Technological Innovations in Immunology

Distinguished Speaker Talks

08:30-08:50	**Title: Automated, label-free $TCID_{50}$ assay to determine the infectious titer of virus-based therapeutics** **Daniel Hochdorfer,** *Boehringer Ingelheim Pharma GmbH & Co. KG, Germany*
08:50-09:10	**Title: Antiviral drug cocktails and pandemics: Past, present and future avenues** **Jocelyn Yelle,** *Antiviral InteliStrat, Canada*
09:10-09:30	**Title: F4/80+ macrophages digression at critical tumor transitions reveals serial combination targets deactivating mouse colorectal liver metastases** **Huan Ren,** *Southern University of Science and Technology, China*
09:30-09:50	**Title: Regulation of mi-RNAs target cancer genes between exercise and non-exercise in rat rheumatoid arthritis induction** **Vimolmas Tansathitaya,** *College of Sports Science and Technology, Mahidol University, Thailand*
09:50:10:10	**Title: Direct virus capture assay for label-free detection of viral particles using a laser microscope** **Adolfo Carloni,** *NTP Nano Tech Projects SRL, Italy*
10:10-10:30	**Title: Diagnosis and prognosis of covid-19 employing biochemical tests and machine learning** **Alexandre de Fátima Cobre,** *Federal University of Paraná, Brazil*

Group Photo 10:30-10:40

Refreshment Break 10:40-10:55

10:55-11:15	**Title: Sequence and phylogenetic analysis of Influenza A and B viruses circulating in Riyadh, Saudi Arabia** **Fahad Nasser Almajhdi,** *King Saud University, Saudi Arabia*
11:15-11:35	**Title: Discover essential host SUMOyaltion pathway for Influenza virus life cycle** **Jiayu Liao,** *Bourns College of Engineering, University of California at Riverside, USA*
11:35-11:55	**Title: Bacterial filtration efficiency and viral filtration efficiency of face masks – the role of bacteriophages in textile testing** **Ludmila Tvrzová,** *Textile Testing Institute, Czech Republic*
11:55-12:15	**Title: *Akkermansia munciphila, Bifidobacter bifidum* and their extra cellular vesicles induce tolerogenic dendritic cells from patients with Crohn's disease** **Shaghayegh Baradaran Ghavami,** *Shahid Beheshti University of Medical Sciences, Iran*
12:15-12:35	**Title: Evidence for the role of a second Fc-binding receptor in placental IgG transfer in nonhuman primates- consequences for immunotherapy** **Yvonne Joy Rosenberg,** *PlantVax Inc., USA*
12:35-12:55	**Title: Detection of Human Papillomavirus in archived bladder and ovarian cancer samples** **Bukhtawar Fatima Malik,** *Atta-Ur-Rahman School of Applied Biosciences (ASAB), NUST, Pakistan*

Group Photo

Lunch Break 12:55-13:30

13:30-13:50	**Title: Beyond the margins of radiation treatment: Immunotherapy in combination with radiotherapy** **Sayeda Yasmin-Karim,** *Brigham and Women's Hospital, Dana Farber Cancer Institute, Harvard Medical School, USA*
13:50-14:10	**Title: Algebraic modelling in virology research** **Oleksandr Letychevskyi,** *Glushkov Institute of Cybernetics of National Academy of Science of Ukraine, Ukraine*

14:10-14:30	**Title: *Pycard* and *Bc017158* candidate genes of *Irm1* locus modulate inflammasome activation for IL-1β production** **Olga Célia Martinez Ibañez,** *Instituto Butantan, Brazil*
14:30-14:50	**Title: HLA sensitization in the era of covid-19 and the impact on transplant laboratory** **Rabab Ali Abdullah Al Attas,** *King Fahad Specialist Hospital-Dammam, Saudi Arabia*
14:50-15:10	**Title: Efficient transfected liposomes co-loaded with pNrf2 and pirfenidone improves safe delivery for enhanced pulmonary fibrosis reversion** **Chang Xin,** *Jinzhou Medical University, China*
15:10-15:30	**Title: Intrathecal delivery of dendritic cell immunotherapy cures breast cancer Leptomeningeal disease and protects against reinoculation in immunocompetent preclinical murine models** **Vincent Law,** *Moffitt Cancer Center and Research Institute, USA*
15:30-15:50	**Title: Therapeutic efficiency of Dexamethasone, Cyprohepatadine and Tetracycline on dermonecrosis induced by *Cerastes cerastes* viper venom** **Oussedik Oumehdi Habiba,** *University of Science and Technology Houari Boumediene, Algeria*
Refreshment Break 15:50-16:05	
16:05-16:25	**Title: Dermoscopic features of cutaneous tuberculosis: A descriptive study unveiling novel findings** **Swati Prasanna,** *Seth G.S. Medical College and K.E.M. Hospital, India*
16:25-16:45	**Title: Covid-19 effect on patients with noncommunicable diseases: A narrative review** **Mai Elaarag,** *Hamad Medical Corporation, Qatar*
16:45-17:05	**Title: Exploring unique immune cell population by dissecting tumor immune microenvironment in hospitalized hepatocellular carcinoma and ovarian cancer patients** **Saif Ullah Afridi,** *Guangzhou Medical University, China*
17:05-17:25	**Title: Isolation and characterization of two novel phages as a possible therapeutic alternative against multi-drug resistant *E. coli*** **Ban Oday Abdulsattar,** *Mustansiriyah University, Iraq*

17:25-17:45	**Title: TGFβ1-high glucose reprogramming in immune cells: Cardio-metabolic consequences** **Kareem Awad,** *University of Turku, Finland*
17:45-18:05	**Title: Immunology of implantation in endometriosis and adenomyosis** **Wolfgang Küpker,** *IVF Baden Baden, Germany*
18:05-18:25	**Title: The association of hypertension with increased mortality rate during the covid-19 pandemic: An update with meta-analysis** **Doaa Mahmoud Eisa Sabir,** *Physician Trainee at Bhealth Company & Volunteer at Surgical Researchs Development at Hamad Medical Corporation (HMC), Qatar*
18:25-18:45	**Title: Cellular dual effects of UVA & controlled drug release** **Julia Li Zhong,** *Bioengineering College of Chongqing University, China*
18:45-19:05	**Title: Analysis of active components and manufacturing technology *Cordyceps militaris* in silkworm** **Yujiao Chen,** *Guizhou Aerospace Intelligent Agriculture, Chongqing University, China*

Panel Discussion

End of Day 1

DAY 2
SEPTEMBER 12, 2023

Scientific Program

Topics: Immunology | Immunology Education | Autoimmunity | Epidemiology | Immunogenetics | Cancer Immunology and Immunotherapy | Immunotherapy | Translational Immunology | Vaccines and Immunotherapy | Cytokines and Chemokines | Transplantation Immunology | Inflammation | Technological Innovations in Immunology

Distinguished Speaker Talks

10:00-10:20	**Title: Epidemiological profile of Ebola virus disease in the Boké region 2014-2018** **Fatoumata Doumbouya,** *Field Epidemiologist, Ministry of Health, Guinea*
10:20-10:40	**Title: Role of mitochondrial DNA biomarker in chronic and late acute graft-versus-host disease in children** **Shima Azadpour,** *University of British Columbia, Canada*

Refreshment Break 10:40-10:55

10:55-11:15	**Title: Comparative characterization of bispecific antibodies with different molecular formats** **Wen Jin Wu,** *U.S. Food and Drug Administration, USA*
11:15-11:35	**Title: Lessons from the covid-19 pandemic. It's time to rewrite the immunology textbooks** **Javdat Muratkhodjaev,** *Institute of Immunology and Human Genomics of Academy of Sciences of Uzbekistan, Uzbekistan*
11:35-11:55	**Title: Increased percentage of apoptotic and CTLA-4 (CD152) expressing cells in CD4+/CD8+ cells in covid-19 patients** **Khalid Ali Nasif,** *King Khalid University, Saudi Arabia*
11:55-12:15	**Title: Sedimentation velocity FDS studies of antibodies in pooled human serum** **Robert T. Wright,** *Janssen Research and Development, USA*
12:15-12:35	**Title: Histological characteristics of chronic allergic rhinitis versus non allergy: Is there a difference in the remodeling?** **Tamara Michelle Acosta Castillo,** *IESS El Batán, Ecuador*

12:35-12:55	**Title: Recovery of potential starter cultures and Probiotics from Fermented Sorghum (Ting) Slurries** **Mathoto Thaoge,** *Tshwane University of Technology, South Africa*

Lunch Break 12:55-13:30

End of the Conference

Closing Remarks

DAY 2

Exclusively for Virtual Speakers

Virtual Presentations Conducted through CISCO Webex

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September 2024 | Rome, Italy

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SCIENTIFIC ABSTRACTS

DAY 1

EURO-GLOBAL SUMMIT ON ADVANCES IN CLINICAL AND CELLULAR IMMUNOLOGY

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Euro-Global Summit on Advances in Clinical and Cellular Immunology

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Automated, label-free $TCID_{50}$ assay to determine the infectious titer of virus-based therapeutics

Daniel Hochdorfer, Ramona Businger, Dominik Hotter, Carina Pfarr and **Johannes Solzin**

Viral Therapeutics Center, Boehringer Ingelheim Pharma GmbH & Co. KG, Germany

A robust and precise infectivity assay is a prerequisite for the development and market supply of virus-based biologics. Like other cell-based assays, traditional infectivity assays suffer from high variability and require extensive hands-on time. Therefore, a faster and more robust method to measure infectivity is needed to fulfill the requirements of a higher sample throughput and speed in drug development. We developed a label-free tissue culture infectious dose 50 ($TCID_{50}$) assay using automated image analysis that determines the cell confluence to discriminate between cytopathic effect-positive and -negative wells. In addition, we implemented semi-automated bench-top pipetting robots for the required pipetting steps to further shorten the hands-on time of the assay. The automated image analysis categorized >99% of the wells similar as operators did via visual evaluation and there was a close correlation between the titers that were determined by using either the automated image analysis or visual evaluation ($r^2 = 0.99$). Thus, here we present a label-free $TCID_{50}$ method with a stable automated image analysis that is ~ 3.6x faster and more standardized compared to the classical $TCID_{50}$ assay.

Biography

Daniel Hochdorfer works as a scientist in the Viral Therapeutics Center within Development at Boehringer Ingelheim. He is currently part of an analytical development team and focuses on bioassays for virus-based therapeutics and on biophysical methods for virus particle characterization, like nanoparticle tracking analysis (NTA), dynamic light scattering (DLS), multi-angle light scattering (MALS), and analytical ultracentrifugation (AUC). Before Daniel joined the pharmaceutical industry, he wrote his PhD thesis at the Institute of Virology in Ulm, Germany, about the entry of the human cytomegalovirus (HCMV) into host cells.

Antiviral drug cocktails and pandemics: Past, present and future avenues

J. Yelle

Antiviral InteliStrat, Canada

The last decades have seen the transmission to humans of quite a few viruses of animal origin (*zoonoses*) with dire consequences. While vaccines represent the ultimate tool to control such pandemics, direct-acting agents (DAAs) have the potential to stop an outbreak before it affects entire populations. These small molecules targeting viral enzymes and processes have been particularly successful and have revolutionized treatment of major viral infections such as HIV/AIDS and hepatitis C virus (HCV), especially when used in the form of cocktails of drugs. The drug cocktail approach, however, takes time to develop. When the SARS-CoV-2 Coronavirus emerged and evolved as a major pandemic, very few antiviral drugs were available as therapeutic agents. This can explain, at least in part, the limited success of DAAs in the early phase of the COVID-19 crisis. New pandemics can be expected in the near future, and they will likely be caused by some RNA viruses again, with known enzyme targets. As we now enter an inter-pandemic phase, we must focus our efforts to develop and optimize multiple drug cocktails against these targets that are associated with RNA viruses, based on our past experience, in order to be ready when new viruses with pandemic potential emerge. There are over 150 antiviral drugs or combination of drugs with various mechanisms of action that have reached the market to this day, but we need a more methodical approach to prepare for next pandemics. In this presentation, we will provide a review of what has been accomplished so far in the development of DAAs for all major families of virus infecting humans along with a view on future avenues, with a focus on emerging viruses and future pandemic threats of viral origin.

Biography

Jocelyn Yelle is a virologist specializing in Retroviruses and Herpesviruses, with a marked interest in antiviral drug discovery. He holds an MSc and a PhD degrees in Virology from Armand-Frappier Institute, a Canadian research center.

After his studies, he launched his career by investigating HIV's ability to establish persistent infections in human cell cultures. He then started a collaboration with a chemist colleague, mounting a multidisciplinary research program focusing on small molecules as potential drugs for HIV/AIDS treatment. With his colleague, he later founded Pharmacor Inc., a small biopharmaceutical company to pursue the same goals. Some of these molecules were eventually acquired by a major pharma.

Dr. Yelle is the Founder and President of Antiviral InteliStrat Inc., a small firm that provides scientific advice to companies and hospital-based research organizations. Antiviral InteliStrat also owns a proprietary database that contains information on thousands of antiviral drugs and vaccines against human viruses.

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F4/80+ macrophages digression at critical tumor transitions reveals serial combination targets deactivating mouse colorectal liver metastases

Huan Ren[1], Ting Qiao[1] and **Xia Li[2]**

[1]School of Medicine, Southern University of Science and Technology, China

[2]Bioinformatics Institute, Harbin Medical University, China

Background: The management of colorectal liver metastases (CRLM) remains a formidable challenge. Macrophages are abundant within the tumor microenvironment and play indispensable roles in immune suppression, angiogenesis, and metabolism. By dynamically analyzing the transformation of tumor-associated macrophages (TAM), derived from Kupffer cells or monocytes *in situ* and systemically at the critical tumor transitions, we aim to optimize the combination targets to cease CRLM growth in a mouse model.

Methods: C57BL/6 mouse CRLM was established by splenic injection of MC38 cells; and separated into tumor phases including tumor initiation, local expansion/ angiogenesis, medium- and high-volume metastases. Bulk and single-cell RNA sequencing was applied on varied CRLM-samples and cells. Data with Flow cytometry, immunohistochemistry, and *in vitro* co-culture experiments confirmed the RNA-seq data analysis by varied bioinformatics methods. Clec4f- and LyZ2-iDTR mice were used to target depletion of Kupffer cells or monocytes during CRLM. The HDAC inhibitor TMP195 or Clodronate liposomes was used to deplete macrophages or divert macrophage polarization *in vivo.*

Results: TAM is the most abundant immune cell, followed by T cells during CRLM growth. In medium tumors, T cells showed exhausted markers and interaction with TAMs. Targeted depletion of Kupffer cells or monocytes did not affect tumor growth but changed T cell quantity within the tumor microenvironment. Depletion of macrophages by liposomes or TMP195 treatment from the tumor transition of angiogenesis significantly distorted tumor vessels and resulted in greatly decreased tumor burdens. Dissection of the metabolic profiles of serial tumor samples and TAMs revealed TAM transformation via the metabolic switch, which initially supported by liver metabolism at initial CRLM angiogenic growth; and T-cell suppression between the medium to high tumor transitions.

Conclusions: The serial combination therapies at tumor initiation and medium-high tumor transitions targeting against TAM metabolic and anti-angiogenic, or immune checkpoint inhibitors may achieve significant efficacy in CRLM.

Biography

Dr. Ren Huan is currently a Professor at School of Medicine, Southern University of Science and Technology, China. She received her master's degree of Immunology in 1997 and her Ph. D in Neuroscience from University of Liverpool, UK 2005. Her research has been focused on tumor immune microenvironment and targeted biotherapy. As a Principal Investigator, Dr Ren has completed 4 major grants supported by National Science Foundation of China (NSFC) and published over 80 scientific research papers and obtained several awards on teaching and research. Dr. Ren has been actively involved in Immunology-related research and teaching in universities including UCSD (University of California, San Diego, USA) and Oxford Brookes University, UK since 1994 and published 25 academic books including Immunology textbooks and research books.

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Regulation of mi-RNAs target cancer genes between exercise and non-exercise in rat rheumatoid arthritis induction

Vimolmas Tansathitaya[1], Witchana Sarasin[2], Tanapati Phakham[2], Vorthon Sawaswong[3], Prangwalai Chanchaem[3] and **Sunchai Payungporn[3]**

[1]College of Sports Science and Technology, Mahidol University, Thailand
[2]Center of Excellence in Systems Biology, Faculty of Medicine, Chulalongkorn University, Thailand
[3]Research Unit of Systems Microbiology, Department of Biochemistry, Faculty of Medicine, Chulalongkorn University, Thailand

Introduction: Rheumatoid arthritis (RA) is classified as an autoimmune inflammatory condition characterized by pain, swelling, and inflammation of the joints, along with stiffness which can reduce function and impair the overall quality of life. Rheumatoid arthritis initiated from chronic inflammatory disorder that can affect not only just the joints but it also damages a wide variety of body systems, including the skin, eyes, lungs, heart and blood vessels. Some patient cases in post- rheumatoid arthritis diagnosis develop cancer later. Moreover, a total of 138 cases of lung and prostate solid tumors were recorded within 12 months of RA diagnosis. Furthermore, those patients diagnosed with RA experienced cancer of greater severity than was the case for patients who did not have RA. Exercise may represent a novel means of mitigating the suffering of RA and cancer patients. A number of studies have sought to examine the application of exercise as a means of inhibiting tumorigenesis.

Methods: The effects of exercise interventions on serum microRNAs were investigated in pristane-induced arthritis (PIA) rat models. Twelve Sprague-Dawley male rats were divided into 4 groups including non-exercise without PIA (N-EX), non-exercise with PIA (N-EX + PIA), exercise without PIA (EX) and exercise with PIA (EX + PIA). Blood samples were collected at the end of the study period to analyze miRNA biomarkers and target cancer gene predictions.

Results: Four significant Rattus norvegicus (rno-microRNAs) may purpose as tumor suppressors were identified as potential target cancer gene candidate expressions within the 4 comparative interventional exercise groups. One rno-microRNA and target cancer gene candidate was up-regulated and 3 rno-microRNAs and their target cancer genes were down-regulated.

Conclusions: Exercise interventions affected rno-miRNAs regulated target cancer gene candidates ITPR3, SOCS6, ITGA6, and NKX2-1 as biomarkers for cancer prognosis in rheumatoid arthritis diagnosis.

Table: *Four miRNAs and target cancer gene candidates*

Table 2. Rno-miRNA expressions and target cancer gene candidates.

MIRNA	TARGET GENES	GENE FUNCTIONS	EXERCISE GROUPS	RNO-MIRNA REGULATION	TYPE OF CANCER	CANCER RISK	REFERENCES
rno-miRNA 877	ITPR 3	Tumor suppressor	EX vs EX + PIA groups	Up	Proteoglycans cancer	↓	genome.jp/kegg ncbi.gov
rno-miRNA 466b-4-3p	SOCS 6	Oncogene	N-EX + PIA vs EX + PIA groups	Down	Leukemia	↑	genecards.org
rno-miRNA 128-2-3p	ITGA9	Oncogene	N- EX vs EX groups	Down	Lung cancer	↑	genecards.org
rno-miRNA 3064-3	NKX2-1	Oncogene	N-EX group vs N-EX + PIA groups	Down	Lung cancer	↑	cancerindex.org ncbi.gov

Biography

In my current role, I serve as a lecturer at Thailand's Mahidol University's College of Sports Science and Technology. My primary research interests concern miRNA and chronic illnesses, as well as fitness. I am also interested in studies on the microbiome in chronic illnesses and exercise, which was presented in an article in 2022. One of my significant study topics concentrated on illnesses and their effects on birth abnormalities acquired by the second and third generations of descendants. MiRNAs and target genes were employed as biomarkers in the research. Tinarathpatra Co Ltd., Thai Health Promotion Foundation, and Mahidol University have all provided me with financial support to study the BDNF gene expressions in amphetamine drug users as part of my ongoing research. This research focused on BDNF gene expression, single nucleotide polymorphism (SNP), mRNAs, miRNAs, and the microbiota to modify miRNAs and target gene expression. After I received my Ph.D. in Health Promotion and Human Services from the University of Cincinnati in the United States, I was inspired to act on another idea. One of my initial thoughts was to look at how genotypes could potentially evolve as lifestyles shifted and how exercise could help mitigate diseases. Since then, I have been motivated to begin examining genetic causes by performing in-depth studies in epigenetics, with a focus on miRNAs and target genes as major indicators.

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Direct virus capture assay for label-free detection of viral particles using a laser microscope

A. Carloni[1], R. Lo Savio[1], S. Piselli[1], C. Bertelli[2] and **M. Pizzato[2]**

[1]NTP Nano Tech Projects SRL, Italy

[2]Department of Cellular, Computational and Integrative Biology (CIBIO), University of Trento, Italy

Since the start of the pandemic of SARS-CoV-2 in 2019, it was immediately evident that early virus detection was crucial to managing the spread of the contagion especially by identifying high-viral load patients as soon as possible. For this reason, the development of new diagnostic tools quickly became a challenge for companies and research groups. Today, real-time reverse transcription PCR (RT-PCR) is considered the gold standard assay for quantitative detection of viral RNA and lateral flow assays (LFA) dominate the market for the qualitative detection of nucleocapsid or spike proteins. However, detection of viral RNA and related proteins in clinical samples does not discriminate between fully formed (infectious) viral particles and fragmented or non-encapsulated (non-infectious) genomic material. Only a specific biosensor targeted on the direct capture of whole virions can deliver this missing information by detecting and quantifying the number of whole virions from swabs possibly in an easy and fast manner. Therefore, this research study focuses on the evaluation of a bioreceptor-based assay, named Direct Virus Capture (DVC), fast, label-free and independent to variants, for the direct capture of SARS-CoV-2 whole virions. A new digital optical laser microscope named Nano Eye Device - Virus Detector (NED-VD), controllable in-situ or even from a remote location, was designed and developed for DVC assay, and specifically adapted to detect virions by light scattering, from samples having a minimum virus amount of ca. 10^5 virions in the reaction volume (20 µL). The working principle of this technology is demonstrated through the detection by evanescent wave scattering of sub-diffractive functionalized gold nanoparticles, and, as a possible biosensing application, we report the detection of spherical viruses, including SARS-CoV-2. The DVC assay combined with NED-VD is potentially extendable for detection of any other viruses having a spherical structure of at least 40 nm diameter.

Biography

Adolfo Carloni is Scientific Director of the company NTP Nano Tech Projects srl (Italy). He has an MSc in Industrial Chemistry from 2004 at Bologna University, Italy. He received two PhDs, one in Chemistry from CNR (National Research Institute) at University of Chemistry in Firenze, Italy in 2008, and one in Health from University of Cranfield, UK in 2010. In 2012 he co-founded NTP Nano Tech Projects with an electrical engineer and a telecommunication engineer. He has since patented a new method of optical laser coupling able to detect nanoparticles used as biomarkers. His research activity focuses mainly on biosensors for viruses, with the design and development of laser based optical devices dedicated to this application. His research interests include: optics, coatings, nanoparticles, surfaces functionalization and laser microscopy. He manages research, design, development, integration and verification of the overall biosensing system, leading colleagues specialized in biology, physics, and bioinformatics.

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Diagnosis and prognosis of covid-19 employing biochemical tests and machine learning

Alexandre de Fátima Cobre[1,2], Mônica Surek[1], Dile Pontarolo Stremel[2], Mariana Millan Fachi[1], Raul Luna Lazo[1], Luana Mota Ferreira[1], Karime Zeraik Abdalla Domingues[1], Thais Pelegrin Garcia[1], Fernando Miguel Stelmach Alves[1], Alexessander Couto Alves[2], Fernanda Stumpf Tonin[4] and **Roberto Pontarolo[1]**

[1]Department of Pharmacy, Federal University of Paraná, Brazil
[2]Department of Biosciences and Medicine, University of Surrey, UK
[3]Department of Forest Engineering and Technology, Federal University of Paraná, Brazil
[4]Health & Technology Research Centre, Polytechnic Institute of Lisbon, Portugal

Objective: This study aimed to implement and evaluate machine learning based-models to predict COVID-19's diagnosis and disease severity.

Methods: COVID-19 test samples (positive or negative results) from patients who attended a single hospital were evaluated. Patients diagnosed with COVID-19 were categorized according to the severity of the disease. Data were submitted to exploratory analysis (principal component analysis, PCA) to detect outlier samples, recognize patterns, and identify important variables. Based on patients' laboratory tests results, machine learning models were implemented to predict disease positivity and severity. Artificial neural networks (ANN), decision trees (DT), partial least squares discriminant analysis (PLS-DA), and K nearest neighbor algorithm (KNN) models were used. The four models were validated based on accuracy (area under the ROC curve).

Results: The first subset of data had 5,643 patient samples (5,086 negatives and 557 positives for COVID-19). The second subset included 557 COVID-19 positive patients. The ANN, DT, PLS-DA, and KNN models allowed the classification of negative and positive samples with >84% accuracy. It was also possible to classify patients with severe and non-severe disease with an accuracy >86%. The following were associated with the prediction of COVID-19 diagnosis and severity: hyperferritinaemia, hypocalcaemia, pulmonary hypoxia, hypoxemia, metabolic and respiratory acidosis, low urinary pH, and high levels of lactate dehydrogenase.

Conclusion: Our analysis shows that all the models could assist in the diagnosis and prediction of COVID-19 severity.

Biography

I have bachelor's degree in pharmaceutical sciences (Lúrio University, Mozambique), a master's in pharmaceutical sciences (Federal University of Paraná, Brazil), and I am currently a PhD student in pharmaceutical sciences (Federal University of Paraná, Brazil). I am currently a visiting student at the University of Surrey in United Kingdom. I have 30 scientific articles published in peer-reviewed journals in the area of Epidemiology, metabolomics and in the field of drug discovery. As of July 20, 2023, I have received 758 citations in scientific literature, and my H-Index = 9. I have 3 book chapters published. In my PhD, which I finished in March 2024, I have successfully applied Artificial Intelligence and Machine Learning in the investigation of risk factors and new biomarkers of COVID-19, as well as in the discovery of new drugs candidates that inhibit the spike protein of the SARS-CoV-2 virus for the treatment of COVID-19.

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Sequence and phylogenetic analysis of Influenza A and B viruses circulating in Riyadh, Saudi Arabia

Fahad Nasser Almajhdi[1], Ibrahim Mohammed Aziz[1] and **Rasha Mohammed Alzayed[1,2]**

[1]King Saud University, Saudi Arabia

[2]Al Jouf University, Saudi Arabia

Influenza viruses are a major public health concern and pose an economic burden worldwide. The extensive mass gathering of pilgrims from all over the globe and the continuous movement of the foreign workforce through country entry borders increase the risk of the spread and evolution of influenza virus outbreaks in Saudi Arabia. Here, we report the sequence and phylogenetic analysis of the H1N1 subtype of influenza A virus (IAV) and influenza B virus (IBV) in clinical samples collected from Riyadh, Saudi Arabia, from 2014/15 to 2019/20 seasons. RNA was extracted from the clinical samples and subjected to RT-PCR analysis for the detection of IAV and IBV. The full-length HA and NA genes were amplified and sequenced. Multiple sequence alignments (both nucleotides and deduced amino acids) were aligned using Clustal W, MegAlign program of Lasergene software. IAV and IBV were found in 35 and 6 samples of the 258 samples screened (13.6% and 2.3% respectively). All IAV strains were subtyped into H1N1 and H3N2. Sequence and phylogenetic analysis results showed that full-length HA and NA genes of the A/H1N1 Riyadh strains were not closely related to any influenza vaccine strains. This study also showed all IBV were classified either B/Yam-like viruses or as B/Vic-like viruses. Amino acids analysis showed 17 mutations of HA1 domain of B/Yam-like and 12 mutations of B/Vic-like Riyadh which are different from their counterparts in vaccine strains recommended for use in the Northern hemisphere. Further studies are needed to verify and understand the significance of these amino acid substitutions for updating influenza vaccines used in Saudi Arabia.

Biography

Proficient in molecular virology and a pioneer in the development of vaccines and diagnostic tools for the identification and prevention of human respiratory viruses and other prevalent viruses in the Saudi population. Aside from research and teaching, I have extensive experience and have made significant contributions in a variety of managerial roles. Professor of Virology, joined King Saud University's Department of Botany and Microbiology in the year 2002. In addition, have an outstanding track record in basic and translational research as a principal investigator of competitive local institutional grants. Collaborator and Co-investigator in a number of international grants and Co-inventor of several patent applications in molecular diagnosis, bringing almost two decades of significant experience in the development of leading research and education programs in molecular virology. Author of more than 47 refereed publications, a membership in several scientific societies. Current Research Interest is focused on the biology of the emerging viruses of human respiratory viruses circulated in Saudi Arabia.

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Discover essential host SUMOyaltion pathway for Influenza virus life cycle

Jiayu Liao[1,2,3,4], Runrui Dang[1], Chuchhu Liu[1], George Way[1] and **Vipul Madahar[1]**

[1]Department of Bioengineering, Bourns College of Engineering, University of California at Riverside, USA
[2]The Stem Cell Center, University of California at Riverside, USA
[3]Institute for Integrative Genome Biology, University of California at Riverside, USA
[4]Biomedical Science, University of California at Riverside, USA

As a pathogen to humans, viruses often take advantage of the host factors for their infection and replication. Identifying and elucidating essential host pathways for viral infection is critical for understanding the viral infection processes and developing novel therapeutics with potential broad-spectrum treatment modalities for anti-viruses, such as influenza A virus (IAV)/ influenza A virus (IBV) and COVID-19.

We have been working on a hypothesis that discovering and blocking host pathway(s) for viruses will be an efficient strategy for anti-viruses with potentially broad activities. We have employed the human SUMOylation pathway to test the hypothesis as a model system for dissecting host-virus interaction. We have taken two approaches to dissect the roles of SUMOylation for influenza viruses. First, we developed a quantitative FRET (qFRET)-based high-throughput screening for discovering human SUMOyaltion inhibitor(s), which could be used to test the SUMOylation requirement for virus life cycle. Second, we developed an *in vitro* qFRET-Mass spec approach to elucidating critical SUMOyaltion sites of influenza virus M1 protein, followed by forward-genetics testings of the virus with mutations of the SUMOylation sites in the life cycle. We found that IAV and IBV can be completely inhibited by the SUMOyaltion inhibitor, and an essential SUMOyaltion site in M1 protein was identified.

An essential host pathway, human SUMOylation, has been discovered for IAV/IBV life cycle. The requirement of the human SUMOylation pathway for viruses is elucidated on the SUMOylation site of the IAV/IBV M1 protein. A host pathway is demonstrated as essential for the virus life cycle for the first time. The blockage of the essential host pathway for viruses could be a novel strategy for future anti-virus therapeutics with a broad spectrum and no drug resistance development.

Biography

Prof. Liao's research focuses on developing novel quantitative FRET (qFRET) technology for basic and translational research, host–virus interaction, inflammation, and diabetes. Prof. Liao joined the University of California at Riverside as a founding faculty of the Bioengineering Department from the Scripps Research Institute, where he discovered the human sweet receptor genes. Before that, Dr. Liao joined the Genomic Institute of Novartis Research Foundation (GNF) as the Founding Scientist of the GPCR platform, where Dr. Liao led an HTS that resulted in the discovery of S1P1-specific agonist (SEW2871), subsequently leading to the FDA-approved drugs, ozanimod from BMS/Celgene/ Receptos and siponimod from Novartis. Prof. Liao was the first to discover the orally available GLP1 small molecule agonist and the human SUMOylation E3 ligase PIAS family. Prof. Liao is a Fellow of the American Institute of Medical and Biological Engineering (AIMBE), and his work has led to more than 5300 citations and 30 patents.

Bacterial filtration efficiency and viral filtration efficiency of face masks – the role of bacteriophages in textile testing

L. Tvrzová, M. Hrubanová, P. Benešovský, H. Doubková, A. Blahová, P. Malčík, P. Dufková, P. Jarmičová and **P. Nasadil**

Textile Testing Institute, Czech Republic

Bacterial filtration efficiency (BFE) is, according to EN 14683 +AC, the main characteristic of medical face masks effectivity and quality. The method is based on the analysis of bacterial aerosol in Andersen cascade impactor (ACI) containing six stages simulating the different parts of the respiratory tract. The aerosol particles are separated on the base of their aerodynamic size and sediment on agar medium in Petri dishes filled in the impactor. The use of the glass Petri dishes is recommended for the correct particle sedimentation in ACI, but the most of laboratories prefer the disposable plastic dishes, actually. In our study, we evaluated the use of plastic dishes in Andersen impactor for the determination of BFE of medical face masks.

The bacterium *Staphylococcus aureus*, used for BFE testing, allows only limited detection of submicron aerosol particles (on the sixth stage of the ACI). This limitation can be overcome by the use of bacteriophage aerosol and the method of viral filtration efficiency (VFE) testing. The bacteriophage Phi-X 174 with *Escherichia coli* host bacterium was chosen for VFE determination. The determined BFE and VFE values correlate well in the case of masks with high filtration efficiency (99% and more). On the other side, lower values of VFE, comparing with BFE, were determined for masks with the filtration efficiency in the range of 95 – 98 %. There were detected higher numbers of plaque forming units (PFU) on the sixth stage of the Andersen impactor in the case of VFE determination in comparison with colony forming units (CFU) in the case of BFE determination. The VFE testing gives more exact information about the ability of tested mask material to filter viral particles carried by submicron aerosol particles (with the ability to penetrate the lungs). It seems appropriate to supplement the testing of face masks with the test of viral filtration efficiency.

Biography

Ludmila Tvrzová is a microbiologist and researcher at Textile Testing Institute in Brno, Czech Republic. Her current work is focused on microbiological methods of textile testing, filtration efficiency testing and the use of bacteriophages in textile testing, above all. She has more than 15 years of experience in microbiology and microbiology teaching (Masaryk University, Brno, Czech Republic). She published a few novel species descriptions and other papers focused on bacterial taxonomy and biodegradation of organic pollutants.

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Akkermansia munciphila, Bifidobacter bifidum and their extra cellular vesicles induce tolerogenic dendritic cells from patients with Crohn's disease

Shaghayegh Baradaran Ghavami[1], Fatemeh Ashrafian[2], Maryam Farmani[2], Hamid Asadzadeh Aghdaei[1], Seyed Mobin Khoramjoo[1], Abbas Yadegar[3], Shabnam Shahrokh[1] and **Mohammad Reza Zali[1]**

[1]Gastroenterology and Liver Diseases Research Center, Research Institute for Gastroenterology and Liver Diseases, Shahid Beheshti University of Medical Sciences, Iran

[2]Microbiology Research Center (MRC), Pasteur Institute of Iran, Iran

[3]Foodborne and Waterborne Diseases Research Center, Research Institute for Gastroenterology and Liver Diseases, Shahid Beheshti University of Medical Sciences, Iran

Objective: According to recent research, tolerogenic dendritic cells (tDCs) have been suggested as a novel treatment option in autoimmune diseases, especially IBD. Furthermore, the immunomodulatory effects of *Akkermansia muciniphila (A. muciniphila), Bifidobacter bifidum* and their extracellular vesicles (EVs) were reported in many studies. Therefore, the current study was designed to evaluate the tolerogenic effects of *A. muciniphila, B.bifidum* and their EVs on DCs from Crohn's disease patients (CD) and healthy controls.

Methods: Monocyte-derived DCs from Crohn's disease patients and healthy individuals were co-incubated with *A. muciniphila, B.bifidum* and their EVs in two different MOI for 24 hours. The expression of co stimulatory molecules and signal-transducing receptors in DCs were assessed by flow cytometry and Real-time PCR, respectively. Moreover, the level of cytokines (e.g. IL-12 and TGF-β) were quantified by ELISA.

Results: Our results showed that induction of semi-maturation markers CD80 and CD86 of DCs by *B. bifidum* MOI (10 and 100) and its EVs (MOI 1 and 10) are disease-dependent. Additionally, *B.bifidum* significantly induced the TGF-β production in DCs from CD patients ($P < 0.05$) and significantly decreased the production of IL-12 in DCs from CD patients at both MOIs compared with untreated DCs. The expression level of TLR2 and integrin ß8 also were significantly increased, the expression of TLR4 & TLR9 were significantly decreased. *A. muciniphila* and its OMV were not association with decrease inflammation in CD patients.

Conclusions: Several experimental and clinical studies have shown the beneficial effects of probiotic bacteria in immunomodulation of mucosal and treatment of inflammatory diseases DCs. In this study *B. bifidum* and its OMV showed the better effect in modulatory function in DCs of CD patients. Interestingly, we understand *A. muciniphila* cannot be proper probiotic for CD patients.

Biography

I am Shaghayegh Baradaran Ghavami. I have a Ph.D. in microbiology. I am the head of the Inflammatory Bowel Disease (IBD) Lab in Gastroenterology and Liver Diseases Research Center, Research Institute for Gastroenterology and Liver Diseases, Shahid Beheshti University of Medical Sciences, Tehran, Iran. I am interested in the interaction between the gut microbiome and the immune system in autoimmune diseases, especially IBD. I believe that the healthy gut microbiota predominantly contributes to gut immunomodulation, host nutrient metabolism, drug metabolism, and protection against pathogen invasion. My lab spotlight on mucosal healing; IBD patients respond to biological therapy and gut microbiome regeneration. Also, one crucial achievement is producing tolerogenic dendritic cells with probiotics from IBD patients. It is essential stipe to develop dendritic cell therapy for autoimmune diseases. I have more than 20 publications. Also, I have collaborated with Italia and Australia University. My main goal is to find helpful biomarkers according to personalize medicine to increase the efficacy of IBD patients' treatment.

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Evidence for the role of a second Fc-binding receptor in placental IgG transfer in nonhuman primates- consequences for immunotherapy

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Transplacental transfer of maternal antibodies provides the fetus and newborn with passive protection against infectious diseases. However, while the role of the highly conserved neonatal Fc receptor (FcRn) in IgG placental transfer in mammals is undisputed, recent reports have suggested that a second receptor may contribute to transport in humans. We compared the transfer efficiency of plant-derived HIV-specific PGT121 and VRC07-523 antibodies and their high (FcRn) affinity YTE and LS-mutants with mammalian counterparts following passive subcutaneous infusion into macaque dams close to parturition. Unexpectedly, while plant and mammalian Abs exhibited comparable efficiency in mice, plant antibodies were essentially unable to cross macaque placentas. This defect was closely associated with poor Fcγ receptor binding and triggering and altered Fc glycans. Results indicate that IgG maternal-fetal transfer across the three-layer primate placenta requires a second Fc receptor and offers a means of providing cytotoxic treatments during pregnancy and has important clinical implications. Overall, this study points to differentiation in the basic mechanisms of inheritance of maternal antibodies among mammals and has important clinical implications. Monoclonal antibodies have become one of the most important and successful types of human therapeutics, and their use and impact during pregnancy have recently been extensively reviewed, revealing the different rates of transfer and clearance of different mAbs. Plant expression systems are fast and scalable and have become increasingly popular for the production of monoclonal antibodies especially for time critical applications. The failure of plant-derived Abs to efficiently cross the placenta in macaques provides a novel strategy for developing biosimilars of therapeutic Ab treatments that are contraindicated during pregnancy. Such therapies may be beneficial to the mother while preventing harm to the fetus and newborn.

Biography

Dr. Rosenberg, the Founder/CEO, PlantVax, Maryland, received her B.Sc Hons (1st Class) at the University of Queensland and her Ph.D. at the Australian National University. She is an immunologist with >25 years experience with rodent and non-human primate models in autoimmunity, infectious disease and chemical defense: in particular the use of macaques in more translational areas towards the development of recombinant therapeutic HIV antibodies as well as pre-and post-exposure treatments against organophosphate nerve agents and insecticides.

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Detection of Human Papillomavirus in archived bladder and ovarian cancer samples

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Atta-Ur-Rahman School of Applied Biosciences (ASAB), NUST, Pakistan

Problem: Human papillomavirus (HPV) is a well-established causative agent of cervical cancer. However, its role in the development of bladder and ovarian cancer is under debate. Current study evaluated the role of high-risk HPV genotypes 16 and 18 in triggering bladder and ovarian carcinomas.

Methods: A total of 80 formalin-fixed and paraffin-embedded (FFPE) archival tissue specimens of both bladder (n = 40) and ovarian carcinoma (n = 40) were tested for the presence of HPV integrants and HPV 16 genotype and HPV 18 genotype.

Results and conclusion: The PCR results showed that 5% (2/40) of bladder cancer samples were HPV positive with equal prevalence of HPV 16 in both sexes (1:1) while 22.5% (9/40) of ovarian cancer samples came positive for HPV with only one positive for HPV 16. These results indicate association of HPV with bladder and ovarian carcinomas, HPV 16 genotype being more prevalent than 18. The study emphasizes that HPV is a serious issue in low- and middle-income countries where existing methods of prevention are still inadequate or costly. Timely HPV screening can help lower the burden of HPV-induced carcinomas. Furthermore, systematic HPV vaccination program among the young population is paramount.

Biography

BS hon's in Applied Biosciences and MS in Health care Biotechnology with Majors in Cancer Biology. Due to strong interest in Cancer biology and deciphering therapeutic approaches for Cancer in general, I prepared Bacterial ghost's of *E.coli* and MRSA (Multi-drug resistant staphylococcus aureus) strains. Later, I Investigated role of HPV-16 and HPV-18 among ovarian cancer and bladder cancer patients. The results of the study revealed the prophylactic approach of HPV vaccination can save patients, from havocs of chemotherapy and Radiotherapy. After moving to Canadian 2016, I worked as a Research Volunteer at St. Joseph's Health care, Hamilton, where I investigated anti-tumor effect of protein CYB5D2 in renal carcinoma cell lines. I am intending to start PhD in the coming September with goal to analyze the effect of diet, exercise and lifestyle changes on ovarian cancer pathogenesis and to present practical approaches to overcome this havoc disease among women.

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Beyond the margins of radiation treatment: Immunotherapy in combination with radiotherapy

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[4]Department of Radiation Oncology and Molecular Radiation Sciences, Johns Hopkins University, USA

Purpose: Persistent immunosuppression in the tumor microenvironment is a major limitation of cancer immunotherapy. On the other hand, radiotherapy is the most important non-surgical modality for cancer treatment. We investigated the use of immunoadjuvant with a low dose of radiation targeting only the gross tumor volume/sub volume for the treated primary and distant untreated secondary tumor along with the effect in immunologically cold tumors.

Methods and Materials: Syngeneic-murine tumor models were generated for aggressive prostate and pancreas cancers. To mimic the metastatic cancer model, two contralateral tumors were implanted in each mouse either subcutaneously (SQ) or one SQ and one orthotopic where only one SQ tumor was treated. Image Guided Radiotherapy (IMRT) along with a (mouse anti-CD40) in one tumor was given. A single dose of radiation was delivered on planning treatment volume (PTV). The identified dose was further evaluated for PTV vs. gross tumor volume, GTV/sub-volume(sv) of IGRT.

Results: Results showed that radiation with immunotherapy administered to the gross tumor sub-volume can effectively boost abscopal responses in both pancreatic and prostate cancers, significantly increasing survival ($P < .0001$ and $P < .001$, respectively). Results also showed equal or superior responses when using field sizes smaller than the gross tumor volume compared with irradiating the whole tumor volume. These results were buttressed by the observation of higher infiltration of cytotoxic CD8+ T-lymphocytes in the treated tumors ($P < .0001$) and untreated tumors ($P < 0.0001$) for prostate cancer. Significantly higher infiltration was also observed in treated tumors ($P < 0.0001$) and untreated tumors $P < 0.01$) for pancreatic cancer. Moreover, the immune responses were accompanied by a positive shift of proinflammatory cytokines in both prostate and pancreatic tumors.

Conclusions: This approach proffers a radioimmunotherapy dose-painting strategy that can be developed for overcoming current barriers of immunosuppression, especially for immunologically cold tumors.

Biography

Sayeda Yasmin-Karim, MD, MS, Ph.D. is currently a Research Fellow in the Department of Radiation Oncology at Dana Farber Cancer Institute, and Brigham and Women's and Hospital Harvard Medical School, in Boston, Massachusetts, USA. Her current research focuses on the innovation of a treatment model for local and metastatic tumours and the development of a cancer vaccine using the synergic action of radiation, immunotherapy, and nanotechnology for different cancer models. She earned numerous awards locally and internationally. She has numerous research publications in different peer-reviewed journals.

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Algebraic modelling in virology research

O. Letychevskyi

Glushkov Institute of Cybernetics of National Academy of Science of Ukraine, Ukraine

Many biological processes are essentially the conversion of certain types of energy into a form suitable for chemical reactions – the effects of quantum mechanics. We consider the modelling of quantum interactions for the study and research of biological phenomena, in particular, the problem of virus–cell interaction.

The technologies for automatic theorem proving, computer reasoning, and machine learning methods are rapidly developing. Based on this state-of-the-art technology, we have developed an unique algebraic modelling method that is significantly more powerful than the imitation modelling methods used in biology.

Our team of scientists created a model of quantum interactions at the levels of electron transitions, synthesis, and the decomposition of molecules. The algebraic method is multi-level; thus, it studies higher-level entities based on quantum models to consider the interaction of proteins and the corresponding elements of cells and viruses.

A multilevel algebraic model makes it possible to consider the behaviour of biological objects in real time by observing not individual scenarios but a set of possible behaviours that can be infinite. This model provides learning the properties of a substance so as to contribute to the search for new compounds applicable to pharmacology, the creation of a vaccine, and the study of virus behaviour.

One of the experiments involves the study of the interaction of enzymes in the cellular environment in cooperation with the Institute of Virology of the Academy of Sciences of Ukraine. The results of modelling have made it possible to study the effect of an enzyme, such as metalloproteinase.

This is the first algebraic modelling of biological phenomena. It allows for modelling in other areas, including cellular breathing, ageing, and resisting to virus intrusion.

Biography

Doctor Oleksandr Letychevskyi is the head of department at the Glushkov Institute of Cybernetics (Kyiv, Ukraine), and professor of Kherson State University. He has worked as a contractor of Motorola and as a researcher at Missouri University (Rolla, USA). His research interests include algebraic approaches in modelling in natural sciences, model-driven development and cyber security of reliable systems. It includes research in quantum physics and biology modelling (virus-cell interaction), blockchain, hardware development subject domains. He is the author of Algebraic Programming System and technology of Insertion Modelling.

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Pycard and *Bc017158* candidate genes of *Irm1* locus modulate inflammasome activation for IL-1β production

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[2]Department of Research, Fondazione IRCCS, Istituto Nazionale dei Tumori, Italy
[2]National Research Council – Institute for Biomedical Technologies, Italy
[3]Department of Medicine and Surgery, University of Milano-Bicocca, Italy
[4]Diagnosis Center, Instituto Pasteur, Brazil
[5]Laboratory of Biophisics, Federal University of São Paulo, Brazil
[6]Laboratory of Immunopathology, Instituto Butantan, Brazil
[7]Laboratory of Development and Innovation, Instituto Butantan, Brazil
[8]Center of New Target Discovery (CENTD), Instituto Butantan/GSK/FAPESP, Brazil
[9]Development and Innovation Laboratory, Center of Innovation and Development, Instituto Butantan, Brazil
[10]ALCHEMY – Inovation, Research & Development Ltd, University of São Paulo, Brazil

AIRmax and AIRmin mouse strains were phenotypically selected on the basis of a high or low acute inflammatory reaction (AIR), respectively, against a non-immunogenic substance. The significant separation of the two strains during the bidirectional selection process, demonstrated that inflammatory reactivity is submitted to genetic control. In addition to this characteristic, these strains differ widely in susceptibility to infections, autoimmune diseases, and cancer, showing that the genetic changes resulting from the selection of the two lines, impacted pathologies where inflammation plays an important role.

Objective: Mapping of Quantitative Trait Loci (QTL) and the identification of the genes responsible for the phenotypic differences between AIRmax and AIRmin.

Methods: Genome-wide linkage analysis of Single Nucleotide Polymorphisms (SNPs) in a cross between AIRmax and AIRmin lines and sequencing of the QTL in the two strains.

Results: A highly significant linkage signal (LOD score peak of 72) for *ex vivo* IL-1β production limited a 4 Mbp interval to chromosome 7. Locus region sequencing revealed 14 SNPs between AIRmax and AIRmin that narrowed the locus to a 420 Kb interval. Variants were detected in non-coding regions of *Itgam*, Rgs10 and *BC017158* genes and at the first exon of *Pycard* gene, resulting in an E19K substitution in the protein ASC (apoptosis- associated speck-like protein containing a CARD) an adaptor molecule in the inflammasome complex. *BC017158* silencing inhibited IL1-β production by stimulated macrophages and the E19K ASC mutation carried by AIRmin mice impaired the *ex vivo* IL-1β response, the formation of ASC specks in stimulated cells and the sensitivity of this strain to develop tumors induced by chemical agents.

Conclusion: Our results delineate a novel genetic factor and a molecular mechanism affecting the acute inflammatory response. IL-1β and ASC specks play major roles in inflammatory reactions, constituting potential targets for new therapeutic strategies for inflammation-related diseases.

Biography

Workplace: INSTITUTO BUTANTAN, Laboratory of Immunogenetics, Avenida. Dr. Vital Brasil, 1500 - CEP 05503-900 - SP, SP.

Education/Training: Doctor in Immunology at University of São Paulo, Brazil, Post Doctor in Immunogenetics, Institut Curie, Paris, France.

Research line: Over several years we study Immunogenetics using a model of "High" and "Low" responder mouse lines, produced by consecutive generations of bidirectional selective breeding, considering quantitative immunological characteristics, such as the production of antibodies against complex antigens and the inflammatory reaction to non-immunogenic substances. Cellular and molecular biology methods are being used to unravel the mechanisms and genes responsible for the phenotypic differences found between the strains.

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HLA sensitization in the era of covid-19 and the impact on transplant laboratory

Rabab Ali Al Attas, Mohammad Awaji, Amani Mohammed, Kenana Alajlan and **Alanoud Alshami**

Histocompatibility & Immunogenetics Laboratory, Department of Pathology and Laboratory Medicine, and Division of Pediatric Nephrology and Kidney Transplant, Multiorgan Transplant Center, King Fahad Specialist Hospital-Dammam, Saudi Arabia

It is well known that several viral infections are capable of triggering formation of HLA antibodies; however, an association between SARS-CoV-2 & development of anti-HLA antibodies is not yet confirmed. In this study, we compared the prevalence of HLA antibody before & after COVID-19 infection in a cohort of 3 groups included 58 healthy nonsensitized employees (HNEs), 130 kidney transplant recipients (KTRs) & 62 kidney transplant candidates.

There were no significant changes observed in HLA class I antibodies in any of the 3 groups, but evaluation of antibodies to HLA class II revealed a significant change in KTR group (P = .0184) after acquiring COVID-19 infection and in HNE group (P = .0043) when compared to the reported prevalence in a similar population. Although we observed the emergence of convalescent de novo donor-specific antibodies in 2 patients, we did not encounter any rejection episodes in KTR group.

In a separate study during COVID-19 pandemic, we observed 22% discordant results out of 445 FCXM performed during an eight months period in our laboratory & another 7% were invalid due to high background negative control. No study has addressed the impact of COVID-19 pandemic on FCXM and the overall pre-kidney transplant workups or described a solution to deal with these non-specific reactivities. Herein, we analyzed all FCXM results in SARS-CoV-2 seropositive patients and addressed how this pandemic affected significantly the pre-kidney transplant workups, highlighting both technical and financial implications.

In conclusion, COVID-19 infection has the potential to produce class II antibodies but with little effect on preexisting sensitization. These antibodies are likely to be transient and not necessarily causing positive crossmatch with the corresponding antigens.

Further evaluation of these antibodies revealed that these antibodies might creating many false positive or invalid crossmatch results. Transplant laboratories must consider this before test interpretations.

Table 1. Demographic Characteristics of the 3 Cohorts Included in the Study

Cohorts	Age (y): Mean ± SEM	Sex: M/F
Healthy nonsensitized employees (n = 58)	36.3 ± 3.4	54/4*
Kidney transplanted recipients (n = 130)	19.4 ± 1.9	90/40
Kidney transplant candidates (n = 62)	23.3 ± 2.8	36/26

*The 4 women were single nulliparous women.
SEM, standard error of the mean.

Table 2: Number of FCXM included in the Study and the Number and Characteristics of Sera that Gave Discordant (false positive) or Invalid (high NC¥) FCXM Results.

	Number	Percentage
Total Number of FCXM investigated	**445**	
Discordant FCXM results	107	22%
Invalid FCXM results	32	7%
All Problematic FCXM	139	
Patients with Discordant FCXM Results	**88***	
Patient Characteristics		
Pediatric patients	26	30%
Adult patients	62	70%
Male/Female	42/46	48%/52%
Sensitized Patient with Weak€ DSA	19	22%
Patient with Negative DSA	69	87%
Characteristic of the Discordant FCXM		
B+T-	57	64%
B+T+	24	27%
T+ B-	7	9%
Total	**88**	**100%**

¥Negative control
[8]19 sensitized patients out of 88 giving discordant FCXM with weak DSA underwent surrogate cells FCXM in addition to the initial FXCM with their corresponding donors
€Weak DSA = MFI less than 2,000

Biography

Academic Degree:

- MBBS
- Clinical Pathology
- Immunopathology & Molecular Genetics
- 2010-2012: Fellowship in Anderson, USA

Board Certification:

- American Board of Medical Laboratory Immunology (D-ABMLI)
- Accredited ASHI- HLA- lab Director, F (ACHI)

70 researches, Oral Presentations in International and National Conferences/Symposia.

25 Abstract for ASHI Meetings and published in Human Immunology

Publications: 28 publications

Efficient transfected liposomes co-loaded with pNrf2 and pirfenidone improves safe delivery for enhanced pulmonary fibrosis reversion

Xin Chang

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Liaoning Provincial Key Laboratory of Marine Bioactive Substances, Jinzhou Medical University, China
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Pulmonary fibrosis (PF) is an interstitial lung disease with a complex pathological mechanism, and there is currently a lack of therapeutics that can heal it completely. Using gene therapy with small molecules provides a promising therapeutic strategy for synergistically reversing PF. However, improving the intracellular accumulation and transfection efficiency of therapeutic nucleic acids is still a critical issue that urgently needs to be addressed. Herein, we developed lipid nanoparticles (PEDPs) with high transfection efficiency coloaded with pDNA of nuclear factor erythroid 2-related factor 2 (pNrf2) and pirfenidone (PFD) for PF therapy. PEDP can penetrate biological barriers, accumulate at the target and exert therapeutic effects, eventually alleviating the oxidative stress imbalance in type II alveolar epithelial cells (AECs II) and inhibiting myofibroblast over activation through the synergistic effects of Nrf2 combined with PFD, thus reversing PF. In addition, we systematically engineered various liposomes (LNPs), demonstrated that reducing the polyethylene glycol (PEG) proportion could significantly improve the uptake and transfection efficiency of the LNPs, and proposed a possible mechanism for this influence. This study clearly reveals that controlling the composition ratio of PEG in PEDPs can efficiently deliver therapeutics into AECs II, improve pNrf2 transfection, and synergize with PFD in a prospective strategy to reverse PF.

Biography

The reporter has been committed to the research and development of new drug therapy systems for a long time, has a solid research foundation in genes, drugs and combined delivery, and has in-depth research and achieved phased results in the development of lung tissue drug delivery systems and the treatment of lung diseases, and has formed a certain theoretical system. At the same time, she has accumulated practical experience in the synthesis, construction and characterization of novel nanoparticles, the construction of mouse models of pulmonary fibrosis, the extraction, identification and culture of various primary cells, and the behavioral and pharmacodynamic evaluation of nano preparations at the *in vitro* and *in vivo* level, and formed a theoretical system for efficient drug delivery based on lung diseases.

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Intrathecal delivery of dendritic cell immunotherapy cures breast cancer Leptomeningeal disease and protects against reinoculation in immunocompetent preclinical murine models

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[2]Clinical Science & Immunology Program, Moffitt Cancer Center and Research Institute, USA
[3]Tumor Biology, Moffitt Cancer Center and Research Institute, USA
[4]Department of Breast Oncology, Moffitt Cancer Center and Research Institute, USA

Background: Approximately 5% of advanced stage breast cancer (BC) patients will develop incurable leptomeningeal disease (LMD). One reason for poor prognoses is the issue of drug accessibility to tumor sites due to the blood brain barrier (BBB) and blood-cerebral spinal fluid (CSF)-barrier. While the Ommaya reservoir is used clinically to overcome this challenge, there has not been an optimized preclinical model that allows researchers to adequately test novel therapies in the CSF space. Here, we examined the intrathecal (IT) delivery of peptide-pulsed DC immunotherapies in HER2+ and TNBC BC-LMD in immunocompetent animal models.

Methods: We developed an MRI-compatible device called the "murine Ommaya" which mimics the Ommaya reservoir and allows repeated IT administration directly into CSF, bypassing BBB. In a joint effort with Dr. Czerniecki, whose lab have developed a pipeline for screening immunogenic MHC class II peptides from tumor-associated oncodrivers and subsequently generating tumor-targeting DCs. We have created a platform to IT deliver peptide-pulsed (HER2- and HER3-peptides) DC immunotherapy directly targeting BC-LMD. BC-LMD mice were randomized into following groups: 1) HER2-DC IT 2) HER3-DC IT 3) HER2/HER3-DC IT. Efficacy evaluation and functional analysis were performed.

Results and discussion: We created a platform to IT deliver peptide-pulsed DC immunotherapy directly targeting BC-LMD. The median survival of untreated BC-LMD was 15 days. All cohorts given IT immunotherapies have prolonged survival ($p<0.001$). Interestingly, HER2/HER3-DC IT was able to rescue disease mice (71% in HER2+ and 28% in TNBC-LMD) and showed complete tumor regression. Some surviving mice were immune to subsequent tumor rechallenge. In mice CSF, we found evidence of T-cells infiltration, and a robust IFN-γ and IL18 response upon treatment.

Conclusions: Our preclinical data supported a clinical trial (approved) of the IT delivery of peptide-pulsed DC in BC patients with LMD.

Biography

Vincent Law is a Senior Research Associate in Peter Forsyth lab in Neuro-Oncology and Tumor Biology departments at the H. Lee Moffitt Cancer Center and Research Institute in Tampa, USA. He earned his graduate degrees at the University of Calgary and had previously worked for the Translational Lab at the Tom Baker Cancer Center in Calgary, Canada. His research of interest is CNS metastasis including leptomeningeal disease, a rare form of metastasis in the meninges. His lab is focusing on understanding the biology of this universally fatal disease and the immune microenvironment in CSF. Currently, the lab is also developing novel therapies in preclinical and Phase I clinical trials.

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September 11-12, 2023 | London, UK

Therapeutic efficiency of Dexamethasone, Cyprohepatadine and Tetracycline on dermonecrosis induced by *Cerastes cerastes* viper venom

H. Oussedik-Oumehdi, A. Khelfi and **F. Laraba-Djebari**

Laboratory of Cellular and Molecular Biology, Faculty of Biological Sciences, University of Science and Technology Houari Boumediene, Algeria

Viperidae venom is characterized by hemorrhage, edema, vital organ failure and tissue damage. *C. cerastes* venom induces a radial spreading dermonecrosis associated with a massive inflammatory process, often leading to huge sequelae, including amputation. The aim of this study was to evaluate the therapeutic effect of some anti-inflammatory medicines on the dermonecrotic activity of the venom.

NMRI Mice were envenomed by an i.d. administration of the venom (48 µg of venom/ 20 g). The control group received a solution of NaCl 0.15 M. The drugs were then administered [cyproheptadine (i.p. route), dexamethasone (i.p. route), and tetracycline (topical application)] to evaluate their healing properties. The animals were humanely sacrificed 72 hours after envenomation, blood samples were collected, centrifuged, and stored until their use for the determination of NO and selenium. Skin samples (100 mg) were collected and homogenized in phosphate buffer. The levels of NO, MDA, H_2O_2, protein carbonyls, protein thiols, selenium, GSH, and the activities of myeloperoxidase (MPO), eosinophil peroxidase (EPO) and catalase were measured in tissue homogenates. Results were analyzed using one-way analysis of variances (ANOVA) followed by post hoc Tukey's test.

C. cerastes venom induced a necrotizing effect with an intense hemorrhage at the site of envenomation. Dermonecrotic lesions indicated a high toxic potency of the venom and its ability to impair all skin layers within an extensive area (17.50 ± 1.78 mm). All used treatments efficiently reduced tissue necrosis. Treatments significantly decreased MPO and EPO activities, and significantly, reduced NO, MDA, H_2O_2 and protein carbonyl levels in skin tissue homogenates. Dexamethasone and tetracycline significantly increased the antioxidant status as indicated by enhanced protein thiols, GSH and selenium levels, and catalase activity.

In conclusion, data suggest that the use of anti-inflammatory medicines would constitute a promising therapeutic strategy to avoid tissue damage and potential permanent sequelae following envenomation.

Biography

Professor Oussedik-Oumehdi Habiba obtained the doctorate in Biochemistry-Immunology in 2007. She is a Research Director within the team « Biomolecules: Mode of Action, Immunotherapy and Immunodiagnosis » directed by Professor Laraba-Djebari Fatima in the Laboratory of Cellular and Molecular Biology, at the Faculty of Biological Sciences of USTHB. She teaches many courses, including Cellular and Molecular Signaling, the Molecular Basis of Pathogenesis and Pharmacotechny. She has several research projects on the elucidation of the mechanisms underlying tissue damage and necrosis induced after viper envenomation, and the application of Immunotherapy and Biotherapy and, currently has a project focusing on the evaluation of biotherapy using nanotechnology in the treatment of the diabetic foot.

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Dermoscopic features of cutaneous tuberculosis: A descriptive study unveiling novel findings

Swati Prasanna and **Vidya Kharkar**

Seth G.S. Medical College and K.E.M. Hospital, India

Cutaneous tuberculosis (TB) is a rare form of extrapulmonary TB that presents diagnostic challenges due to the limited effectiveness of conventional techniques in detecting the causative agent, Mycobacterium tuberculosis. The application of dermoscopy in analyzing infective granulomas such as cutaneous TB remains relatively unexplored. A study was conducted involving 31 patients diagnosed with cutaneous TB. Among the participants, 14 were males and 17 were females, with a mean age of 31 years (ranging from 6 to 71 years). Live images were captured using a Dinolite AM4113ZT dermoscope, employing adjustable polarization and magnifications of 50x and 200x. The most prevalent subtype observed was lupus vulgaris, accounting for 32.26% of the cases, followed by scrofuloderma (22.58%), papulonecrotic tuberculid (16.13%), tuberculosis verrucosa cutis (9.68%), lichen scrofulosorum (6.45%), erythema induratum (6.45%), and resolved lupus vulgaris (6.45%). In all patients, yellowish-orange globules, indicative of dermal granulomas, were consistently observed, representing a prominent feature (100%). Other notable findings included white scales (38.71%), white structure less areas (77.42%), patulous follicles with plugging (25.81%), white streaks (61.29%), and milia-like cysts (45.16%). Distinct vascular patterns, such as hairpin-shaped vessels with dots (22.58%) and linear vessels (35.48%), were also consistently observed. Additionally, newer findings included the crown of vessels and perifollicular pallor in lichen scrofulosorum, as well as radiating white streaks in papulonecrotic tuberculid. The dermoscopic insights gained from this study provide valuable diagnostic information for cutaneous TB and highlight the potential of dermoscopy as a quick and non-invasive tool in identifying these infective granulomatous disorders.

Biography

Swati Prasanna was born on November 4, 1995, in Chhattisgarh, India. She secured an All India Rank (AIR) of 425 in the National Eligibility cum Entrance Test (NEET) and pursued her MBBS at Seth G.S. Medical College and KEM Hospital, one of India's top medical institutions. With an impressive AIR of 170 in NEET, she went on to specialize in Dermatology, completing her MD at the same institute. Swati has published research papers in renowned peer-reviewed journals, focusing on lichen sclerosus, cutaneous tuberculosis, and metal hypersensitivity syndrome. Her research findings have been presented at international conferences in 2023, earning her the prestigious Prof D K Gupta Award and scholarships for International Dermacon and International Leprosy Congress. She is an active member of the Indian Association of Dermatologists, Venerologists and Leprologists (IADVL) and the Association of Cutaneous Surgeons of India (ACSI). Her primary interests lie in Dermatosurgery and Clinical Dermatology.

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Covid-19 effect on patients with noncommunicable diseases: A narrative review

Mai Elaarag[1], Ahmad R. Al-Qudimat[1,2], Mohamed B. Al Darwish[1], Raed M. Al-Zoubi[1,3,4], Mohamed Amine Rejeb[1], Laxmi K. Ojha[1], Abdulqadir J. Nashwan[5], Timoor Alshunag[2], Karam Adawi[2], Abdelfettah El Omri[1], Omar M. Aboumarzouk[1,6,7], Aksam Yassin[1,8] and **Abdulla A. Al-Ansari[1,9]**

[1]*Department of Surgery, Surgical Research Section, Hamad Medical Corporation, Qatar*
[2]*Department of Public Health, Qatar University, Qatar*
[3]*Department of Biomedical Sciences, College of Health Sciences, Qatar University, Qatar*
[4]*Department of Chemistry, Jordan University of Science and Technology, Jordan*
[5]*Nursing Department, Hamad Medical Corporation, Qatar*
[6]*College of Medicine, Qatar University, Qatar*
[7]*School of Medicine, Dentistry, and Nursing, the University of Glasgow Glasgow, UK*
[8]*Center of Medicine and Health Sciences, Dresden International University Dresden, Germany*
[9]*Hamad General Hospital, Hamad Medical Corporation, Qatar*

Background and Aims: On March 11, 2020, the WHO has declared COVID-19 a global pandemic, affecting our day-to-day lives. Physical distancing and lockdown made significant obstacles to populations, particularly healthcare systems. Most healthcare workers were reallocated to COVID-19 facilities. Noncommunicable disease patients were given low priority and are at a higher risk of severe COVID-19 infection, which disrupted the treatment and disease management of these patients. This review aimed to assess the effect of COVID-19 on different types of noncommunicable diseases and the severity it may cause to patients.

Methods: We have conducted a review of the literature on COVID-19 and noncommunicable diseases from December 2019 until January 2022. The search was done in PubMed and Cochrane for relevant articles using variety of searching terms. Data for study variables were extracted. At the end of the selection process, 46 papers were selected for inclusion in the literature review.

Results: The result from this review found that the COVID-19 pandemic has affected the efficiency of the patient's treatment indirectly by either delaying or canceling sessions, which solidified the need to rely more on telemedicine, virtual visits, and in-home visits to improve patient education and minimize the risk of exposure to the patients. The major and most common types of noncommunicable diseases are known to be related to the severe outcomes of COVID-19 infection. It is strongly recommended to prioritize these patients for vaccinations against COVID-19 to provide them with the protection that will neutralize the risk imposed by their comorbidities.

Conclusion: We recommend conducting more studies with larger population samples to further understand the role of noncommunicable diseases (NCDs) in this pandemic. However, this pandemic has also affected the efficiency of NCDs treatment indirectly by delaying or canceling sessions and others.

Biography

I am Mai Elaarag, a BSc with focus areas in health sciences and biology graduate. I was born in Canada but home to me is Qatar, the country I grew up in. I work as a Clinical Research Officer at Hamad Medical Corporation in Qatar and recently got accepted into a MSc in Clinical Research program. My interest in science started during my high school, biology was the only subject I enjoyed studying for while my interest in research started after I graduated university. The achievements that I am proud of is having 6 publications in just one year, I wouldn't have done this without my patience and stubbornness to strive to the better, in addition to my colleagues and mentors at work. I hope to complete my PhD in the future and to make an impact on this big research world.

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Exploring unique immune cell population by dissecting tumor immune microenvironment in hospitalized hepatocellular carcinoma and ovarian cancer patients

Saif Ullah Afridi[1,2,4], Zhiyuan Wu[1], Guohe Song[2], Meiying Zhang[2], Shyamal Goswami[2], Huijuan Yang[3] and **Xiaoming Zhang[2]**

[1]Department of Pediatric Intensive Care Unit, Guangzhou Institute of Pediatrics, Guangzhou Women and Children's Medical Center, Joint Center for Infection and Immunity, Guangzhou Medical University, China
[2]The Center for Microbes, Development and Health, Key Laboratory of Molecular Virology and Immunology, Institut Pasteur of Shanghai, Chinese Academy of Sciences, China
[3]Department of Gynecological Oncology, Shanghai Cancer Center, Fudan University, China
[4]Section Biochemistry & Molecular Genetics Department of Physical Therapy, Faculty of Allied Health Sciences, Kohat University of Science and Technology, Pakistan

Backgrounds: Worldwide cancer is among the top ten leading causes of mortality and morbidity. Determination of accurate disease staging plays a vital role in prognostic evaluations and therapeutic decisions. Although numerous strategies have been tested so far, the complex interactions in between tumors and their growing microenvironment remain to be elucidated well.

Methods: Here-in, we dissected the Tumor Immune Microenvironment in hospitalized HepatoCellular Carcinoma (HCC) and Ovarian Cancer (OVT) Patients using standard techniques including FACS, 10X Genomics (blood / cells) and mFIHC (Tissues) analysis etc.

Results: To assess the plasticity and phenotypes of immune cells within the OVT and HCC Tumor Immune microenvironment at single-cell level, we identified two distinct immune cell populations known is HLA-DR^{hi} Treg (OVT) and CD68+CD206+CCL18+ macrophages (HCC) in two different cancer types. First we recognized that the HLA-DR^{hi} Treg population in the peripheral blood was significantly increased in cervical squamous cell carcinoma (CSCC) patients compared to pre cancer patients and healthy donors. Quantitative multiplexed immunohistochemistry revealed that an increase in the number of tumor infiltrating HLADR^{hi} Tregs is associated with unfavorable classical risk parameters of advanced disease stage and stromal invasion. Notably, we also identified a subset of M2 macrophage with high expression of CCL18 and transcription factor CREM that was enriched in advanced HCC patients, and potentially participated in tumor progression.

Conclusions / Learning Points: In the current study, we identify and characterized two unique populations of highly activated and immunosuppressive HLADR^{hi} Tregs (in CSCC patients) and M2 like CD68+CD206+CCL18+ macrophages (in HCC patients). An increased HLADR^{hi} Treg and CD68+CD206+CCL18+ macrophages frequency may be a potential biomarker to stratify CSCC / HCC patients and to evaluate therapeutic efficacies in personalized immuno-oncology studies.

Biography

Dr. Saif Ullah Afridi is working as an Associate Professor & Head of Department at the Faculty of Life Sciences, Sarhad University of Science & Information Technology (SUIT), Mardan Campus, Khyber Pakhtunkhwa, Pakistan. He has recently completed his Ph.D. in Molecular Medicine with an Immunology specialization (2015) from University of Karachi, Pakistan. Recently, he completed his Postdoc Research training (June 2018-2021) in Cancer Immunology & infections at the Institute Pasteur of Shanghai – Chinese Academy of Sciences (IPS-CAS), Shanghai China. Dr. Afridi has published around 20 ISI indexed research articles & 2 book chapters and completed 3 Research Projects (1 million $) as a Principal Investigator with numerous awards.

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Isolation and characterization of two novel phages as a possible therapeutic alternative against multi-drug resistant *E. coli*

Ban O. Abdulsattar and **Abdulrahman A. Abdulhussein**

Department of Biology, College of Science, Mustansiriyah University, Iraq

Escherichia coli is one of the most common pathogens around the world, causing a wide range of infections. Most strains are multidrug resistant to antimicrobial therapy, leading to therapeutic options limitation. Because of increasing numbers of antibiotic resistance bacteria and lack of efficient control methods for multidrug resistant bacteria dissemination, phages are one of the promising alternatives that target bacteria specifically and effectively. Their highly specific host ranges and ability to kill only the target pathogenic bacteria selectively characterize phages. However, several challenges and limitations in phage therapy regarding management of multidrug resistant bacteria require more investigation. In this study, two novel lytic phages referred to as AAA1 and AAA2 were isolated from the Tigris River, Baghdad, IRAQ, characterized for their lytic efficiency, functional stability and characteristics against multidrug resistant *E. coli* host. Phage AAA1 lysed drug resistant *E. coli* whereas AAA2 showed no lytic activity. The two phages were stable in the temperature range of 4°C to 37°C. The tolerance of AAA1 phage to pH level was higher than AAA2. The AAA1 phage is a promising candidate to treat or control multi-drug resistant (MDR) *E. coli* strains.

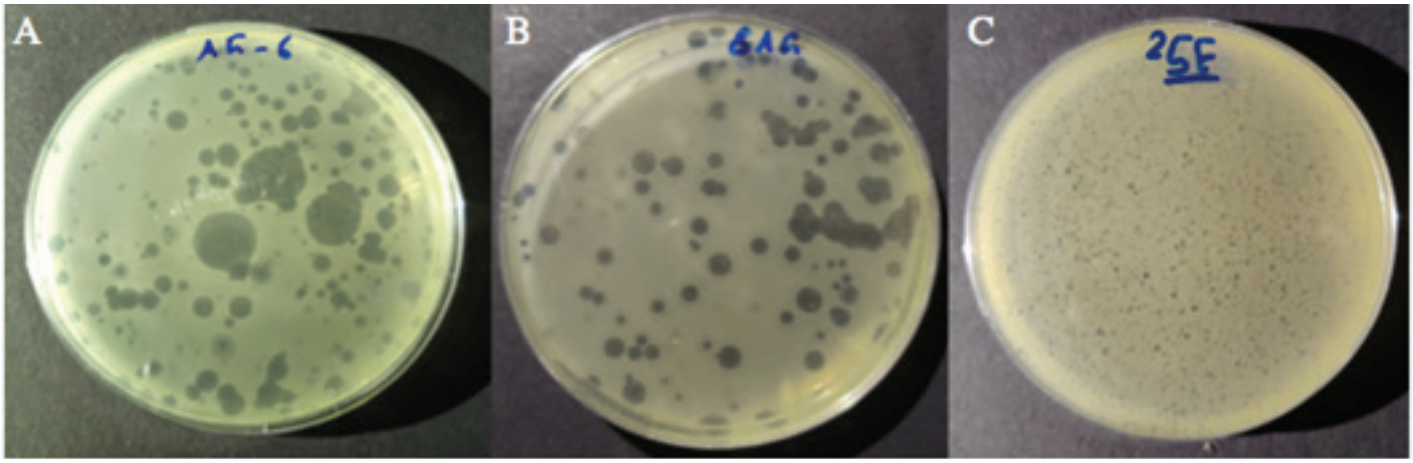

Figure 1. *Morphological observation of plaques. (A): Phages isolation resulted in various plaque size; (B) Morphologies of AAA1 plaque; (C): Morphologies of AAA2 plaque.*

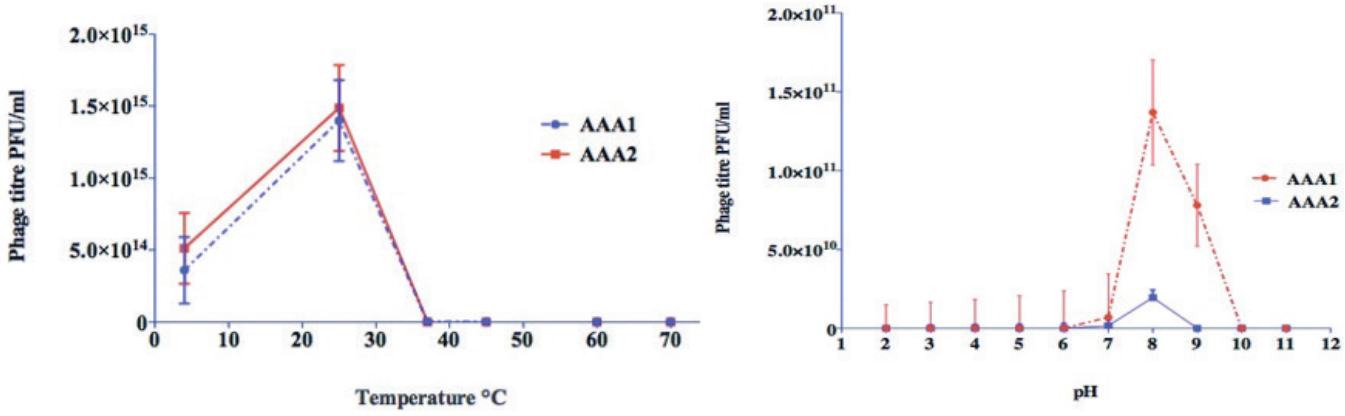

Figure 2: *Thermal and pH stability of the isolated phages.*

Biography

Academic Achievements and Qualifications:

- PhD in Microbiology/Virology, School of Biological Sciences/ University of Reading/UK, 2017. Thesis title: Coronavirus proteins and their directed evolution to inhibit virus replication
- M.Sc. in Medical Microbiology, Microbiology Department/ College of Medicine/ Baghdad University, 2008. Thesis title: The effect of Carnberry juice and Lactobaciili on Pseudomonas aeruginosa isolated from urinary tract infectios
- B.Sc in Microbiology, Biology department/College of Science/ Baghdad University, 1995

Working Positions at Mustansiriyah University, Iraq (2001-present):

- Assistant professor in Microbiology/ gene therapy 2020
- Lecturer 2011 to 2020
- Assistant lecturer 2008 to 2011
- Lab assistant from 2001-2008

Teaching

- Entomology lab
- Pathogenic bacteriology lab
- Genetic engineering lab
- Clinical analysis lab
- Pathogenic bacteriology
- Nanotechnology

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TGFβ1-high glucose reprogramming in immune cells: Cardio-metabolic consequences

Kareem Awad

Institute of Biomedicine, Faculty of Medicine, University of Turku, Finland
Department of Therapeutic Chemistry, Institute of Pharmaceutical and Drug Industries Research, National Research Centre, Egypt

The diversity of metabolic reprogramming mechanisms in immune cells widely contributes to consequences on the cardio-vascular system. This deteriorative consequences are of complex nature and rely on heterogeneous pathogenic/non-pathogenic stimuli (1, 2). We aimed at studying the effect of hyperglycaemia on transforming growth factor beta 1 (TGFβ1) in immune cells and were able to demonstrate its dual role in monocytes/Macrophages.

Furthermore, our results show how different pathogenic stimuli may modulate metabolism in immune cells and to what extent this could affect cardio-vascular deteriorative consequences. Results show specific glycolysis/stimulus pattern suspecting a leading a role of TGFβ1 signaling under different glucose concentrations in human monocytes/macrophages.

In conclusion, hyperglycaemia is an essential metabolic factor that based on the environmental stimuli of the immune cells may contribute to deteriorative cardio-metabolic consequences.

Biography

My research concerns human immune cells responses to different pathogenic and non-pathogenic stimuli as well as the interaction of these cells with the surrounding nerves or vascular neighboring cells. So, my previous work within years of experiences in different scientific schools in Egypt, Finland and Germany focused on the responses of these cells to pathogens such as influenza viruses' strains as well as signals from abnormal environmental contexts such like hyperglycaemia or tumor cells. In this sense, I targeted diseases such as diabetes, influenza virus infection and cancers specifically the brain tumor glioblastoma. My last degree obtained from Cairo University is my PhD in Pharmaceutical Sciences "Biochemistry", holding at the moment the position of a researcher at the National Research Centre of Egypt. More about my publications can be found on https://orcid.org/0000-0003-1007-9632.

Immunology of implantation in endometriosis and adenomyosis

Wolfgang Küpker and **Jon Aizpurua**

IVF Baden Baden, Germany

With the delineation of the pathogenetic background of endometriosis and adenomyosis fertility problems of patients displaying with this disease are characterized in particular with regard to the immunology of the preimplantation endometrium.

Results of a specific immuno-mapping of the endometrium will be presented and the success of different regimens of immune-therapy.

Biography

Between 1973 and 1979 Professor Dr. Wolfgang Küpker (MD, PhD) studied art history, philosophy and German literature at the University of Freiburg, then theology and philosophy at the Universities of Göttingen and Zürich. From 1979–1985 he studied human medicine at the Free University of Berlin, followed by clinical training at the University Schleswig Holstein in Lübeck where he finally served as Vice Chairman of the Department of Obstetrics and Gynecology until 2003. From 2003 to 2006 he was Chairman of OB/Gyn at the Central Hospital in Bremen Nord. Since 2007 he held a position as Director of the Department of Minimal Invasive Gynecology, Endometriosis and Reproductive Medicine at the Klinikum Mittelbaden in Bühl and Baden Baden. Since 2020 he is Medical Director and CEO of IVF Baden Baden.

He performed extensive research in the field of Reproductive Medicine and Endometriosis at the University of Schleswig Holstein in Lübeck and has been maintaining close scientific collaboration with the Free University Bruxelles and the Rockefeller University and Weill Cornell Medical Center in New York. He published more than 300 articles and book chapters. He gives frequently lectures, nationally and internationally.

His particular specializations and interests are in Operative laparoscopy, Operative oncology, Endometriosis, Assisted Reproduction and Male infertility.

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The association of hypertension with increased mortality rate during the covid-19 pandemic: An update with meta-analysis

Doaa M Sabir[1], Ahmad R. Al-Qudimat[1,2], Ayisha Ameen[1], Heba Alkharraz[1], Mai Elaarag[1], Ayisha Althani[1], Kalpana Singh[1], Wassim M. Alhimoney[1], Raed M. Al-Zoubi[1,3,4] and **Omar M. Aboumarzouk[1,5,6]**

[1]Surgical Research Section, Department of Surgery, Hamad Medical Corporation, Qatar
[2]Department of Public Health, QU-Health, College of Health Sciences, Qatar University, Doha
[3]Department of Biomedical Sciences, QU-Health, College of Health Sciences, Qatar University, Qatar
[4]Department of Chemistry, Jordan University of Science and Technology, Jordan
[5]College of Medicine, Qatar University, Qatar
[6]School of Medicine, Dentistry and Nursing, The University of Glasgow, UK

Background and Aim: The impact of multiple risk factors on COVID-19 mortality has been previously reported in multiple systematic reviews and meta-analyses. The aim of this review is to provide a comprehensive update on the association between hypertension (HTN) and mortality in patients with COVID-19.

Methods: A systematic review and meta-analysis were performed and followed the Preferred Reporting Items for Systematic Reviews (PRISMA) guidelines. A search was achieved using PubMed, Scopus, and Cochrane Databases for research publications on hypertension, COVID-19, and mortality published between December 2019 and August 2022.

Results: A total of 23 observational studies involving 611,522 patients from 5 countries (China, Korea, the UK, Australia, and the USA) were included in our study. The confirmed number of COVID-19 with HTN cases in each study ranged from 5 to 9964. The mortality ranged from 0.17% to 31% in different studies. Pooled results show that the mortality rate of COVID-19 among the included studies ranges from a minimum of 0.39 (95% CI 0.13–1.12) to a maximum of 5.74 (95% CI 3.77–8.74). Out of the 611,522 patients, 3119 died which resulted in an overall mortality prevalence of 0.5%. Subgroup analyses indicated that patients with COVID-19 who have hypertension and male patients had slightly less risk of mortality than female patients [the percentage of men>50%; OR 1.33: 95% CI (1.01, 1.76); the percentage of men≤50%: OR 2.26; and 95% CI (1.15, 4.48)]. Meta-regression analysis results also showed a statistically significant association between hypertension and COVID-19 mortality.

Conclusion: This systematic review and meta-analysis suggests that hypertension may not be the only risk factor associated with the increased mortality rate during the COVID-19 pandemic. In addition, a combination of other comorbidities and old age appears to increase the risk of mortality from COVID-19.

Biography

Mai's Biography

I am Mai Elaarag, a BSc with focus areas in health sciences and biology graduate. I was born in Canada but home to me is Qatar, the country I grew up in. I work as a Clinical Research Officer at Hamad Medical Corporation in Qatar and recently got accepted into a MSc in Clinical Research program. My interest in science started during my high school, biology was the only subject I enjoyed studying for while my interest in research started after I graduated university. The achievements that I am proud of is having 6 publications in just one year, I wouldn't have done this without my patience and stubbornness to strive to the better, in addition to my colleagues and mentors at work. I hope to complete my PhD in the future and try to make an impact on this big research world.

Doaa's Biography

I'm Dr. Doaa Mahmoud Eisa Sabir, a Sudanese living in Qatar. I received my MBBS degree in 2019 from Al Gazera University in Sudan. Consequently, I completed a 1 year of internship at Hamad Medical Corporation (HMC) in 2021. I had the opportunity to work during the COVID-19 pandemic at HMC for 6 months. I'm glad to mention that I passed IFOM exam, plab1 exam, OET exam and TOEFL exam. In addition, I participated in multiple research studies in different roles, such as, data collection, writing the manuscripts and analyzing the results. And this has immensely increased my interest in the research field leading to me achieve 3 publications, and I'm eager to enrich my future career with more publications and effective studies. Currently, I am working as a physician trainee at B Health company in Qatar.

Cellular dual effects of UVA & controlled drug release

Julia Li Zhong[1], Mengqi Liu[1], Yu Ren[1], Yujiao Chen[1], Xiao Huang[1], Chao Qi[1], Zhiyong Chen[2] and **Zailiang Yang[2]**

[1]Key Laboratory for Biorheological Science and Technology of Ministry of Education, Bioengineering College of Chongqing University, China
[2]Tumor Section, Fuling Hospital, Chongqing University China

Both solar UV radiation and radio therapy cause significantly skin and potential internal damage. Solar UV has two sides: either beneficial or harmful effects. In order to have and medicine administration simultaneously for skin dermatitis, Acetyl-11-keto-β-boswellic acid (AKBA) loaded Zinc Oxide (ZnO) nanoparticles of which drug release behavior is UV-controlled. Such nanoparticles can not only reflect UV but also transfer the energy to release AKBA which presents an excellent antioxidant and anti-inflammatory effects. In addition, they are biocompatible to skin cells. Due to ROS production original from both radio-therapy and UVA irradiation, we are currently seeking in combining radiation dermatitis protection and medicine administration simultaneously for radiation protection and therapy by using SOD as well as AKBA to load into nano-micro needle to reduce the side effects of the radiation therapy, which is potential beneficial and clinical relevance.

Biography

Julia Li Zhong (Professor, PhD & MD)

- Professor of Skin-Photobiology, Bioengineering College of Chongqing University.
- Key member of of Chinese Society of Free Radical Biology and Medicine.
- Chinese Society of Photobiology, Head of Experimental Dermatology of Chongqing.
- 50 papers in journals such as *Free Radical Biology & Medicine, Oxid Med Cell Longev.,* etc.
- Invited speaker/host: ISUP & ESP conference, 2023, 2019, 2017.
- SKIN@Bath Symposium, 2024, 2022, 2019, 2017.
- Supervised 18 master students and 9 Ph.D. students.

Research Interest:

- Photobiology. UVA radiation human skin cells and mouse model; Skin care (beauty products) & SPA medicine.
- Dermatology, UVA therapy and drug release: Iron chelation therapy. Skin diseases such as psoriasis and cancer related research etc.

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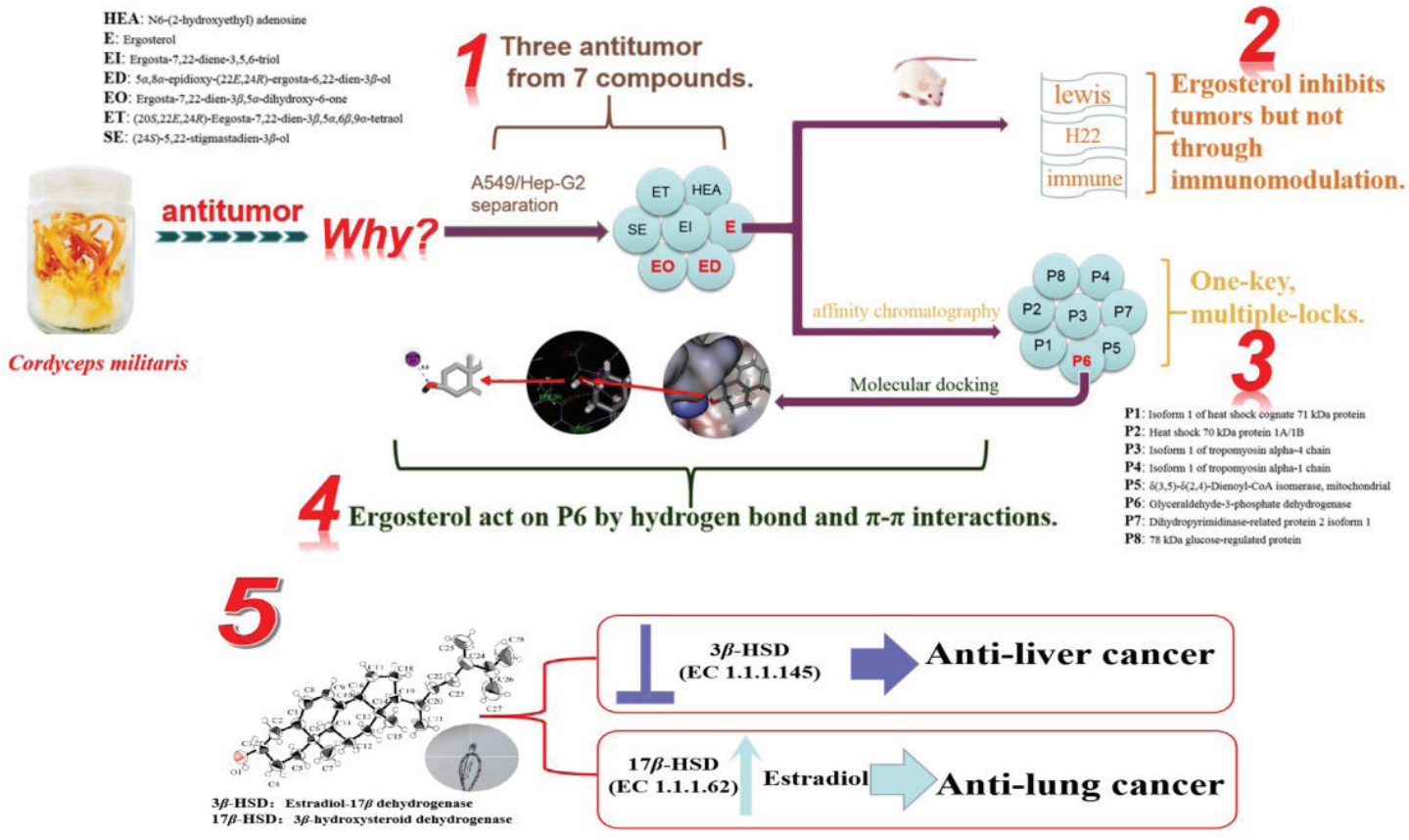
Analysis of active components and manufacturing technology *Cordyceps militaris* in silkworm

Yujiao Chen, Jun Cao, Guixue Wang and **Julia Li Zhong**

Guizhou Aerospace Intelligent Agriculture, Chongqing University, China

The chemical composition and efficacy of *Cordyceps militaris* are similar to that of natural *Cordyceps sinensis*, but the content and activity of chemical components are different due to different strains, cultivation methods and extraction and separation methods. However, large-scale cultivation, active ingredient production and medicinal use are the key and difficult points in the industrial research of *C. militaris*. In this study, the silkworm chrysalis was used as raw material to carry out the large-scale cultivation of *C. militaris*, manufacturing technology of active components, the gene sequencing of fruiting body, enzyme gene analysis of secondary metabolic pathway, the main active components and medicinal evaluation, and the anti-liver cancer application research. To sum up, the solid-state large-scale culture technology of *C. militaris* Haining strain was established. The content of cordycepin, N6- (2- hydroxyethyl)



adenosine, and ergosterol in the obtained fruiting body were relatively high. Furthermore, the genome of *C. militaris* HN was mapped in detail at chromosome level, and 19 key enzymes of HN ergosterol metabolism pathway provided the foundation for its biosynthesis. Based on solvent extraction and industrial chromatography technology, a one-step production process of cordyceps polysaccharide, high-purity cordycepin, N6-(2-hydroxyethyl) adenosine and ergosterol was established. These active ingredients/monomers prove that *C. militaris* HN can improve sleep quality and inhibit lung cancer growth through multi-component interaction in mice. It is preliminarily clarified that *C. militaris* HN can down-regulate the expression of 3 *β*-hydroxysteroid dehydrogenase in HepG2 cells by ergosterol, and then play a role in inhibiting the growth of liver cancer, which provides a new mechanism for the application of *C. militaris* HN as raw materials for liver cancer drugs. These conclusions provide technical support for large-scale culture of *C. militaris*, the preparation of effective components and medicinal use.

Biography

Assistant Director, The National Engineering Research Center of Supercritical Fluid Technology and Equipment, China Aerospace Science and Industry Corporation. Doctor of engineering, *Bioengineering College of Chongqing University*. Deputy general manager and chief engineer, *Guizhou Gui'an Academy of Precision Medicine Co. Ltd.* Deputy chief engineer, *Guizhou Aerospace Intelligent Agriculture Co. Ltd*. Director of college of biological engineering alumni association of chongqing university. Deputy secretary-general, Chinese Medicine Modernization Community, China Association of Chinese Medicine (2017-2022). Mainly engaged in the modernization of *Traditional Chinese Medicine*, gene sequencing in the field of scientific research and research results transformation related work.

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SCIENTIFIC ABSTRACTS

DAY 2

EURO-GLOBAL SUMMIT ON ADVANCES IN CLINICAL AND CELLULAR IMMUNOLOGY

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Euro-Global Summit on Advances in Clinical and Cellular Immunology

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Epidemiological profile of Ebola virus disease in the Boké region 2014-2018

Fatoumata Doumbouya[1], Claude Ngona Mandro[2] and **Salomon Corvil[3]**

[1]Field Epidemiologist, Ministry of Health, Guinea
[2]Field Epidemiology Training Program Mentor, AFENET, Guinea
[3]Field Epidemiology Training Program Resident Advisor, AFENET, Guinea

Introduction: Of the 28610 confirmed cases of Ebola Virus Disease and 11308 deaths recorded during the Ebola outbreak between 2014 and 2016 in West Africa, 3811 (13%) confirmed cases and 2543 (22%) deaths were recorded in Guinea. Since the occurrence of the Ebola epidemic in the Boké region, no data analysis was done to characterize the cases to guide the ministry during future outbreaks hence the description of this profile.

Methods: A descriptive analysis was performed. The National health security agency of the Ministry of health database was used. The WHO definitions of suspected, probable and confirmed cases were adopted. Data were analyzed using EPI-Info 7.2 and Excel. Proportions, ratios, incidence, median and ranges were calculated.

Results: There were 67 laboratory-confirmed and 23 probable cases. Median age: 30 (0 to 85) years. Were more affected: 50 years and older with a cumulative incidence of 10 cases/100,000 inhabitants followed by 30 to 49 years old with 7 cases/100,000 inhabitants. Housewives: 11 (12%) and health care workers: 6 (7%) were most representative. Cumulative incidence was highest in the prefecture of Boffa with 9 cases/100,000 inhabitants followed by Fria with 8 cases/100,000 inhabitants and Boké with 4 cases/100,000 inhabitants. All of these areas were large conglomerations, two of which (40%) are mining areas and one (20%) is a fisherman.

Conclusions: Housewives, health care workers, mining areas and fishermen were the most affected by the outbreak due to the movement of the population. We recommended the correct use of personal protective equipment by health care workers, define the case definition algorithm for early detection of cases, strengthen surveillance at the coastal level, carry out vaccination among high-risk persons such as housewives and health care workers.

Biography

Dr. Fatoumata Doumbouya has a master in Field Epidemiology Training Program (FETP) from the Ki-Zerbo University of Ouagadougou. She has previously completed intermediate and frontline FETP tiers. Currently she is working for the African Field Epidemiology Network (AFENET) as a mentor at frontline and intermediate FETP building capacity of Ministry of Health and Livestock staff to early detection and outbreak response. Prior to this position, she worked for the same organization as a poliomyelitis consultant. Her main role was active case finding for acute flaccid paralysis and other immunization preventable diseases including the coordination of activities vaccination supplement. For the Ministry of Health, Dr. Doumbouya worked at the Boké Regional Health Directorate as the epidemiological surveillance officer. She presented at several international conferences such as AFENET scientific conference 2018 in Maputo, Global TEPHINET scientific conference 2019 in USA and the epidemiology congress of Canada in 2021.

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Role of mitochondrial DNA biomarker in chronic and late acute graft-versus-host disease in children

Shima Azadpour[1,2], Sayeh Abdossamadi[2], Bernard Ng[3], Elena Ostroumov[2], Geoffrey D.E. Cuvelier[4] and **Kirk R. Schultz[2]**

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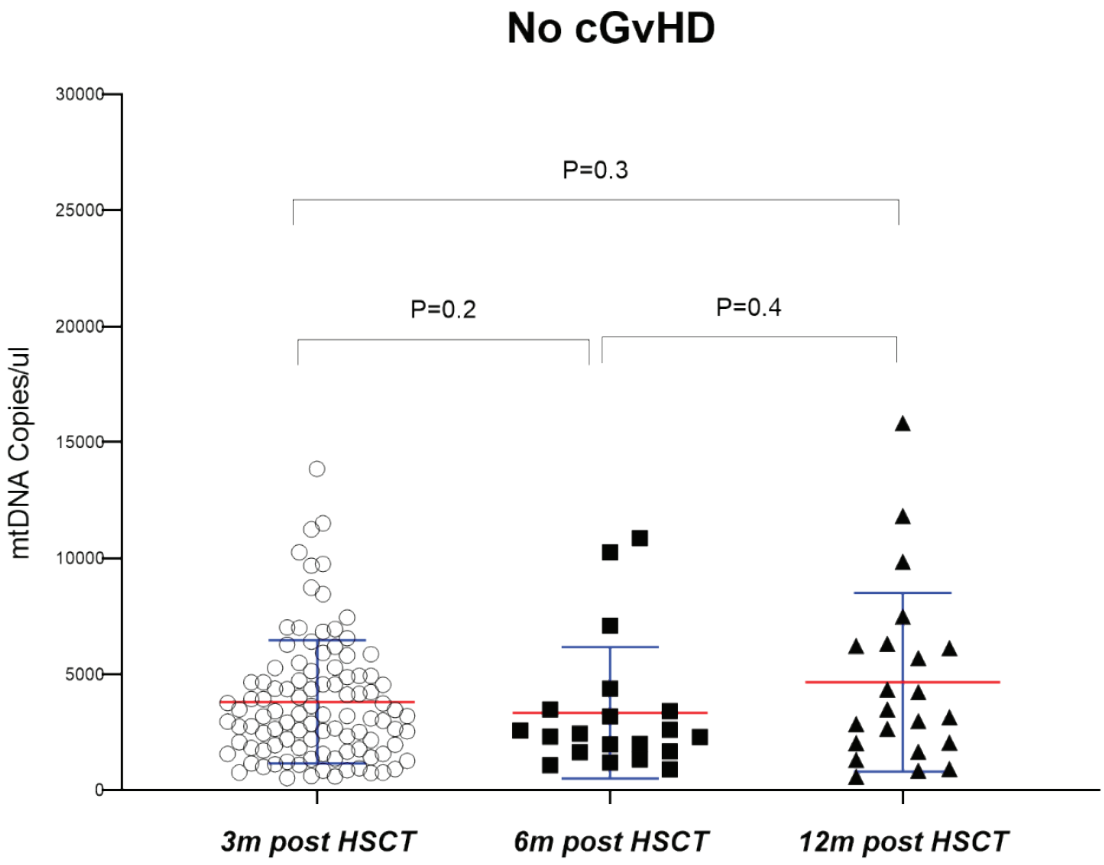
[2]Michael Cuccione Childhood Cancer Research Program, British Columbia Children's Hospital Research Institute, University of British Columbia, Canada
[3]Department of Statistics, Centre for Molecular Medicine and Therapeutics, British Columbia Children's Hospital, University of British Columbia, Canada
[4]Pediatric Blood and Marrow Transplantation, Cancer Care Manitoba, University of Manitoba, Canada

Background: Chronic graft-vs.-host disease (cGvHD) is a major long-term complication of hematopoietic stem cell transplantation (HSCT) resulting in high levels of morbidity and mortality post-HSCT. Few biomarkers for prediction and early diagnosis of cGvHD are available. Previously, we found that mitochondrial DNA (mtDNA) is elevated in adults with chronic graft-versus-host disease (cGvHD), acting as an endogenous source of TLR9 agonists to augment B cell responses. To further evaluate the role of mtDNA in cGvHD, we evaluated mtDNA plasma expression in a large pediatric cohort from the ABLE study.

Methods: Plasma cell-free mtDNA (cf-mtDNA) copy number was isolated from plasma and quantified using digital PCR by amplification of MT-CO1 and MT-ND1 human mitochondrial genes. Two assays probe with FAM and VIC fluorescent dyes were used to increase accuracy and efficiency. Two evaluations were performed: a) before the onset of cGvHD or late aGvHD at day and b) at the time of onset cGvHD.

Results: Comparing day 100 samples in patients developing late acute GvHD after day 100 to the 3-month samples in controls with no cGvHD/no late acute GvHD, higher levels of cell-free mtDNA were found in the late acute GvHD cohort associated with VIC - MT-CO1 assay. Most significant was that plasma mtDNA concentrations were elevated in patients at the onset of cGvHD. There was no significant elevation of plasma cell-free mtDNA at day 100 after HSCT in patients who later developed cGvHD compared with no cGvHD controls with mtDNA measured by the VIC - MT-CO1 assay.

Conclusions: Our study shows that cf-mtDNA level is increased at day 100 after HSCT in patients later developing late acute GVHD after day 100 (before the onset of cGvHD) and at the onset cGvHD. Measurement of mt-DNA may have the potential as a diagnostic biomarker to guide therapy.



Biography

Dr. Shima Azadpour is currently an Assistant Professor at the Department of Hematology, Abadan University of Medical Sciences, Abadan, Iran. She obtained her Ph.D. in Hematology at the University of Tehran, Iran. She was working in the Michael Cuccione Childhood Cancer Research Program, at BC Children's Hospital, Department of Pediatrics, University of British Columbia, Vancouver, as part of her internship program.(2019-2023) She is doing research on developing approaches in pediatric blood and immune disorders, doing a hematology research project related to bone marrow transplantation in children's leukemia and GVHD to save children and adolescents from life-threatening childhood blood diseases, Hematology Laboratory investigations.

Comparative characterization of bispecific antibodies with different molecular formats

Wen Jin Wu

Division of Biotechnology Review and Research, Office of Biotechnology Products, Office of Pharmaceutical Quality, Center for Drug Evaluation and Research, U.S. Food and Drug Administration, USA

We generated two IgG1-like bispecific antibodies (BsAbs) that have different molecular formats, symmetrical DVD-Ig and asymmetrical knob-in-hole (KIH), targeting the same antigens, EGFR and PD-L1. We compared some key quality attributes and biological activities of these two formats of BsAbs. While both formats of BsAbs bound EGFR and PD-L1, the binding affinity of the KIH format was weaker than the DVD-Ig format in Biacore binding assays. Both DVD-Ig and KIH BsAbs had similar ELISA and cell surface binding activities, comparable to mAbs. Results showed that anti-EGFR/PD-L1 BsAbs exhibited *in vitro* and *in vivo* antitumor proliferation activity, but there was a difference in the potencies of the respective BsAb formats (DVD-Ig and KIH) when different cells or assays were used. This study provides evidence that the potency of the BsAbs targeting the same antigens can be affected by the respective molecular features, and selection of appropriate cell lines and assays is critically important for the assay development and potency testing of BsAbs.

Biography

Dr. Wen Jin Wu is a Senior Investigator in Office of Biotechnology Products (OBP), Center for Drug Evaluation and Research (CDER) at FDA. He earned his M.D. from Wannan Medical College, China, and his PhD from Cornell University. Dr. Wu was recruited as a Principal Investigator in Division of Monoclonal Antibodies, OBP at FDA in 2004. In addition to the regulatory duty as a product quality reviewer, Dr. Wu directs an independent research program at FDA. His laboratory studies the roles of ERBB family receptors in breast cancer progression and HER2-targeted antibody therapeutics and immune checkpoint inhibitor. His laboratory designs and produces different molecular formats of bispecific antibodies using genetic engineering approaches, characterizes bispecific antibodies using physiochemical and biological methods, and develops appropriate bioassays for bispecific antibodies. He has published research papers in highly reputed journals, including Journal of Biological Chemistry, Nature, Cell, Molecular Cancer Therapeutics, Cancer Research, mAbs, Cancers and has been invited to deliver speeches in the national and international conferences.

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Lessons from the covid-19 pandemic. It's time to rewrite the immunology textbooks

Javdat Muratkhodjaev

Institute of Immunology and Human Genomics of Academy of Sciences of Uzbekistan, Uzbekistan

The history of any scientific discipline moves from one paradigm to another as new facts and discoveries are accumulated that cannot be described within the existing theory. So in immunology, such a time has come. The discoveries in the late 90s of the 20th century of the mechanisms of CRISPR-Cas and RNA interference summed up the theoretical basis, and the current COVID-19 pandemic provided gigantic factual material for the creation of a new theory of antiviral protection.

It became clear that high titers of antibodies against SARS-Co2 are directly related to the severity of the disease, according to reports from the Bureau of Statistics in the United States, Australia and Western Europe, widespread vaccination leads to increased mortality, and analysis of the incidence of COVID by age directly indicated the aggravating role of the immune system in viral infections. All this forces us to reconsider the old dogmas of immunology. One such dogma is that the memory of infection is formed only by T- and B-cells. Immunologists are well aware that this is only part of the picture and that innate immunity can remember and learn. It has long been known that bacteria, plants, and invertebrates lacking T and B cells are capable of developing systemically acquired resistance.

In all kingdoms of the living world, there is a single mechanism of antiviral protection based on the use of small RNAs. In my report, I will dwell on the mechanisms of this RNA-dependent antiviral defense in detail.

Biography

Higher Education & Work Experience

- 1981-1987--Tashkent State Medical Institute, Student, First-class Degree with distinction
- 1987-1993--Institute of Physiology and Biophysics of the Academy of Sciences of the Republic of Uzbekistan. Assistant, Postgraduate, Senior Research Worker 14 scientific publications, July 1993 –Degree of Doctor of Philosophy (Ph.D.) in Biology
- 1993-2000--"Bristol-Myers Squibb", USA (pharmaceutical company). Consultant, Representative, Area Manager, Country Manager Uzbekistan
- 2000-2018--"Metroplex Trading International", GB (pharmaceutical company). Head of Representative Office
- 2018-2020--"Genex", Uzbekistan (pharmaceutical company). Head of department (R&D)
- 2020- to Present -- Institute of Immunology and Human Genomics of the Academy of Sciences of the Republic of Uzbekistan. Head of department (International Relations).

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Increased percentage of apoptotic and CTLA-4 (CD152) expressing cells in CD4+/CD8+ cells in covid-19 patients

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[10]Department of Otorhinolaryngology, Qena Faculty of Medicine, South Valley University, Egypt
[11]Department of Clinical and Chemical Pathology, Qena Faculty of Medicine, South Valley University, Egypt

Coronavirus infectious disease 2019 (COVID-19) confirmed cases are characterized by T lymphopenia. Total apoptotic and cytotoxic T-lymphocyte antigen-4 (CTLA-4) expressing cells among CD4+/CD8+ cells were analyzed in 24 COVID-19 patients (16 out-patients and 8 in-patients) and 18 healthy volunteers using flow cytometry to detect their possible role in T lymphopenia. Hospitalized patients did not show significant difference compared to non-hospitalized patients. While the percentage and absolute count of CD4+/CD8+ cells were significantly reduced in COVID-19 cases compared to healthy control ($P < .05$), the proportion of apoptotic and CTLA-4 expressing CD4+/CD8+ cells were significantly up-regulated in COVID-19 patients ($P < .05$). In addition, apoptotic and CTLA-4+/CD4+ cells were directly related to dyspnea duration, chest CT score, ferritin, and C-reactive protein and inversely correlated with platelet count in COVID-19 patients. While apoptotic and CTLA-4+/CD8+ cells were directly related to lymphocyte count in COVID-19 patients. The apoptotic and CTLA-4+ cells were directly related to each other in CD4+/CD8+ cells ($P < .05$). White blood cells (WBCs) (×103/L), eosinophils (ratio and count), lymphocyte ratio, neutrophil ratio, neutrophil/lymphocyte ratio, neutrophil/CD4 ratio, neutrophil/CD8 ratio, CD4+ cells ratio, and CTLA-4+ cells percentage), and CD8+ cells (ratio, count, total apoptotic cell, and CD152 + cells) were all found to be significantly altered in association with COVID-19. Total lymphopenia and depletion of CD4+/CD8+ cells are characterizing COVID-19 patients. Increased apoptosis and CTLA-4 expression in CD4+/CD8+ cells in COVID-19 and their correlations with reduced cell count and severity indicators as CRP and ferritin can be used for diagnosis and follow up of the clinical severity. Our current study proposes promising future diagnostic and therapeutic targets.

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Sedimentation velocity FDS studies of antibodies in pooled human serum

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[2]*Janssen Research and Development, USA*
[3]*Interactive Technology, USA*
[4]*Harvard Medical School, USA*

Studying high concentration environments like human serum is of high interest to the pharmaceutical world. The fluorescence detection system designed by AVIV Biomedical fitted for the analytical ultracentrifuge (AU-FDS) enables the performance of experiments via tracer or BOLTS protocols. This protocol allows for the behavior of a fluorescently labeled protein to be determined in highly concentrated solution environments. In this study, we compare six pooled human serum samples by AUC sedimentation velocity (SV) techniques in order to demonstrate the potential of this technology for characterizing therapeutics antibodies in serum. Control experiments by FDS SV on serum alone reveal a bilirubin-HSA complex whose sedimentation is slowed by solution nonideality and exhibits a Johnston-Ogston (JO) effect due to the presence of high concentrations of IgG. Sedimentation velocity experiments with absorbance optics on diluted serum samples verify the HSA-IgG composition as well as a significant IgM pentamer boundary at 19s. Fluorescently labeled (Alexa-488) Simponi (golimumab) was used as a tracer to investigate the behavior of a therapeutic monoclonal antibody (mAb) in serum as well as the sedimentation behavior of total IgG in serum. Serum dilution experiments allow extrapolation to zero concentration to extract s^0; while direct global boundary fitting with SEDANAL verifies the utility of a matrix of self- and cross-term phenomenological nonideality coefficients (k_s and BM_1) and the source of the JO effect. The best fits include weak reversible association (~4 x 10^3 M^{-1}) between Simponi and total human IgG. Secondary mAbs to human IgG and IgM verify the formation of a 10.2s 1:1 complex with human IgG and a 19s complex with human IgM pentamers. These results demonstrate that AU-FDS allows a range of approaches for investigating therapeutic antibodies in human serum.

Biography

Senior Scientist of the biophysics group in the Biologics Discovery department of Janssen Research & Development (Spring House, PA, USA). Technical responsibilities include analytical ultracentrifugation, high concentration liquid formulation, analytical size exclusion chromatography, viscosity, and human serum stability studies. Research focus is to drive discovery of antibody and antibody-like therapeutic modalities toward NME. Education includes undergraduate studies (2013) at Belhaven University (Jackson, MS, USA) and a Ph.D. (2018) in the biochemistry department from the University of Mississippi Medical Center (USA).

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Histological characteristics of chronic allergic rhinitis versus non-allergy: Is there a difference in the remodeling?

Tamara Michelle Acosta Castillo[3], Carlos Ríos-Deidán[1], Maria-Soledad Reyes[2], Edgar-Escalante-Fiallos[4] and **Diana Villacrés-Silva[4]**

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[2]Pathology Unit, Ecuadorian Institute of Social Security Sangolquí, Ecuador
[3]Otorhinolaryngology Unit, IESS El Batán, Ecuador
[4]Otorhinolaryngology Unit, Carlos Andrade Marin Specialties Hospital, Ecuador

Demonstrate the histological remodeling changes in the turbinates, identify the frequency of the two forms of rhinitis in the samples studied and determine the remodeling difference found in the two variants. Patients attended an otolaryngology service at the Social Security Hospital of city Sangolqui-Ecuador from February 2016 to June 2017. The allergic variant was determined when eosinophils were found by higher magnification field and non-allergic when they were not found in the submucosal segment. Epithelial, inflammatory and stromal markers were analyzed. One hundred twenty histopathological samples were analyzed, 75% presented allergic rhinitis, the age averaged 36.2 years. When we compared between the allergic and non-allergic variants: epithelial and stromal markers we had significant difference, as well as between each of its components; except fibrosis. In relation to the inflammatory pattern, there were significant difference between the number of mast cells and stromal markers with eosinophils>10 by field. The allergic type corresponded to 75% of patients with persistent severe rhinitis who underwent turbinectomy. Regarding remodeling, there was a statistically significant difference in favor of the allergic variant. Eosinophilia greater than 10 was directly related to mastocytosis and subepithelial edema.

Table 1 Organization of qualitative data to carry out statistical calculations

Epithelial markers											
MB thickening				Globet cells				Squamous metaplasia			
0	x	xx	xxx								
< 5 µm	5–10 µm	10–15 µm	> 15 µm	0–25	26–50	51–75	76–100	Absent	Mild	Moderate	Marked
0	1	2	3	0	1	2	3	0	1	2	3
Stromal markers											
Edema								Fibrosis			
Absent		Mild		Moderate		Marked		Present		Absent	
0		1		2		3		0		1	
Inflamatory markers											
Eosinophil number				Mast cells number				Eosinophil cumulus			
0	x	xx	xxx								
	< 10 eos	10–20 eos	> 20 eos	0	X	XX	XXX	Present		Absent	
0	1	2	3	0	1	2	3	0		1	

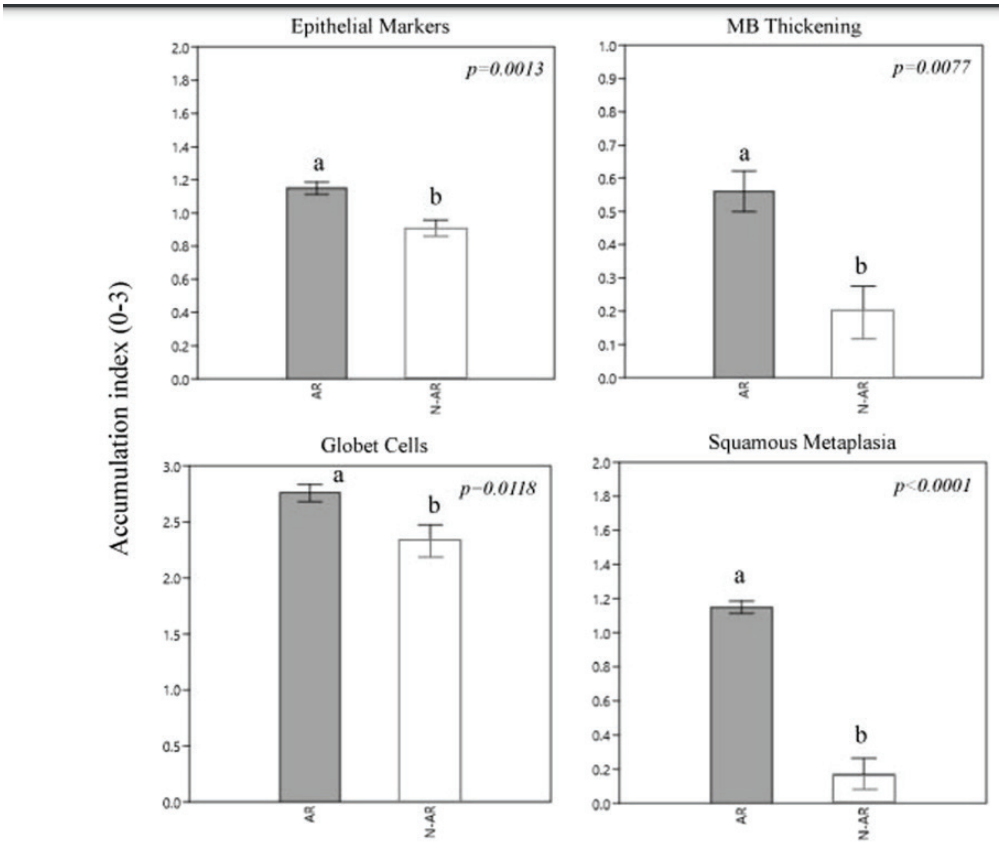

Fig. 1 Epithelial markers and their comparative analysis between allergic and non-allergic after Mann Whitney U test

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Recovery of potential starter cultures and Probiotics from Fermented Sorghum (Ting) Slurries

M. Thaoge, S. Rapoo and **P. Budeli**

Department of Biotechnology and Food Technology, Tshwane University of Technology, South Africa

Fermented foods are thought to provide a source of probiotics that promote gut health. Consequently, isolation and characterization of fermented food strains and their applications in a controlled fermentation process or as probiotics present a new facet in this area of research. Therefore, the current study sought to identify dominant strains in sorghum-fermented foods (ting) and characterize their probiotic potential *in vitro*. Recovered isolates were identified as *Lactobacillus helveticus, Lactobacillus amylolyticus, Lacticaseibacillus paracasei, Lacticaseibacillus paracasei subsp paracasei, Lactiplantibacillus plantarum, Levilactobacillus brevis, Loigolactobacillus coryniformis* and *Loigolactobacillus coryniformis* subsp *torquens* based on the their 16S rRNA sequences. Increased biomass was noted in seven out of nine under a low pH of 3 and a high bile concentration of 2% in vitro. Bactericidal activities of isolated LABs presented varying degrees of resistance against selected pathogenic bacteria ranging between (1.57 to 41 mm), (10 to 41 mm), and (11.26 to 42 mm) for *Salmonella typhimurium ATTC 14028, Staphylococcus aureus* ATTC 6538 and *Escherichia coli ATTC8739,* respectively. Ampicillin, erythromycin, mupirocin, tetracycline and chloramphenicol were able to inhibit growth of all selected LABs. Thus, isolates recovered from ting partially satisfy the potential candidacy for probiotics by virtue of being more tolerant to acid and bile, antibacterial activity and antibiotic resistance.

Biography

Dr. Mathoto Thaoge is the Head of the Department (HOD) of Biotechnology and Food Technology at the Tshwane University of Technology (TUT). She has an MSc in Microbiology (University of Limpopo) and a PhD in Food Science (University of Pretoria). She has worked at the Council for Scientific and Industrial Research (CSIR), University of Limpopo and at the University of Pretoria, She then moved into the policy space to support research in the South African National System of Innovation (NSI) at a national level. Between 2006 and 2015 she worked between the National Research Foundation (NRF) and the Department of Science and Innovation (DSI). Her current research is in the use of prebiotics/probiotics, fermentation technologies and the use of biotechnology to improve the safety, nutritional and functional properties of foods, in order to address nutritional, food security and food safety challenges in the Southern African region. She is supervising several postgraduate students.

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