Joint Event
International Conference on

# Infectious Diseases

&

International Conference on

# Clinical Microbiology

March 20-21, 2023
Belstay Roma Aurelia,
Rome, Italy

**Scisynopsis LLC**
Atlanta, GA 30326
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# Conference Programme

# Conference Programme

**March 20-21, 2023, Belstay Roma Aurelia, Rome, Italy**

## Day 1, March 20, 2023

**Meeting Hall: Parioli 2**

9.00 - 9.45 **Registrations**

9.45 - 10.00 **Introduction**

## Keynote Presentation

10.00 - 10.45 **Mohamed Al-Ibrahim,** Pharmaron CPC, USA

**Title:** Controlled Human Infection Models in Infectious Disease Research

## Oral Presentations

Session Chair: **Mohamed Al-Ibrahim,** Pharmaron CPC, USA

Session Chair: **Sergey V. Suchkov,** Institute for Biotech & Global Health of Ros BioTech, and A.I. Evdokimov MGMSU, Russia

**Sessions:** Infectious Diseases | Coronavirus Disease (COVID-19) | Bacterial Infectious Diseases | Fungal Infectious Diseases | Viral Infectious Diseases | Veterinary Diseases | Paediatric Infectious Diseases | Nosocomial Infections and Control | Urinary Tract Infections | Blood Infectious Diseases | Sexually Transmitted Diseases | Neuro Infectious Diseases | Epidemiology | Orthopaedic Infections | Sepsis/Septicemia | Infectious Diseases Prevention, Control and Cure | Vaccines and Vaccination | Rare Infectious Diseases | Surgical Site Infections | STD and HIV Infection | Viruses and Cancer | Disinfection and Sterilization | Plants Diseases and Infection Control

10.45 - 11.15 **Francois Kiemde,** Health Sciences Research Institute, Burkina Faso

**Title :** Impact of an Electronic Algorithm using Two-step Malaria Rapid Diagnostic Test and Bacterial Biomarkers Point-of-care Tests for the Management of Febrile Diseases in Children under 5 Years in Burkina Faso

## Group Photo: 11.15 - 11.30

**Networking and Refreshments @ Bar: 11.30 - 12.00**

12.00 - 12.30 **Hans Rudolf Pfaendler,** Ludwig-Maximilians University Munich, Germany

**Title:** The Rapid Carbalux Inhibition Assay to Improve Antibacterial Therapy

12.30 - 13.00 **Isaac Darko Otchere,** University of Ghana, Ghana

**Title :** Variable Physiology of West Africa Specialist *Mycobacterium* Tuberculosis Complex (MTBC) Genotypes Highlights Potential Implications of Genomic Diversity of the MTBC

13.00 - 13.30 **Sissy T. Sonnleitner,** Dr. Gernot Walder GmbH, Austria

**Title:** Studies on the Evolution of a SARS-CoV-2 Variant of Concern – The Story of Immune Escape in an Immunocompromised Patient

13.30 - 14.00 **Andres Baena,** University of Antioquia, Colombia

**Title:** Predictive Model of Active Pulmonary Tuberculosis (APTB) Severity Based on a Combination of Inflammatory Markers, Bacterial Variants and a New TB Score

**Lunch @ Seguimi: 14.00 - 15.00**

15.00 - 15.30 **Mirza Kovacevic,** Cantonal Hospital Zenica, Bosnia and Herzegovina

**Title:** COVID-19 Associated Coagulopathy in Septic Critically Ill Patients - A Retrospective Cohort Study

15.30 - 16.00 **Emilie Burel,** APHM (Hospital of Marseille - IHU), France

**Title:** Sequential Appearance and Isolation of a SARS-CoV-2 Recombinant between Two Major SARS-CoV-2 Variants in a Chronically Infected Immunocompromised Patient

## Poster Presentations

16.00 - 16.20 **Cristina Sapaniuc,** “Sf. Parascheva” Infectious Diseases Hospital, Romania

**Title:** Imported Malaria – 12 year Experience of a University Hospital in Romania

16.20 - 16.40 **Rola Ghanem,** Jordan Ministry Of Health, Jordan

**Title :** Antimicrobial Resistance Surveillance System in Jordan: Establishment and Initial Results

16.40 - 17.00 **Sumalee Kondo,** Thammasat University, Thailand

**Title:** Distribution of Extended-Spectrum β-Lactamase and Other Resistant Genes among Patients who Underwent Abdominal Surgery

**Networking and Refreshments @ Bar: 17.00 - 17.30**

17.30 - 17.50 **Amel Abdulghani,** Doncaster and Bassetlaw Teaching Hospitals NHS Foundation Trust, United Kingdom

**Title :** Second Discitis within 4 Months, Different Level with Different Organism

17.50 - 18.10 **Gyunam Kim,** Cellivery Therapeutics, Inc., South Korea

**Title:** Intracellular Delivery of Nuclear Localization Sequence Mitigates COVID-19 by Inhibiting Nuclear Transport of Inflammation Associated Transcription Factors and Attenuating Cytokine Production

18.10 - 18.30 **Lilija Kovalchuka,** Institute of Food Safety, Animal Health and Environment BIOR, Latvia

**Title:** Distribution of DR/DQ Haplotypes in Patients with Lyme Neuroborreliosis

## Day 1 Concludes

## Day 2: March 21, 2023

## Meeting Hall: Parioli 2

## Keynote Presentation

10.00 - 10.45 **Wanessa Melo,** National Physical and Technological Sciences Center, Lithuania

**Title:** Antimicrobial Photodynamic Therapy (aPDT): An Approach to Overcome *Candida albicans* Biofilm Matrix

## Oral Presentations

Session Chair: **Rola Ghanem,** Jordan Ministry of Health, Jordan

Session Chair: **Wanessa Melo,** National Physical and Technological Sciences Center, Lithuania

**Sessions:** Clinical Microbiology | Medical Microbiology | Cancer and Microbes | Sexually Transmitted Diseases | Immunology and Vaccination | Rare Infectious Diseases | Pathogenesis | Dental Infections | Bacteriology | Virology | Antibiotics and Resistance | Pharmaceutical Microbiology | Mycology | Food Microbiology | Industrial and Applied Microbiology | Coronavirus COVID 19 | Air Borne and Infectious Diseases | Antimicrobial Agents | Nosocomial Infections | Microbial Evolution | Microbiome | Paediatric Infections | Plant Beneficial Microbes

10.45 - 11.15 **Ludmila Czarkwiani Wozniakowska,** Children's Memorial Health Hospital, Poland

**Title:** Treatment Procedures of Lyme Disease in Patients with Symptoms of Significant Conduction Disorders in Peripheral Nerves.

**Networking and Refreshments @ Bar: 11.15 - 11.45**

11.45 - 12.15 **Sergey V. Suchkov,** Institute for Biotech & Global Health of Ros BioTech, and A.I. Evdokimov MGMSU, Russia

**Title:** Personalized and Precision Medicine (PPM) as a Unique Healthcare Model to Secure the Human Healthcare, Wellness and Biosafety: Through The View of Infectious Disease Management

12.15 - 12.45 **Edith Fernandez-Figueroa,** National Institute of Genomic Medicine, Mexico

**Title :** Molecular Diagnosis for Neglected Tropical Diseases in LATAM: from Expensive to Cheap Techniques

**Lunch @ Seguimi: 12.45 - 13.45**

## Poster Presentations

13.45 - 14.05 **Mohammed Sheikh,** UHD-University of Human Development, Sulaymaniyah, Iraq

**Title:** Molecular Characterization and Phylogenetic Analysis of Foot and Mouth Disease Virus Isolates in Sulaimani Province, Iraq

14.05 - 14.25 **Roba Attar, University of Jeddah, Saudi Arabia**

**Title :** Assaying for Antiviral Activity of the Folkloric Medicinal Desert Plant *Rhazya stricta* on Coronavirus SARS-CoV-2

14.25 - 14.45 **Filip Orwat,** Polish Academy of Sciences, Poland

**Title :** Isolation and Characterization of Specific Phages against *Acinetobacter baumannii*

14.45 - 15.05 **Saidbeg Satorov,** Medical-Social Institute of Tajikistan, Tajikistan

**Title:** *In vitro* Antiviral Activity against Influence Strains of Tajik Endemic Plants Ferula Violacea Korovin

15.05 - 15.25 **Naseebh N. Baeshen,** University of Jeddah, Saudi Arabia

**Title :** *In silico* Screening of Some Compounds Derived from the Desert Medicinal Plant *Rhazya stricta* for the Potential Treatment of COVID-19

15.25 - 15.45 **Agnieszka Laudy,** Medical University of Warsaw, Poland

**Title :** New Phenylenediboronic Acid Derivatives – Direct Antibacterial and Beta-lactamase Inhibitory Activity

15.45 - 16.05 **Enrique Noa Romero,** National AIDS Research Laboratory, Cuba

**Title :** Biological and Molecular Characterization of SARS-CoV-2 Virus Isolates from Cuban Patients with COVID-19

16.05 - 16.25 **Otto Cruz Sui,** National AIDS Research Laboratory, Cuba

**Title :** Adequate Correlation between the Neutralization Assay and the Umelisa SARS-CoV-2 Anti RBD

**Networking and Refreshments @ Bar: 16.25 - 17.00**

**Day 2 Concludes followed by Panel Discussion - Awards & Closing Ceremony**

# Virtual Programme

# Virtual Programme

## March 20-21, 2023, Virtual Program

### Day 1 March 20, 2023 GMT (London Time: 10.00 - 16.05)

9.45 - 10.00 **Introduction**

## Keynote Presentation

10.00 - 10.30 **Daphne Lopez,** Vellore Institute of Technology, India

**Title:** Analytics on the Impact of Climate in the Transmission of Vector Borne Diseases

## Oral Presentations

10.30 - 10.55 **Nazlee Samodien,** University of Cape Town, South Africa

**Title:** Utility of a Syndromic Pneumonia Molecular Diagnostic Assay for Antimicrobial Stewardship: Ally or Adversary?

10.55 - 11.20 **Aristotle Koutsiaris,** University of Thessaly, Greece

**Title:** Covid-19 and Microcirculatory Thrombosis

11.20 - 11.45 **Sumeet Kumar,** Mahatma Gandhi Memorial Medical College and Maharaja Yashwantrao and Associated Hospitals, India

**Title:** MuCovid-21 Study: Mucormycosis at an Indian Tertiary Care Centre During Covid-19 Pandemic

11.45 - 12.10 **Andrei A. Bunaciu,** AAB_IR Research Company, Romania

**Title:** Fourier Transform Infrared Spectroscopy Used in Viruses' Detection

12.10 - 12.35 **Ibezim Emmanuel Chinedum,** University Of Nigeria Nsukka, Nigeria

**Title:** The Place of Omega 3 Fatty Acids in Optical and Cardiac Health

12.35 - 13.00 **Baharak Akhtardanesh,** Shahid Bahonar University of Kerman, Iran

**Title:** Canine Brucellosis and Male Dog Infertility

**Lunch (13.00 - 13.30)**

13.30 - 13.55 **Ndifontiayong Adamu Ndongho,** Dschang University, Cameroon

**Title:** Seroprevalence of HBV and HCV in HIV Patients and Immune Response after 24 months of HAART in HIV/HBV or HIV/HCV Co-Infections

13.55 - 14.20 **Suja Aarattuthodi,** Mississippi State University, USA

**Title:** Profiling of Viruses Aids the Development of Efficient Management Strategies

14.20 - 14.45 **Lee-Ann Sampson,** National Health Laboratory Service, South Africa

**Title:** Penicillin Susceptible Staphylococcus aureus: Inter-Rater Agreement in Interpreting the Penicillin Zone Edge Test.

14.45 - 15.10 **Hafiza Farhat,** Gomal University D.I Khan, Pakistan

**Title:** Evaluation of Antibacterial Potential of Endophytic Fungi and GC-MS Metabolic Profiling of *Talaromyces assiutensis*

15.10 - 15.35 **Lucke-Wold Brandon,** University of Florida, USA

**Title:** The Neutrophil to Lymphocyte Ratio in Poststroke Infection: A Systematic Review and Meta-Analysis

## Keynote Presentation

15.35 - 16.05 **Huang Wei Ling,** Medical Acupuncture and Pain Management Clinic, Brazil

**Title:** Why is SARS-CoV-2 Infection Just the Tip of an Iceberg?

## Day 1 Concludes

## Day 2 March 21, 2023 GMT (London Time: 10.00-14.25)

## Keynote Presentations

10.00 - 10.30 **Mohammad Zubair,** University Of Tabuk, Saudi Arabia

**Title:** Biofabrication of Titanium Oxide Nanoparticles from Ochradenus Arabicus to Treat Biofilm Based Diabetic Foot Infections Caused by Drug Resistant Staphylococcus aureus and Pseudomonas aeruginosa: Potential Role as Novel Antipathogenic Drug

## Oral Presentations

10.30 - 10.55 **Andreea Cristina Stoian,** University of Medicine and Pharmacy of Craiova, Romania

**Title:** COVID-19 in Patients with Neurological Diseases

10.55 - 11.20 **Anis Al-Maleki,** Universiti Malaya, Malaysia

**Title:** The Essential Roles of Metabolic Reprogramming and Genetic Variation in The Development of Antimicrobial Resistance In Helicobacter pylori

11.20 - 11.45 **Kavita Pandey,** Jaypee Institute of Information Technology, India

**Title:** Polycystic Ovary Syndrome Feature Extraction Using Design of Experiments

11.45 - 12.10 **Muyingo Yusuf,** Kiwoko Hospital, Uganda

**Title:** Prevalence, Bacterial Profiles and Factors Associated with Surgical Site Infection Among Post-Operative Mothers at Kawempe National Referral Hospital, Uganda

12.10 - 12.35 **Asit Kumar Chakraborty,** Vidyasagar University, India

**Title:** Biotechnological Explorations of Phyto-drugs, Saponin-polybromophenol of Cassia fistula bark and Tepentine-glycosides of Suregada Multiflora Root against MDR Bacterial Infections

12.35 - 13.00 **Hafiza Farhat,** Gomal University D.I Khan, Pakistan

**Title:** Evaluation of Nematicidal Potential of Endophytic Fungi Associated with Healthy Plants and GC-MS Metabolic Profiling of *Fusarium solani*

13.00 - 13.25 **Uroosa Ejaz,** Shaheed Zulfikar Ali Bhutto Institute of Science and Technology, Pakistan

**Title:** Detection of Adhesive Surface Proteins in MRSA Isolates Obtained from Karachi, Pakistan

13.25 - 13.50 **Nachappa Sivanesan Uthraraj,** East Kent Hospital University Foundation trust, United Kingdom

**Title:** Neonatal Septic Arthritis – Analysis from A Nosocomial Outbreak in an Nicu

13.50 - 14.15 **Mohammad Zubair,** University of Tabuk, Saudi Arabia

**Title:** Study of Stress Level Among the University Students in the Kingdom of Saudi Arabia During and After Lockdown

## Poster Presentations

14.15 - 14.30 **Hema Merai,** National Health Service, UK

**Title:** Erdheim-Chester Disease: An Incidental Finding in an Asymptomatic 69-year Old

14.30 - 14.45 **Nazlee Samodien,** University of Cape Town, South Africa

**Title:** Prevalence of Colistin Resistance amongst Gram-negative Bacteria at Groote Schuur Academic Hospital in South Africa: Retrospective Study and Literature Review

14.45 - 15.00 **Fatemeh Fallah,** University of Medical Sciences, Iran

**Title:** The Co-Colonization of Fungal and SARS-CoV-2 in Mini BAL Samples of the Hospitalized Children in One Year

**Day 2 Concludes Followed by Vote of Thanks**

# Day 1

# Keynote Presentations

# CONTROLLED HUMAN INFECTION MODELS IN INFECTIOUS DISEASE RESEARCH

**Mohamed Al-Ibrahim**
*Pharmaron CPC, USA*

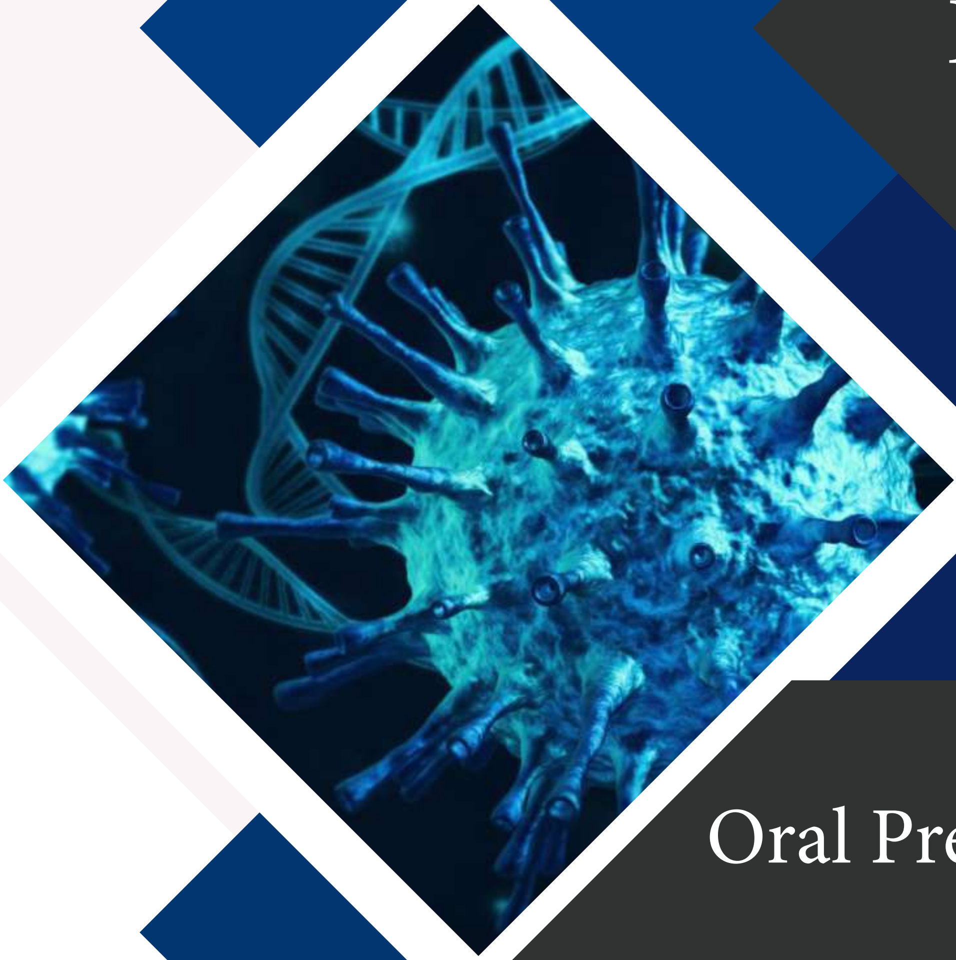
## Abstract:

Purposeful infection of individuals with pathogenic organisms has been practiced for centuries to gain medical knowledge on disease pathogenesis and host immunity. Edward Jenner is given credit for the first documented scientific observations following inoculation of his gardener's son, first with material from cowpox lesions and subsequently when challenged with material from a smallpox patient. In the early 1900's Walter Reed's team experimented with inoculations using yellow-fever virus carrying mosquitoes. During the last 5 decades Controlled Human Infection Models (CHIM) have evolved to address ethical, scientific and safety concerns among the scientific community and public at large. Established CHIMs include those using viral, bacterial, and parasitic pathogens providing researchers the opportunity for controllable replicable procedures and standardized reporting of results. This research platform is also useful when there is a lack of a suitable disease animal model and, while it does not replace field trials, CHIMs are an effective means of reaching go-no-go decisions on utility of vaccine or therapy candidates in the shortest time frame while exposing a limited number of participants. Several CHIMs will be discussed to highlight selection of volunteers, access to challenge dose, safety, and medical management. Limitations of this type of research will be reviewed including differences in participants' health profiles with those of endemic populations such as baseline health status, coinfection, nutrition, and microbiome content.

## Biography

Mohamed Al-Ibrahim is Senior Physician Investigator at Pharmaron Clinical Pharmacology Center in Baltimore, Maryland and Adjunct Professor of Medicine, University of Maryland School of Medicine. He received his medical degree from Baghdad College of Medicine (1967) and training in internal medicine and Infectious disease and immunology at the University of Maryland and New York University Schools of Medicine. His research area of interest is early phase drug development with a focus on vaccines and anti-infectives.

# Day 1



## Oral Presentations

# IMPACT OF AN ELECTRONIC ALGORITHM USING TWO-STEP MALARIA RAPID DIAGNOSTIC TEST AND BACTERIAL BIOMARKERS POINT-OF-CARE TESTS FOR THE MANAGEMENT OF FEBRILE DISEASES IN CHILDREN UNDER 5 YEARS IN BURKINA FASO

**Francois Kiemde, Fla Koueta, Athanase M. Some, Daniel Valia, Berenger Kabore, Toussaint Rouamba, Seydou Sawadogo, Macaire Nana, Diane Y. Some, Nadine A. Kone, Adelaide Compaore, Antonia W Bere, Massa dit Achille Bonko, Gautier Tougri, Sylvie Yeri Youl, Henk Schallig and Halidou Tinto**

*Institut de Recherche en Sciences de la Santé, Burkina Faso*

## Abstract:

**Background:** In low and middle incomes countries (LMICs) such as sub-Saharan Africa (SSA), the management of febrile diseases remains challenging given the lack of practical diagnostic tools to screen the real cause of fever, except malaria. Currently, diseases are managed basing on clinical signs and symptoms, leading to inappropriate prescription of antimicrobials. This situation is exacerbating by the limits of malaria rapid diagnostic tests (RDT) to correctly diagnose malaria infections. In order to improve the management of febrile diseases in children under 5 years, this study has been conducted.

**Material and Methods:** The study was conducted at the Field Station of Sigle, set-up by the Clinical Research Unit of Nanoro (CRUN). All patients from 6-59 months aWending the outpatient clinic of the health facility of Bologho in the health district of Nanoro (Burkina Faso), with documented fever or history of fever within the pass 7 days were invited to participate to the study. Participants were randomized to receive either the intervention package or standard practice. The intervention package was constituted by the following PoC tests: two-step malaria RDT detection PfHRP2 and pLDH, CRP, white blood cells (WBC) count, oximetry, Group A Streptococcus, and Salmonella/Shigella.

**Results/Finding:** After six months of implementation (March-August 2022), 172 and 173 participant were enrolled respectively in e-Algorithm arm and standard practice system. Malaria was diagnosed in 33.14% (57/172) of children in e-Algorithm arm by using sequential diagnostic and 38.73% (67/173) in standard practice system by using PfHRP2. In e-Algorithm arm, antibiotics were prescribed in 43.60% (75/172) of participants *versus* 73.99% (128/173) in standard practice system, corresponding to a reduction of 30.39% of antibiotic prescription. In intervention arm, 66.67% (38/57) of children with positive malaria RDT received antibiotics *versus* 46.27% (31/67) in standard practice system, corresponding to an increase of 20.40% of antibiotic prescription. However, antibiotic prescription was reported in 32.17% (37/115) of children with negative malaria RDT in e-Algorithm arm *versus* 91.51% (97/106), corresponding to a reduction of 59.34% of antibiotic prescription. In total, 15 (4.35%) unscheduled visits were reported in both arms (e-Algorithm: 8; standard practice system: 7).

**Conclusion:** Electronic algorithm including two-step malaria RDT and PoC tests for bacterial infections has potential to improve the management of febrile diseases in children under 5 years presenting at outpatient

clinic and reduce inappropriate prescription of antibiotics. Nevertheless, CRP test is not suitable for the to discriminate patients that antibiotic prescriptions in children with malaria infection.

## Biography

Biologist by background, Francois Kiemde is a Postdoc Scientist working as research associate at the "Institut de Recherche en Sciences de le Santé-Unité de Recherche Clinique de Nanoro" (IRSS-URCN), a public research center based in Nanoro, Burkina Faso. His research activities focused on malaria parasite biology and antimicrobial resistance, are currently oriented towards the diagnostic of these pathogens in settings without laboratory facility. He has been involved in several research activities in this topic. He mainly worked in the field of management of febrile diseases and more recently in the implementation of point-of-care tests for the management of febrile diseases in primary health centers without laboratory facility.
He worked at IRSS-CRUN from July 2009 to September 2014 as field supervisor in several research projects. From December 2014, he has been recruited as research assistant at IRSS-CRUN. From October 2014 to June 2019, he has been recruited as PhD fellow at KIT-Biomedical Research, Amsterdam, and subsequently by the Academic Medical Centre in Amsterdam (AMC) in May 2015, where he worked on the etiologies of fever episode in children under 5 years of age. After obtained his PhD in June 2019, he went back in Burkina Faso to strength the capacity of his home institute and appointed as research associate. In January 2022, he has been designed has Head of the field station of Siglé, set-up by IRSS-CRUN.
In June 2014, Dr Kiemde successfully obtained a small grant from the International Society of Infectious Diseases (ISID) to investigate the capacity of natural killer cells to lyse erythrocytes infected by *Plasmodium falciparum*, and to determine the factors associated with cytotoxicity. In 2017, his research team won the discovery award from NESTA Foundation to encourage their joint research. In 2019, he successful won an EDCTP Career Development Followship for three years (December 2020 to November 2023). He is also involved in several research projects as co-investigators. He actively prepare his registration in the grade of Research Master at Africa and Malagasy Council for Higher Education (CAMES) in 2024.

# THE RAPID CARBALUX INHIBITION ASSAY TO IMPROVE ANTIBACTERIAL THERAPY

**Hans Rudolf Pfaendler**
*Ludwig-Maximilians University Munich, Germany*

## Abstract:

Every year, several million people die from infectious diseases caused by Gram-negative bacteria. For over thirty years, carbapenems, e.g. imipenem or meropenem, were effective antibiotics. Only recently has their widespread use led to bacteria becoming resistant to carbapenems, largely due to acquired carbapenemases, enzymes that hydrolyze and inactivate carbapenems during hospitalization. To maintain effective therapy, several potent carbapenemase inhibitors have been developed, such as avibactam, relebactam, zidedactam, nacubactam, or vaborbactam. They were combined with cephalosporins or carbapenems. The new dual compositions are effective against bacteria with class A or C carbapenemases. However, they were not able to overcome resistance caused by inherent class B metallo-beta lactamases, nor (by and large) resistance caused by class D OXA carbapenemases. Because the "new" bacterial strains often produce multiple unknown carbapenemases selected from hundreds of variants, scientists are concerned that unlimited clinical use of carbapenem-inhibitor combinations may give rise to new bacteria that are ultimately multiresistant to antibiotics. Therefore, rapid phenotypic case testing for carbapenemases is mandatory. For rapid results, the CarbaLux standard assay has been recommended for the detection of all carbapenemases in bacteria from primary culture plates. It is performed using plastic tubes filled with a fluorescent carbapenem substrate. When the substrate is hydrolyzed or inactivated by extracted bacterial enzymes, the fluorescence disappears. The new CarbaLux inhibition test is applied after a positive standard test, or the two tests are performed simultaneously. In addition to the extraction buffer, an inhibitor solution is added to a fresh original tube, then the bacteria are suspended and the tube(s) are kept at 36°C. Fluorescence is observed under a UV laboratory lamp for a period of several minutes to one hour. Fluorescence obtained indicates an effective inhibitor, while a dark tube indicates an ineffective inhibitor. We tested the five new commercial inhibitors and two conventional inhibitors with 16 characterized Gram-negative bacteria. The test results provide information on the extent of antibiotic preservation by the added inhibitors. A positive *in vitro* inhibition result suggests using the same approved inhibitor and a carbapenem for antibiotic therapy. Rapid phenotypic testing for carbapenemases benefits patients and hospitals and can help prevent the development and spread of further resistance.

## Biography

Hans Rudolf Pfaendler received his PhD in 1971 in Basel under Professor Cyril A. Grob for the study of organic reaction mechanisms. His knowledge in practical microbiology, which Pfaendler acquired during repeated part-time jobs at the Cantonal Food Control. also stems from this period. He then continued his studies on reaction mechanisms as a postdoctoral fellow at the Shionogi Research Laboratory, Osaka, with Dr. Hiroshi Tanida. 1972, he started working for seven years at the Woodward Research Institute in Basel under Harvard professor and Nobel laureate R. B. Woodward. During this work, the first totally synthetic beta-lactam antibiotic was prepared and named penem, due to its combined structural elements from penicillin (penam) and cephalosporin (cephem). After the untimely death of R. B. Woodward in 1979, Pfaendler joined the pharmaceutical research department of CIBA-GEIGY AG in Basel. In 1982, he received an appointment as professor at the University of Munich. During many years of giving the traditional Experimental Lecture in Organic Chemistry, which goes back to Justus-von-Liebig, he gained a thorough overview of the life sciences. Pfaendler has remained true to his field of research: the chemical synthesis of biologically active compounds. This includes the stable oxapenems as potent beta-lactamase inhibitors. The most recent research in the field of diagnostics was carried out in collaboration with Dr. Schmidt, who as a senior physician has many years of experience in microbiology. Fluorescent carbapenems were first prepared by Dr. Gregor Golz as part of his doctoral thesis at Ludwig-Maximilians University in Munich.

# VARIABLE PHYSIOLOGY OF WEST AFRICA SPECIALIST *Mycobacterium tuberculosis* COMPLEX (MTBC) GENOTYPES HIGHLIGHTS POTENTIAL IMPLICATIONS OF GENOMIC DIVERSITY OF THE MTBC

**Isaac Darko Otchere**[1,2], **Ceesay F.B. Sainey**[1], **Basit Abdul Musah**[1], **Amanda Tetteh**[1], **Luiz de Carvalho**[2] **and Dorothy Yeboah-Manu**[1]
[1]*University of Ghana, Ghana*
[2]*The Francis Crick Institute, United Kingdom*

## Abstract:

Tuberculosis (TB) is caused by group of bacilli called *Mycobacterium tuberculosis* complex (MTBC). The human-adapted MTBC are the ubiquitous *M. tuberculosis* sensu-scricto or MTBSS (lineages (L)1-4 & 7) and the West Africa restricted *M. africanum* or MAF (L5 and L6). Studies into carbon and nitrogen metabolism of the pathogen is paving way for discovery of novel biomarkers for development of new effective control tools. However, all these efforts are based on MTBSS to the neglect of MAF (causing over 40% TB in some countries). We used West Africa dominant MTBC genotypes to determine the potential influence of genomic diversity on growth physiology when using specified sources of carbon and nitrogen. We carried out comparative-mutational analysis of genes encoding specific carbon and nitrogen metabolism enzymes among the isolates. We observed at the lineage level that L4 grows significantly better followed by L5 then L6 irrespective of the source of nitrogen or carbon. This observation is also supported by the number of lineage-specific mutations identified from our *in silico* comparative mutational analysis supported by the SIFT analysis. At the sub-lineage, we observed a very high within-lineage diversity among the five L5 and 3 L6 genotypes used in the study whereas the 3 L4 genotypes (including H37Rv) were basically the same. Following these with gene expression analysis using RNAseq of isolates under limited carbon and/or nitrogen sources, we observed general downregulation of genes in the presence of limited carbon sources compared to up-regulation of genes in the presence of limited nitrogen sources. This observation suggests remodelling of metabolism among the MTBC irrespective of genotype when forced to use specific nitrogen source. Nevertheless, the observed growth pattern of each genotype positively correlates with the gene expression under specified growth conditions. Slow growth of MAF irrespective of carbon/nitrogen sources may negatively impact the generalised treatment-regimen targeting rapidly dividing MTBC cells. MAF associated TB cases might require a longer period of therapy compared to TB caused by MTBSS.

## Biography

Isaac Darko Otchere is a Senior Research Fellow of at the Bacteriology Department of the Noguchi Memorial Institute for Medical Research (NMIMR). After receiving his PhD from the University of Ghana, he has been working on tuberculosis (TB) research focusing on the use of high throughput technologies to study the basis of bacterial pathogenesis and drug resistance whilst searching for new therapeutics and biomarkers for development of vaccines and diagnostics. He has a broad background in Biochemistry and practical training in biostatistics, bioinformatics, and pathogen genomics. His future aspirations are to use the invaluable applications of bioinformatics and biostatistics 1) to explore mycobacterial pathogenesis and disease control especially in the search of new biomarkers for vaccine and new therapeutic drugs and 2) to transfer the skills acquired while working on tuberculosis to other bacterial diseases.

# STUDIES ON THE EVOLUTION OF A SARS-COV-2 VARIANT OF CONCERN – THE STORY OF IMMUNE ESCAPE IN AN IMMUNOCOMPROMISED PATIENT

**Sissy Therese Sonnleitner, Martina Prelog, Stefanie Sonnleitner, Eva Hinterbichler, Hannah Halbfurter, Dominik BC Kopecky, Giovanni Almanzar, Stephan Koblmüller, Christian Sturmbauer, Leonard Feist, Ralf Horres, Wilfried Posch and Gernot Walder**
*Dr. Gernot Walder GmbH, Austria*

## Abstract:

Different scenarios explaining the emergence of novel variants of concern (VOC) of the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) have been reported, including their evolution in scarcely monitored populations, in animals as alternative hosts, or in immunocompromised individuals. Here we report SARS-CoV-2 immune escape mutations over a period of seven months in an immunocompromised patient with prolonged viral shedding. Signs of infection, viral shedding and mutation events are periodically analyzed using RT-PCR and next-generation sequencing based on nasopharyngeal swabs, with the results complemented by immunological diagnostics to determine humoral and T cell immune responses. Throughout the infection course, 17 non-synonymous intra-host mutations are noted, with 15 (88.2%) having been previously described as prominent immune escape mutations (S:E484K, S:D950N, S:P681H, S:N501Y, S:del(9), N:S235F and S:H655Y) in VOCs. The high frequency of these non-synonymous mutations is consistent with multiple events of convergent evolution. Thus, our results suggest that specific mutations in the SARS-CoV-2 genome may represent positions with a fitness advantage, and may serve as targets in future vaccine and therapeutics development for COVID-19.

## Biography

Sissy Therese Sonnleitner studied biology at KF University Graz, specializing in immunobiology and phylogenetics. After successfully graduating, she took up employment as a laboratory manager at Dr. Gernot Walder GmbH in Außervillgraten in 2009. She has been actively involved in the development of the laboratory and routine diagnostics from the beginning and for many years. She is particularly familiar with the isolation and cultivation of pathogens in the BSL-3 and with the development of new technologies, such as the current Next-Generation Sequencing. She heads a small research group of the laboratory Dr. Gernot Walder - Infektiologie.tirol and is currently completing her doctoral studies in medical sciences at the Medical University of Innsbruck.

# PREDICTIVE MODEL OF ACTIVE PULMONARY TUBERCULOSIS (APTB) SEVERITY BASED ON A COMBINATION OF INFLAMATORY MARKERS, BACTERIAL VARIANTS AND A NEW TB SCORE

**Andres Baena, Juan C Ocampo, Juan F Alzate, Luis. F Barrera and Hanna M Henao**
*University of Antioquia, Colombia*

## Abstract:

APTB is a chronic inflammatory disease with a high incidence and mortality worldwide. It is known that Post-tuberculosis sequelae is associated with disease severity and has consequences in the patient´s quality of life. We studied and follow a cohort 121 APTB patients from Colombia during their treatment at T0 (before treatment), T2 (2 months of treatment) and T6 (At the end of treatment). By using a modified version of the TB score and a pulmonary X-ray algorithm we classified the patient´s disease as mild (Mi), moderate (Mo) and severe (S). We measured 13 cytokines by flow-cytometry with the LEGENDplex™ inflammatory panel 1 in addition to LXA4 and CHIT-1. We analyzed the genome of 88 *Mycobacterium tuberculosis* (MTB) clinical isolates by WGS and determined the different bacterial variants. We obtained all the information from 108 APTB patients in which 24.7% Mi, 46.29% Mo and 29.62% S. Notably, the S patients showed significantly higher levels of IL-6 at T0 compared to the Mi patients, and higher levels of de IL-6, IFN-γ, IL-33, and CHIT-1 of the S patients compared to Mi patients at T2. Moreover, we obtained high quality WGS of the 88 MTB clinical isolates and using TB profiler, and we found that all of them belong to the lineage 4 (L4) and to the main sub-lineages 4.1.2 and 4.3.3. The MTB variants contained 132 polymorphisms that were associated with the S patients and with the production of CHIT-1. Many of the polymorphic variants were located in virulent genes such as kdpD, rv3083, rv3084, rv3085, rv3089, PE_PGRS30 and rv1787. With these results we propose an integrative model that may allow us to early classify the severity of a patient in order to prevent the post-treatment sequelae with the application of an early anti-inflammatory intervention.

## Biography

Andres Baena is a biologist from the National University of Colombia with a Ph.D. degree from the Albert Einstein College of Medicine in New York, currently working as a full professor in the department of Microbiology and Parasitology at the Medical School of the University of Antioquia in Colombia. His research interests are cantered in the understanding the immune response against *Mycobacterium tuberculosis*(Mtb)the causing agent of Tuberculosis (TB). Mtb is a clever pathogen that is considered the major killer of humans during all the recorded history. Although TB is a curable disease we have not be able to eradicate this disease from the planet. He believe that the solution to this problem rely in the generation of an effective vaccine against TB. He is currently working with different glycolipids in combination with TLR and NLR adjuvants to improve Tuberculosis vaccines such us BCG. Additionally, he was looking for some of the Mtb genes and pathways using dual RNAseq, that are involved in the immune evasion mechanisms of Mtb that could be use as targets for vaccine and drug design in the future.

# COVID-19 ASSOCIATED COAGULOPATHY IN SEPTIC CRITICALLY ILL PATIENTS - A RETROSPECTIVE COHORT STUDY

**Mirza Kovacevic**
*Cantonal Hospital Zenica, Bosnia and Herzegovina*

## Abstract:

**Objective:** To determine the relationship between coagulation disorders and septic condition in COVID-19 critically ill patients.

**Methods:** Data including age, sex, comorbidities, quick Sequential Organ Failure Assessment (qSOFA) score, inotropes requirement, laboratory findings: platelets, neutrophils, lymphocytes, procalcitonin (PCT), C-reactive protein (CRP), fibrinogen, D-dimer, sepsis-induced coagulopathy (SIC) and disseminated intravascular coagulation (DIC) score were recorded on the day of admission and on the day of starting of invasive mechanical ventilation. Primary outcome was to establish CAC with sepsis; secondary outcome measure was incidence of CAC in septic COVID-19 critically ill patients.

**Results:** The most common COVID-19 associated coagulopathy in septic patients were INR values (p=0.019) for Group 2, followed by the values of inflammatory parameters PCT (p=0.002) and lymphocytes (p=0.011) also for Group 2. The statistical significance of SIC score was observed for both groups of patients, Group 1 (p=0.007), Group 2 (p=0.012). Norepinephrine (p=0.000) and dobutamine (p=0.000) for Group 2, qSOFA for both groups (p=0.000) were also statistically significant.

**Conclusion:** The observed coagulation abnormalities met the criteria for a SIC (sepsis-induced coagulopathy) diagnosis.

## Biography

Mirza Kovacevic was Born on October 31, 1988 in Tuzla, Bosnia and Herzegovina. Primary and secondary school finished in Gračanica, Bosnia and Herzegovina. He obtained his medical degree at Faculty of Medicine at the University of Tuzla, and graduated at the same University in 2013. Employed at the Cantonal Hospital Zenica in the Department of Anesthesiology, Resuscitation and Intensive Care since 2013. Anesthesiology residency training started in 2015. Final year of his residency training finished at the Clinic for Anesthesiology, Resuscitation at University Medical Center Tuzla. Specialist exam passed in 2020 in Tuzla and acquired the title of specialist of anesthesiology, resuscitation and intensive care. His postgraduate (doctoral) studies began in 2019 year at the University of Tuzla. Since then, he have been actively involved in scientific research. As the author and co-author of several published scientific and professional papers. Before and during his doctoral studies, he was a lecturer at numerous domestic and international symposia and congresses, with membership of the Association of Anesthesiologists of the Federation of BiH.

# SEQUENTIAL APPEARANCE AND ISOLATION OF A SARS-COV-2 RECOMBINANT BETWEEN TWO MAJOR SARS-COV-2 VARIANTS IN A CHRONICALLY INFECTED IMMUNOCOMPROMISED PATIENT

**Emilie Burel, Philippe Colson, Jean-Christophe Lagier, Anthony Levasseur, Marielle Bedotto, Philippe Lavrard-Meyer, Pierre-Edouard Fournier, Bernard La Scola and Didier Raoult**
*APHM (Hospital of Marseille - IHU), France*

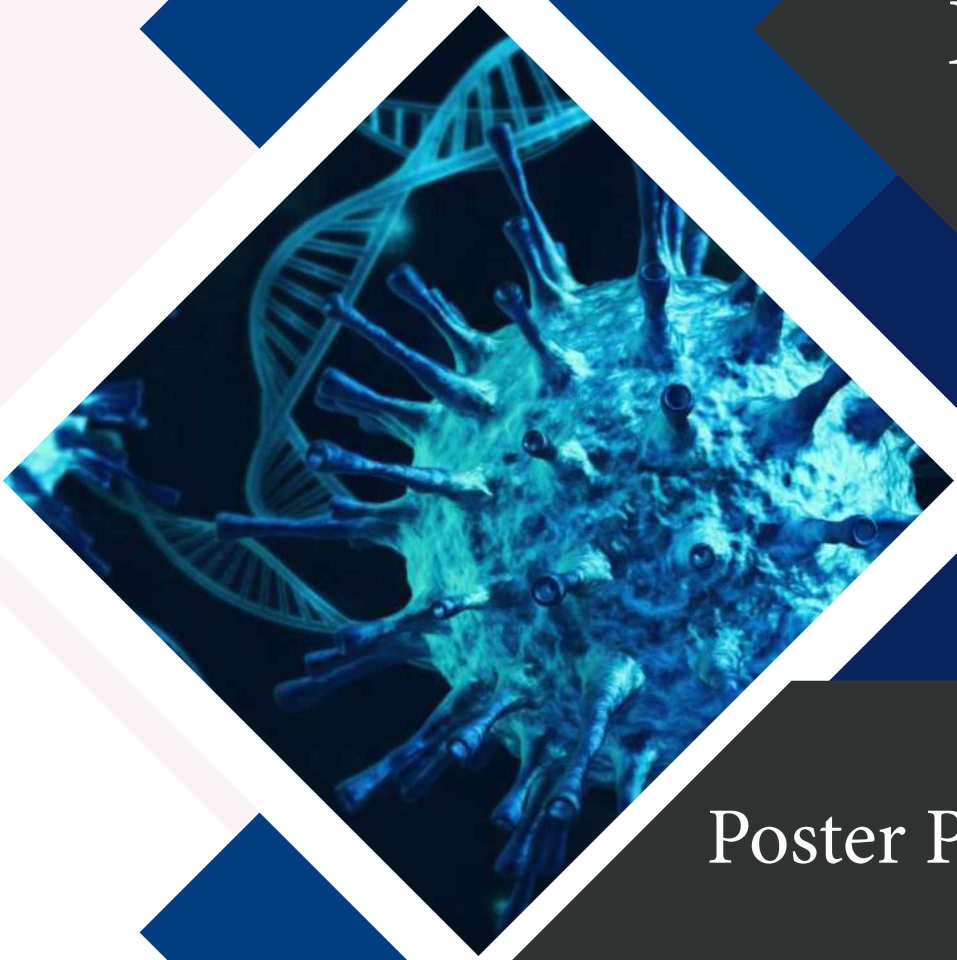
## Abstract:

Genetic recombination is a major evolutionary mechanism among RNA viruses, and it is common in coronaviruses, including those infecting humans. A few SARS-CoV-2 recombinants have been reported to date whose genome harbored combinations of mutations from different mutants or variants, but only a single patient's sample was analyzed, and the virus was not isolated. Here, we report the gradual emergence of a hybrid genome of B.1.160 and Alpha variants in a lymphoma patient chronically infected for 14 months, and we isolated the recombinant virus. The hybrid genome was obtained by next-generation sequencing, and the recombination sites were confirmed by PCR. This consisted of a parental B.1.160 backbone interspersed with two fragments, including the spike gene, from an Alpha variant. An analysis of seven sequential samples from the patient decoded the recombination steps, including the initial infection with a B.1.160 variant, then a concurrent infection with this variant and an Alpha variant, the generation of hybrid genomes, and eventually the emergence of a predominant recombinant virus isolated at the end of the patient's follow-up. This case exemplifies the recombination process of SARS-CoV-2 in real life, and it calls for intensifying the genomic surveillance in patients coinfected with different SARS-CoV-2 variants, and more generally with several RNA viruses, as this may lead to the appearance of new viruses.

## Biography

Emilie Burel studied archaeology and evolutionary biology before specializing in genetics and physiology. She is currently working as a hospital engineer at the bioinformatics platform of the "Institut Hospitalo Universitaire" of Marseille. She is currently completing her PhD thesis focusing on viral genomes evolution.

# Day 1



# Poster Presentations

# IMPORTED MALARIA – 12 YEAR EXPERIENCE OF A UNIVERSITY HOSPITAL IN ROMANIA

**Sapaniuc Cristina, Georgiana-Alexandra Lacatusu and Carmen Manciuc**
*"Sf. Parascheva" Infectious Diseases Hospital, Romania*

## Abstract:

Malaria currently affects approximately 240 million people worldwide, and over 2 billion individuals are at risk. The most vulnerable group is represented by children under 5 years old. We analyzed the files of the patients admitted in the "Sf. Parascheva" infectious diseases hospital, Iasi, Romania, from the 1st of January 2010 to the 24th August 2022. During the mentioned period, a number of 11 patients diagnosed with Malaria were admitted to our clinic, approximately 1 patient per year. All of them are male, with an equal distribution according to the area of origin. The age ranged from 23 to 60 years, with an average of 43 years. Malaria was imported from Africa. 2 patients had Nigerian nationality and 9 patients had Romanian nationality. One of them is a priest, 3 went to Africa for personal interest and 5 were soldiers. *Falciparum malaria* prevailed, in 6 patients, followed by *plasmodium malariae* in 3 patients, *plasmodium falciparum* and ovale in one patient, and *plasmodium vivax* in one patient. Patients presented anemia, leukopenia/occasionally leukocytosis, eosinophilia, and thrombocytopenia. The hospitalization period varied between 3 and 21 days, with an average of 12 days. Three patients were transferred to the Institute of Tropical Diseases "Victor Babes" in Bucharest for additional clinical-biological investigations and specialized treatment, our hospital not being a tropical diseases Hospital. Of the 8 patients treated in our clinic, 3 received antimalarial treatment with Chloroquine and 5 with Mefloquine. The evolution was 100% favorable, with the remission of the symptoms, the normalization of the blood count, no patient needing care in the intensive care unit.

**Conclusion:** Malaria remains one of the most important global health problems of the century so always have to think about it when we have a patients that was recently in a tropical area. "Where did you come from?" is a must question in our anamnesis.

## Biography

Sapaniuc Cristina is Infectious Diseases resident doctor at "Sf. Parascheva" Infectious Diseases Clinical Hospital, Iasi, Romania; PhD student at "Grigore T. Popa" University of Medicine and Pharmacy, Iasi, Romania; member of European AIDS Clinical Society (EACS).

# ANTIMICROBIAL RESISTANCE SURVEILLANCE SYSTEM IN JORDAN: ESTABLISHMENT AND INITIAL RESULTS

**Rola Ghanem, Lora Alsawalha and Sameeh M. Abutarbush**
*Jordan Ministry of Health, Jordan*

## Abstract:

**Background:** AMR is a global concern and antibiotics are becoming increasingly ineffective. The aim of this study is to describe the development and activities of the Jordan Antimicrobial Resistance Surveillance System (JARSS).

**Methods:** The available documentation on the development and activities of the JARSS were reviewed. These included system establishment and organization, AMR surveillance sites and training, data management, and initial JARSS results.

**Results:** The JARSS was officially launched in July 2019, although activities started late 2018 and included establishing and strengthening the structure of the surveillance, where the multi-sectoral National Coordinating Center (NCC) was established from members of involved sectors to oversee the AMR surveillance.

Initially there were eight AMR surveillance sites and consisted of eight hospitals that were affiliated with public, private, military and academic sectors. They were trained on basic epidemiological principles and methods of surveillance, use of WHONET Software for surveillance of AMR and standardized SOPs for pathogen Identification, antimicrobial susceptibility testing and quality control. AMR data was sent on monthly basis to the NCC. Data of the first year (2018/2019) of the surveillance was analyzed using WHONET software.

A total of 21,813 priority pathogens were collected from all clinical specimens at the eight surveillance sites. *Escherichia coli* (51.8%) constituted about half the isolated pathogens followed by *Klebsiella pneumonia* (14%), *Acinetobacter sp*. (10%), *Staphylococcus aureus* (10%), *Pseudomonas aeruginosa* (8%), *Enterococcus faecalis* (5%), *E. faecium* (1%) and *Streptococcus pneumonia* (0.8%). About 58.6% of the priority pathogens were isolated from urine, 10.7% isolated from pus and 8.3% isolated from blood.

*Acinetobacter sp.* showed high resistance rate to carbapenems, third generation cephalosporin and aminoglycosides. There was a variation in vancomycin resistance among the *Enterococci sp.* where 45.3% of *E. faecium* isolates were vancomycin resistant *versus* only 1.1% of *E. faecalis* isolates. Of the *Enterobacteriaceae spp*., *K. pneumonia* showed higher carbapenem resistance (10.4%) then *E. coli* (2.3%). Production of extended spectrum beta-lactamases (ESBL) in *E. coli* (53.2%) was higher than that in *K. pneumonia* (50%). The highest resistance rate for *P. aeruginosa* isolates was observed against carbapenem (30.7%). About 52.6% of *S. aureus* isolates were methicillin resistant. For *Streptococcus pneumonia*, Penicillin G resistance was observed in 12.2% of the isolates and higher resistance rate reaching up to 31% was observed against clindamycin.

**Conclusion:** The high levels of AMR for several important bacterial species reported to JARSS show that AMR is a serious challenge in Jordan.

## Biography

Rola Ghanem is the Head of Central Public Health Laboratory at Jordan MoH and National Glass AMR focal point. She holds M.Sc degree in Clinical Microbiology and Immunology. During the past 20 years Rola worked as Medical Lab specialist and senior lab manager in private and governmental medical laboratories. She is responsible of managing CPHL activities by coordinating with different lab unites' supervisors' all public health related lab activities and tests, enforce and ensure adherence and application of international standard on all infectious diagnostic testing, oversee all confirmatory testing process in term of quality and safety measures. As the Global Antimicrobial resistance surveillance System (GLASS) focal point; Rola coordinate surveillance activities; provide technical support to AMR surveillance sites. As Rola is Jordan GLASS focal point she is responsible for sharing the national AMR data on the WHO Global platform (GLASS) since 2017. Rola coordinate with national and international partners (eg WHO, CDC, MediLabSecure,) multiple Laboratories capacity building activities and monitor the implementation of the decided ones. Rola has been represented Jordan in many regional and international Public health related activities and participated in many international meetings held for strengthening labs capacities and strategic planning.

# DISTRIBUTION OF EXTENDED-SPECTRUM β-LACTAMASE AND OTHER RESISTANT GENES AMONG PATIENTS WHO UNDERWENT ABDOMINAL SURGERY

**Sumalee Kondo, W Phornsiricharoenphant, P Phokhaphan, C Ngamphiw, S Tongsima, L Na-rachasima, A Apisarnthanarak, W Ruangchai and P Palittapongarnpim**
*Thammasat University, Thailand*

## Abstract:

Extended-spectrum β-lactamase-producing *Enterobacterales* (ESBL-PE) are a serious global health problem. We screened for ESBL-PE from rectal swabs of patients who underwent abdominal surgery. ESBL-producers were isolated from 31 out of 104 patients. Whole genome sequencing was conducted on 46 representative strains from 17 patients. Resistance genes and sequence types (ST) were examined by sequence analysis. Sequence types of the isolates were identified, and there were some unknown types. ST of EPE strains were varied while EKP strains were mainly ST14 and ST15. The strains isolated from 8 out of 17 patients were the same ST at both pre- and post-abdominal surgery. The most prevalent *bla* in *E. coli* were *bla*EC (67.49%), *bla*CTX-M (63.04%) and *bla*TEM (32.61%), whereas *bla*SHV was the most prevalent in only K. pneumoniae (21.74%). The fecal ESBL producers isolated from swabs taken prior to and after abdominal surgery illustrated persistence of colonization in patients' guts. The results revealed antibiotic resistance genes including class A (*bla*CTX-M, *bla*TEM, *bla*Z), class C (*bla*SHV, *bla*MIR *bla*DHA and *bla*EC) and class D (*bla*OXA). The most prevalent *bla*CTX-M, *bla*TEM, *bla*SHV, and *bla*OXA variants were *bla*CTX-M-15, *bla*TEM-1B, *bla*SHV-28, and *bla*OXA-1. Interestingly, *bla*CMY-2, the most common pAmpC β-lactamase genes reported worldwide, and mobile colistin resistance genes, mcr, were detected. The isolates were mostly multidrug resistance. The isolates harboring the two genes including *bla*CMY-2 and *mcr* are concerning because they may cause potentially high risk of infections during abdominal surgery. It is imperative that healthcare professionals monitor, reduce intra-abdominal surgery site infection, and prevent transmission of prolonged fecal ESBL carriages at high risk. In addition, prevention and control of resistance gene transmission is needed to reduce the spread of the mobile resistance genes.

## Biography

Sumalee Kondo graduated from Medical Technology. Khon Kaen University, Thailand (1981–1984) and worked for Faculty of Medicine, Prince of Songkla University, Thailand (1984-2003). She received Master degree in Medical Microbiology at University Kebangsaan Malaysia, Malaysia (Dec 1988 - Mar 1991). and doctoral degree from University of Sydney, Australia (Jul 1992 - Feb 1997) and works at Division of Molecular Genetics and Molecular Biology, Department of Preclinical Sciences, Faculty of Medicine, Thammasat University, Thailand (2003-present). Research of interest are Molecular Biology, Molecular Genetic and Molecular epidemiology. Current research topics focus on antibiotic resistance of bacteria, including Methicillin-resistant *S. aureus* and Extended-spectrum β-lactamase - producing Enterobacterales. Antimicrobial activity of herbal plants. Research output include publications in high impact factor and patents of hand gel and cream containing herbal extracts with effective antibacterial activity against resistant bacteria including gram positive and gram negative bacteria and procedure and proportion of products preparation. Research award include an honourable mention award of Faculty of Medicine Meeting 2011, 2015 and 2020, the 2nd runner up award of the Faculty of Medicine Meeting 2016 and 2017. National Research Award 2022 "Development of Herbal Drugs for Chronic Diseases From Benjakul Extract". University publication award 2020.

# SECOND DISCITIS WITHIN 4 MONTHS, DIFFERENT LEVEL WITH DIFFERENT ORGANISM

**Amel Abdulghani, Kenneth Agwuh and Jasdev Sawhney**
*Doncaster and Bassetlaw Teaching Hospitals NHS Foundation Trust-Doncaster, United Kingdom*

## Abstract:

**Background:** *Corynebacterium striatum* is part of the commensal skin flora and has been recognised as opportunistic pathogen. It has been associated with infective endocarditis and prosthetic infection, but rarely in discitis. In this case report, we will discuss discitis caused by *Corynebacterium striatum* in a patient who was earlier treated with penicillin based antibiotics for discitis due to *Pseudomonas aeruginosa*.

**Case description:** 82 years old gentleman with medical history of rheumatoid arthritis who was treated at a neighbouring hospital for C2-C3 discitis associated with epidural abscess and repatriated to our hospital to complete is antibiotic therapy and rehabilitation. The epidural abscess was surgically drained and grew *Pseudomonas aeruginosa*, he was treated with 6 weeks of intravenous piperacillin-tazobactam and then had a further 6 weeks course of oral ciprofloxacin. Patient improved clinically and in his inflammatory markers. On completion of initial treatment weeks later, patient spiked temperature and was unwell associated with rising inflammatory markers. Two sets of serial blood cultures were taken and positive for *Corynebacterium striatum*. Repeat MRI spine showed a secondary discitis L2-L3. He was then treated with intravenous vancomycin for 6 weeks before switching to oral Linezolid.

**Discussion:** This case highlights *Corynebacterium striatum* causing discitis which is an unusual causal organism. Patients with Rheumatoid arthritis should be investigated for spinal infection if evidence of degenerative spinal disease, as these individuals are prone to low grade infection in the form of recurrent discitis. This case also illustrated penicillin and ciprofloxacin resistant *Corynebacterium striatum*. This could be due to the prolong use of these antibiotics, which the patient was treated with in the first discitis episode.

## Biography

Amel Abdulghani has graduated in Medicine from University of Manchester, UK in 2016. She worked in general medicine and rotated in different medical speciality such Renal, haematology, respiratory, Rheumatology and cardiology. Recently she developed interest in Microbiology. She working in Microbiology at Doncaster Royal infirmary.

# INTRACELLULAR DELIVERY OF NUCLEAR LOCALIZATION SEQUENCE MITIGATES COVID-19 BY INHIBITING NUCLEAR TRANSPORT OF INFLAMMATION ASSOCIATED TRANSCRIPTION FACTORS AND ATTENUATING CYTOKINE PRODUCTION

**Gyunam Kim, Dongho Kim, Dasom Shin, Sanghyeon Yu, Seokwon Lee and Jieun Kim**
*Cellivery Therapeutics, Inc., South Korea*

## Abstract:

The outbreak of infectious severe and acute respiratory syndrome (SARS)-CoV-2 which induces coronavirus disease 19 (COVID-19) causes patients to develop acute respiratory distress syndrome (ARDS) and even death by triggering uncontrolled immune responses. Dysregulated immune responses impair healthy organs by over-production of pro-inflammatory cytokines, which are called “cytokine storm”. In this study, an improved cell-permeable nuclear import inhibitor (iCP-NI) has been developed by fusing sequence-optimized advanced macromolecule transduction domains (aMTDs) and nuclear localization sequence (NLS) originated from human NF-κB to treat the cytokine storm mediated organ failure and death in COVID-19. Intracellularly delivered NLS inhibits nuclear transport of various inflammation-associated transcription factors (IATFs) such as NF-κB, NFAT, AP-1 and STAT1/3 which results in suppressed expression of pro-inflammatory cytokines and chemokines. In brief, iCP-NI decreased lethality of RNA virus infection mimetic pneumonitis animals by protecting lung structure from inflammation-mediated destruction via reduction of the inflammatory cytokines. Continuously, iCP-NI significantly attenuates severity of SARS-CoV-2 infected hamster model. Inhibition of viral replication is proved with quantitative PCR by reducing level of RdRp gene (log7.04 *vs* log5.79). Likewise, levels of inflammatory cytokines such as *TNF-α* and *IL-17A* in lungs are significantly decreased and thereby, lung structures are protected from inflammation-mediated damages. As a result, iCP-NI facilitates intracellular delivery of NLS to suppress pro-inflammatory cytokines and chemokines production, demonstrating a potential as a therapeutic agent to control COVID-19-related hyperimmune responses.

## Biography

Gyunam Kim (M.S.) is now charged senior researcher at the division of new drug development Cellivery Therapeutics, Inc (Seoul, South Korea). He majored in functional gemonics at Yeungnam University (Gyeongsan-Si, South Korea). He has been the team leader of the immune disease team for 3 years and has been developing treatments for various immune diseases (COVID-19, Sepsis). The iCP-NI, which his team is developing, is currently undergoing phase 1 clinical trials in the United States as a treatment for COVID-19.

# DISTRIBUTION OF DR/DQ HAPLOTYPES IN PATIENTS WITH LYME NEUROBORRELIOSIS

**Lilija Kovalchuka[1], Sandra Gintere[2] and Angelika Krumina[1,2]**
[1]_Institute of Food Safety, Latvia_
[2]_Riga Stradiņš University, Latvia_

## Abstract:

**Introduction:** The association of viral, parasitic infections with host human leukocyte antigens (HLA) has been partially investigated. The type and strength of this association differs among different populations, as well as among racial and/or ethnic groups. The genes encoding the HLA-DR, -DQ heterodimer molecules, have been found to have the association with Lyme borreliosis (LB) risk, although there is cumulative evidence for the effect of other gene loci within the major histocompatibility complex (MHC) gene region.

**Objective:** The purpose of this study was to determine of HLA -DRB1/DQA1/DQB1 haplotypes in patients with Lyme neuroborreliosis (LNB).

**Materials and Methods:** The study included 29 LNB patients and 100 control (healthy) persons. The diagnosis was confirmed and imposed Latvian Infectology Center. Immunogenetic examinations were performed RSU Clinical Immunology and Immunogenetic Laboratory. HLA genotyping performed by PCR with sequence-specific primers (SSP). Statistical analysis of data was performed by Microsoft Office Excel 2003 and ARLEQUIN 3.11 software. Odds ratios and 95 % confidence intervals were computed by standard methods.

**Results:** The frequency of haplotypes: _DRB1*07:01/DQA1*02:01/DQB1*05:02-05:04 (9.6 vs_ 1.1 percent; odds ratio, 5.2; p=0.003), _DRB1*07:01/DQA1*02:01/DQB1*06:02-06:08_ (11 _vs_ 2.9 percent; odds ratio, 4.1; p=0.053), and _DRB1*04:01/DQA1*02:01/DQB1*04:01-04:02_ (13.1 _vs_ 5.2 percent; odds ratio, 4.0; p=0.062), were significantly increased in LNB patients compared with the control groups. Although, p value was less than 0.05 only in _DRB1*07:01/DQA1*02:01/DQB1*05:02-05:04_ haplotype. Whereas, the haplotype of DRB1*11:05/_DQA1*03:04/DQB1*03:04_ (2.6 _vs_ 4.2 percent; odds ratio, 0.3; p=0.068) was smaller in LNB patients and significantly higher in controls.

**Conclusion:** This data suggests that HLA-DR/DQ haplotypes may have a considerable effect on susceptibility/or protection to Lyme neuroborreliosis Knowledge of the mechanisms of genetic protection against infectious diseases and predisposition to them is one of the important steps to combat them in endemic areas, and may be the key to future vaccines.

## Biography

Lilija Kovalchuka graduated from Riga Stradiņš University with a degree in Molecular Biology and Biochemistry. Currently works as a senior expert at the Institute of Food safety, animal health and environmental “BIOR”. Participated in the international program “European bank genomic and clinical, genetic and immunogenetic database of Ankylosing Spondylitis and the other spondylarhropathies”. Also in the scientific project “The studies of Latvian population genetic pool and their use in diagnostic of human pathology and prevention”; and the project “Acute and chronic borreliosis (Lyme disease) specific, immunogenetic, clinical, radiological diagnosis, prediction of disease course , patients’quality of life verification borreliosis caused by the prevention of disability and the public health by reducing the burden Latvian”. Author of 18 scientific articles and one patent.

# Day 2

# Keynote Presentation

# ANTIMICROBIAL PHOTODYNAMIC THERAPY (aPDT): AN APPROACH TO OVERCOME *Candida albicans* BIOFILM MATRIX

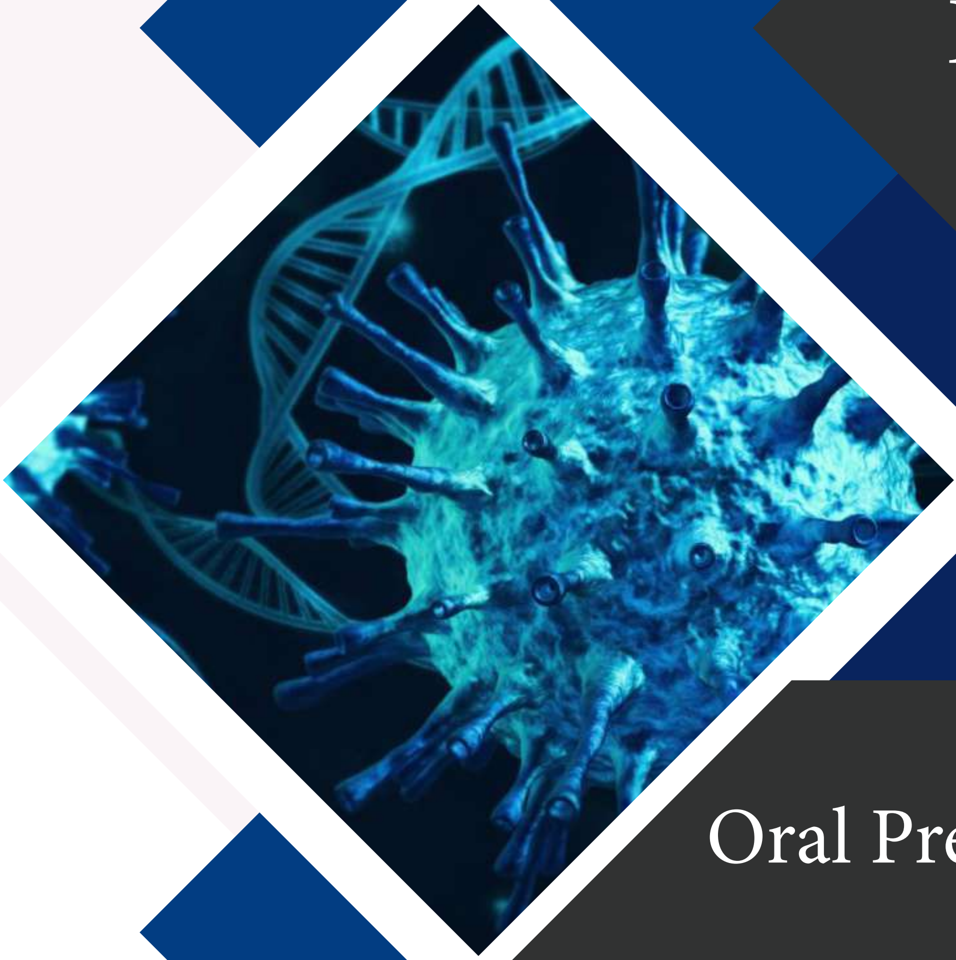
**Wanessa de Cassia M.A. Melo**
*State Scientific Research Institute Center of Physical and Technological Sciences (FTMC), Lithuania*

## Abstract:

Currently, biofilms have been the cause of a wide variety of infections in the human body, reaching 80% of all microbial infections. *Candida albicans* is considered to be one of the most commonly identified resistant pathogen that causes biofilm infections. The biofilms are intrinsically resistant to conventional antifungal therapeutics, the host immune system, and other environmental factors, making biofilm-associated infections a significant clinical challenge. This resistance is directly related to the extracellular polysaccharide (EPS) matrix that acts as both a physical barrier to drug penetration and as a stabilizer of the overall architecture of the biofilm. The development of new approaches is urgent, and aPDT has been shown as a promising candidate. aPDT involves the synergistic combination of a photosensitizer (PS), molecular oxygen and visible light of an appropriate wavelength to produce highly reactive oxygen species (ROS), which leads to the oxidation of several cellular components. Thus, this work aimed to evaluate the aPDT effect on *Candida albicans* biofilm matrix and its components (proteins and carbohydrates), using the wellknown methylene blue as a photosensitizer. *C. albicans* biofilms were illuminated at 630 nm with a light dose of 20 $Jcm^{-2}$ after incubation with 1.0 mg $mL^{-1}$ MB. As result, *C. albicans* biofilm suffered 60% and 3.52 CFU $mL^{-1}$ log10 reduction in its metabolism and viability, respectively. These results were compared to the significant reduction of ECM components as follows, 72.36% of proteins and 82.87% of carbohydrates. These results were also visualized by electronic micrography, showing a reduced number of cells and no matrix surrounding them. The effect of the red light or MB alone did not cause any significant effect against *C. albicans* biofilm matrix and its metabolic activity. We may suggest that the aPDT is able to cause EPS disruption and consequently *C. albicans* biofilm reduction.

## Biography

Wanessa Melo has completed PhD in Science with a focus on Microbiology at the University of São Paulo – Brazil (Department of Bioengineering). Part of her work was accomplished at Harvard Medical School – USA (Department of Health Science and Technology). Additionally, she has graduation in Biomedicine, Master's degree and post-doctoral in Biotechnology. She also has experience as director of the Biomedicine course and professor of microbiology. Currently, Wanessa Melo occupies the position of principal investigator at FTMC, Vilnius – Lithuania. The aim of her work is to search for new strategies to overcome biofilm infection on medical devices. She has published several papers in reputed journals, a few chapters of books and has been serving as an editorial board member of a reputed journal.



# Day 2

# Oral Presentations

# TREATMENT PROCEDURES OF LYME DISEASE IN PATIENTS WITH SYMPTOMS OF SIGNIFICANT CONDUCTION DISORDERS IN PERIPHERAL NERVES

**Ludmila Czarkwiani Wozniakowska and Barbara Golinska and Sylwia Stepniewska**
*Children's Memorial Health Institute, Poland*

## Abstract:

Lyme disease has been a known disease from years and unfortunately it is spreading quickly. We know that early diagnosis and use of antibiotic therapy, especially in the initial stage after infection, is effective in the most patients. In our work we dealt with the problem of late diagnosis of Lyme disease in a patient with extensive neurological symptoms – neuroborreliosis in the form of significant tetra paresis, more severe in the lower limbs and its treatment. These symptoms did not pass, and were even growing despite antibiotic therapy, physical rehabilitation, electrostimulation and administration of a series of injection with vitamin B1, B2 and B12. In this article we discuss the methodology and results of the treatment of this patient with use of iontophoresis and Nivalin injections.

## Biography

Throughout Ludmila Czarkwiani's medical life, she dealt with Neurology and Neurophysiology (EEG, EMG and EP) working mainly in neurosurgery clinics-first in the Central Teaching hospital of the Warsaw Medical University and then as the head of the department of neurophysiology and diagnosis of nervous system diseases, which she treated in this hospital. Currently, for several years, she have been working in the neurosurgery clinic at the children's memorial health Institute. In her work, she dealt with patients in the ward and outpatients, as well as neurophysiological intraoperative monitoring and teaching students and doctors. She is always willing to take up new challenges and therefore cooperate as a neurophysiologist, with otolaryngologists, phoniatrics – recently with the world hearing center in Kajetany, as well as with orthopaedists and surgeons. She have learned a lot from all of them and still learning, as she look for new ways to apply neurophysiology and treat her patients.

# PERSONALIZED AND PRECISION MEDICINE (PPM) AS A UNIQUE HEALTHCARE MODEL TO SECURE THE HUMAN HEALTHCARE, WELLNESS AND BIOSAFETY: THROUGH THE VIEW OF INFECTIOUS DISEASE MANAGEMENT

**Sergey Suchkov, William Thilly, Maria Studneva1, Shawn Murphy, Veronika Medvedeva1, Daniel Scherman, Andrew D. Miller, Elena Antonova, Hiroyuki Abe, Daryl Pritchard, Alan Wu, Carlos Malpica and Abner Notkins**

*Institute for Biotech & Global Health of Ros BioTech and A.I. Evdokimov MGMSU, Russia*

## Abstract:

Policy formation in the field of individual health promotion and protection is one of the priority tasks of national healthcare systems. Canonical health care is becoming increasingly unaffordable in most of the countries, yet it remains ineffective in preventing or effectively treating chronic diseases (including infectious ones). The medicine of the XXI century is Personalized & Precision Medicine (PPM), by protecting and preserving human health throughout the life. In this regard, an upgraded model of healthcare service, which includes the philosophy, principles and armamentarium of PPM and aimed at identifying the disorder at its early (subclinical) stage, is being created and set up.

PPM focuses on predictive and preventive measures that contribute to the development of individualized strategies for managing a healthy lifestyle that stabilize morbidity rates and can help to improve the working capacity of the population. PPM provides procedures for disease prediction and for the prediction of consequences and complications. In this regard, the biomarker-based analysis is intended as a first step towards a more personalized and precision treatment and clinical utility.

With the increase in antimicrobial agent resistance and a decreasing antimicrobial pipeline, there is a need for coordinated efforts to promote appropriate use of antimicrobial agents. Such “antimicrobial agent stewardship” measures encourage the appropriate use of antimicrobials by promoting the selection of the optimal drug regimen. PPM can help solve the crisis of antimicrobial resistance (AMR) by changing the way antimicrobial agents are developed and prescribed.

Improved patient (or persons-at-risk) outcomes with the application of the above-mentioned biomarker tests must consider not only increased survival or quality of life, but also improved clinical decision support (CDS) & making leading to the avoidance of unnecessary therapy or toxicity captured within the rapid learning system.

Opportunities exist at every stage of disease initiation and progression to develop a Personalized Health Plan (PHP) addressing lifestyle, risk modification and disease management, and later, Personalized Health Management & Wellness Program (PHM & WP). So, a combination of genomic and phenome-related biomarkers is becoming of great significance to be applied in PPM and need to be translated into the daily practice to predict

risks of the disease chronification and thus of disabling.

Meanwhile, advances in biomedical informatics and IT technologies brought on and suiting the goal by applying mathematical modeling to secure constructing and maintaining unified biobanks and databanks necessary for personal health monitoring, for instance, by the increasing availability of electronic medical records (EMRs), electronic patient registry (EPR, telemedicine and mHealth tools and cloudy technologies have allowed for the proliferation of data-centric tools and inter-hospital network communications armamentarium, especially in the context of personalized & precision healthcare (PPH).

Advances in genomics and computing are transforming the capacity for the characterization of biological systems. The set would include the use of genome-based approaches to inform molecular diagnosis and individual-level treatment regimens. In addition, advances in the speed and granularity of pathogen genome generation have improved the capability to track and understand pathogen transmission, leading to potential improvements in the design and implementation of population-level public health interventions. So, we outline several trends that are driving the development of PPM-based epidemiology of infectious disease and their implications for the ability to respond to outbreaks.

Going beyond the detection of the pathogen is crucial to transforming the diagnosis of microbial infections. Consideration of the evolutionary and ecological principles between the host and their microbiome might provide “new strategies for restoring and maintaining human health.” Innovative diagnostics that can identify host, microbiome, environmental and pathogen biomarkers are crucial to PPM-based approach. That Big Data can then be used to design optimal therapeutic strategies for patients that can restore them to health by coordinating agents that can target the pathogen, the host and the microbiome thereby intervening appropriately in the ecological balance in the patient. These strategies bring us a step closer to developing personalized therapies that exclusively remove disease-causing infectious agents. And we would advocate the preservation of our beneficial microbes and provide an overview of promising alternatives to broad-spectrum antimicrobials. Specifically, we emphasize that the newest approaches can not only improve patient care, but preserve antimicrobial agents for the future. We can advance directly to the phase of preclinical validation of disease biomarkers and their underlying mechanisms, and the results can be translated into precision diagnosis enabling patient stratification for individualized therapy. Taken together, the activities proposed will demonstrate the clinical feasibility and advantages of PPM in managing chronic and acute infectious diseases.

As you might see from the above-mentioned, PPM has drastically changed and is keeping on changing the landscape of healthcare. In reality, PPM is the new revolution in medicine which is dramatically modifying the traditional paradigm in medicine with huge consequences for health care systems. And putting PPM-tools in a public health perspective requires an apprehension of the current and future public health challenges.

A symbiotic relationship between infectious diseases, their risks, epidemiological studies, public health and PPM may exist. And this approach will be possible only with the integration of data across levels of influence and analytic wisdom in using those data toward better identification of disease and lifestyle risks. So, often overlooked, is the most fully realized application of PPM so far: in infectious diseases, where advances in genomics are already changing both medical and public health practice.

PPM has indeed arrived for the diagnosis of infectious diseases. More than that, it has arrived once and for all in the areas of clinical microbiology, molecular epidemiology and many other areas. Epidemics of the most diverse viruses will continue to occur due to factors that we are not completely able to control. The difference now is that we have powerful PPM-based technologies and tools to win this fight. In this connection, the healthcare providers, public policy sector, and consumer industries will be required to develop new and creative models and products. And, no doubt, next generations will speak about the XXI century as a time, when medicine became preventive and personalized, and its outcomes – predictive and guarantied.

## Biography

Sergey Suchkov was born in the City of Astrakhan, Russia, in a family of dynasty medical doctors.In 1980, graduated from Astrakhan State Medical University with MD. From 1980 through 1983 has been working as Res Associate, and from 1983 through 1985 as Senior Res Associate at the Inst of Medicical Enzymology, USSR Academy of Medical Sciences. In 1985, maintained his PhD at the Sechenov University. From 2021 through 2021, is a Professor and Chair (full-time job) of the Dept for Personalized Medicine, Precision Nutriology & Biodesign of Moscow State University for Food Industry (MGUPP), Moscow, Russia.

Professor and Chair, Dept for Personalized Medicine & Precision Nutriciology and Scientific Director of the Institute for Global Health, Moscow State University for Food Industry (MGUPP),Moscow,RussiaProfessor, Department for Clinical Allergology & Immunology, A.I.Evdokimov . Moscow State University of Medicine & Dentistry, Moscow, Russia. Member, EPMA (European Association for Predictive, Preventive and Personalized Medicine), Brussels, EU Member, PMC (Personalized Medicine Coalition), Washington, DC, USA. Member, ISPM (International Society for Personalized Medicine), Tokyo, Japan. Member, American Chemical Society (ACS), Washington, DC, USA

## MOLECULAR DIAGNOSIS FOR NEGLECTED TROPICAL DISEASES IN LATAM: FROM EXPENSIVE TO CHEAP TECHNIQUES

**Edith Fernandez-Figueroa**
*National Institute of Genomic Medicine, Mexico*

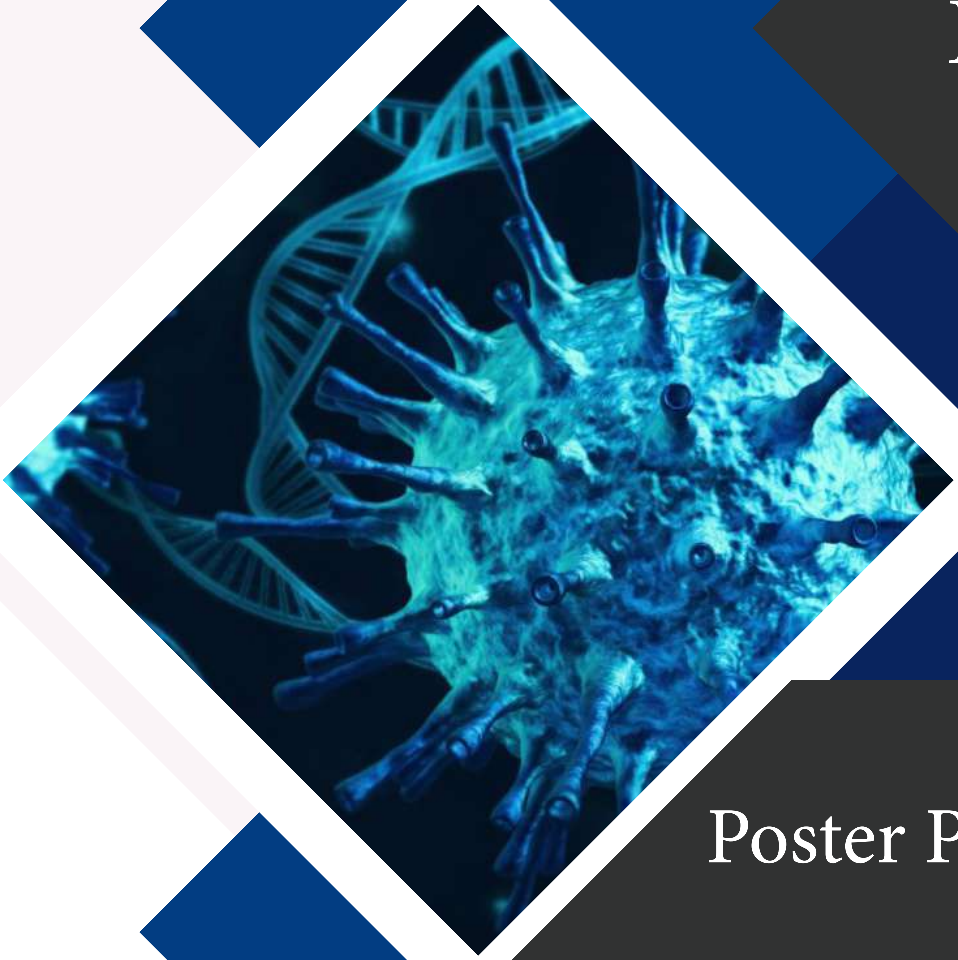
### Abstract:

Neglected Topical Diseases (NTDs) are related to poverty and affect more than a billion people worldwide. These diseases are endemic to regions that have limited access to healthcare, and, hence, despite available treatments and unfortunately can be fatal. The diagnostics are the approach to identify and possibly quantify a specific microorganism. Based on the variety of biomolecular ways for detection of antibodies or nucleic acid, can be used different kind samples such serum, blood, tissues, etc. But also, can be used several techniques to identify the causal agent of a disease. Particularly, the cases of Leishmaniasis and Chagas disease in LATAM increase and in several countries the number of cases is underestimated due to the lack of cheap, rapid, and accessible diagnoses for populations at risk. The diagnoses for these diseases are diverse and the more specific they turn out to be more expensive or require specialized equipment that is not found in any laboratory. This is the reason why the development of easy-to-use diagnoses for patients is required, but above all, access to them and know better the epidemiology of diseases, as well as the timely treatment of patients.

### Biography

Edith Fernandez had been working in the molecular diagnosis of Leishmaniasis and Chagas diseases in Mexico, as well as the study of the immune response to *Leishmania mexicana* in human macrophages. Currently, works in collaboration with other research centers to improve molecular and serological diagnosis in regions that are active foci of Leishmaniasis and Chagas Disease.

# Day 2



# Poster Presentations

# MOLECULAR CHARACTERIZATION AND PHYLOGENETIC ANALYSIS OF FOOT AND MOUTH DISEASE VIRUS ISOLATES IN SULAIMANI PROVINCE, IRAQ

**Mohammed Omar Baba Sheikh, Peshnyar Atta Rashid, Zhino Raheem and Ari Salahadin Marouf**

*UHD-University of Human Development, Sulaymaniyah, Iraq*

## Abstract:

Foot-and-mouth disease (FMD) is transboundary disease and endemic in Iraq. The current study can be considered as the first molecular characterization of serotype O in Iraq. The present investigation reported the determination of FMDV serotype O from local farms in Sulaimani districts outbreaks. Samples were collected from suspected cattle. The virus was primarily detected with RT-PCR directly from mouth epithelial samples. The direct sequencing and subsequent analysis of amplified PCR products for the VP1 gene indicated the circulation of serotype O of FMD in studied areas. Moreover, phylogenetic analysis revealed that the field isolated serotype O belonged to topotype ME-SA and lineage PanAsia II and clustered with Pakistan and Iran isolates (KU365843 and KY091283) with identity (96.00%, 95.00%) respectively. Furthermore, according to the phylogenic tree, the field isolates had different lineage with the three O/Manisa vaccine strains and Iraq/2000 strains. These findings highlighted the continuous circulation of serotype O of FMD in the region.

## Biography

Mohammed sheikh has his expertise in identification and evaluation of veterinary viral disease, its open and contextual assessment models are based on responsive constructive and approach to reducing and raising awareness of transboundary diseases in countries. He has built this model after years of experience in research, evaluation, and teaching in veterinary institution.

# ASSAYING FOR ANTIVIRAL ACTIVITY OF THE FOLKLORIC MEDICINAL DESERT PLANT *Rhazya stricta* ON CORONAVIRUS SARS-COV-2

**Roba Attar, Mohammed N. Baeshen, Thamer A. Bouback, Abdulaziz O. Albeshri, Naseebh N. Baeshen, Alaa Karkashan, Basma Abbas, Abdullah A. Aljaddawi, Yaaser Q. Almulaiky, Sara H. Mahmoud, Noura M. Abo Shama, Mohamed A. Ali, Moayad Baadhaim, Samer Zakri, Khaled Alsayegh, Arif Mohammed and Nabih A. Baeshen**
*University of Jeddah, Saudi Arabia*

## Abstract:

The emergence of superbugs and resistant pathogens poses a challenge in scientific and medical research as they threaten public health worldwide. Many herbal natural products currently used in therapies have been suggested to exert antimicrobial, antiviral and even virucidal activities against a vast majority of impervious pathogens. *Rhazya stricta*, a folk medicinal desert plant from Saudi Arabia was recently revealed to exhibit bactericidal activity against multidrug-resistant (MDR) microorganisms. The pandemic caused by the severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) is a threat to public health worldwide. Hence, we examined the antiviral activity of *R. stricta* against the virus. The *R. stricta* water extract was prepared at the traditional dose. The antagonistic effects of this extract against pathogens have been proven in previous studies, and those against SARS-CoV-2 were shown in the present study. Therefore, we explored the effects of the plant extracts and fractions against the virus for future drug development. All plant extracts showed antiviral effects against SARS-CoV-2 in the Vero E6 cell lines. Non-alkaloids showed the strongest effect against the virus, followed by weak base alkaloids and finally strong base alkaloids. A cytotoxicity assay was performed to explore the safest dose with the strongest antiviral effects. The non-alkaloid extract derived from *R. stricta* leaves is a promising antiviral candidate for the development of potential drugs with appropriate activity against COVID-19 and other lifethreatening diseases.

## Biography

Roba Mohammed Saeed Attar is currently an assistant professor in the faculty of the College of Science at the University of Jeddah in Saudi Arabia since 2019. has earned a Ph.D. in Genetics/Virology/Microbiology in 2019. My primary areas of specialty are microbiology as well as biotechnology. I am working in teaching Microbiology, Virology, and Immunology under the Department of sciences. Highly motivated researcher interested in viral infections, Interactions between viruses and their hosts (with emphasis on emerging viruses), Discovery of novel antiviral approaches, Viral mutation and drug resistance and vaccine development research. To further my goal of becoming a professor, I need to develop my research skills to the point where I am able to carry out independent studies in my chosen field. In addition, I will be able to improve my talents, which I have earned via my prior working and studying experience, as well as attend to new fascinating and professional challenges.

# ISOLATION AND CHARACTERIZATION OF SPECIFIC PHAGES AGAINST *Acinetobacter baumannii*

**Filip Orwat, Natalia Bagińska, Martyna Cieślik, Marek Harhala, Barbara Owczarek, Norbert Łodej, Andrzej Górski and Ewa Jończyk- Matysiak**
*Polish Academy of Sciences, Poland*

## Abstract:

**Introduction:** *Acinetobacter baumannii*, due to their resistance to currently available antibiotics, have been classified as a critical priority group of pathogens. They are opportunistic bacteria that most often cause infections in long-term hospitalized and/or immunocompromised patients. In addition, the ability of these strains to form biofilms contributes to the colonization of, e.g., catheters applied in patients. Therefore, there is a need to look for an alternative method of treating infections caused by *A. baumannii*. Phage therapy could become such an alternative.

**Material & Methods:** In order to search for active (preferably lytic) phages specific for *A. baumannii*, a total of 461 environmental samples and municipal sewage were collected and tested on multidrug-resistant bacterial strains belonging to *Acinetobacter spp*. (*A. ursingii* n=1, *A. pitti* n=2, *A. johnsonii* n=2 and *A. baumannii* n=132) and six belonging to other species. Phage isolation, lytic spectrum, adsorption rate, as well as phage titer were evaluated with the use of the standard plate method. Phage morphology and dimensions were determined based on Transmission Electron Microscopy. Genome sequencing and bioinformatic analysis of phage genomes were also performed.

**Results:** A total of 20 *Acinetobacter*-specific phages were obtained (2 new phages during the project and 18 as a part of research conducted in the Bacteriophage Laboratory). Genetic studies have shown that among 18 bacteriophages 12 of them are individual phages that were used in further research. The phages displayed species specificity, and their lytic spectrum was 11-75%. The maximum adsorption of phage particles to host bacterial cells (individually for each phage) was obtained within 3 to 17.5 min, and ranged from 40 to 82%. The phage lysates revealed good stability at a low temperature. Their titer after 12 months of incubation at 4°C, -70°C and -70°C with an addition of 25% glycerol decreased 1-4 orders of magnitude whereas active phages were not detected after 4 months of lysate incubation at 25°C. On the basis of genetic studies, it was determined that 11 out of 12 tested phages are temperate, and only one of them is lytic (Acba_6). Additionally, based on International Committee on the Taxonomy of Viruses (ICTV) recommendations, we proposed a taxonomic classification of the studied phages. Acba_3, Aclw_9, Acba_18, Acba_14, Acba_11 and Acba_13 phages were classified as *Shemyakinvirus* in the *Junivirinae* subfamily, while Acba_1, Acba_16, Acba_4, Acba_15 and Aclw_8 were classified as *Vieuvirus* in the *Junivirinae* subfamily.

**Conclusion:** The above data suggest that phages obtained from environmental samples may have therapeutic potential. The conducted research will allow development of the composition of the phage preparation for the treatment of urinary tract infection caused by *A. baumannii* which will be evaluated in the course of further research.

**Funding:** The presented studies were supported by Norway Grants, SMALL GRANT SCHEME Call, NOR/SGS/ACIPHAGE/0192/2020-00.

## Biography

Filip Orwat was graduated from the Wrocław University of Environmental and Life Sciences in the field of biotechnology. He has been working in Insitiute of Immunology and Experimental Therapy in Wrocław for six years. He is currently doing laboratory work related to phages. During his work in the Bacteriophage Laboratory, he became a co-author of 5 publications, in cluding 3 original ones.

# *In vitro* ANTIVIRAL ACTIVITY AGAINST INFLUENCE STRAINS OF TAJIK ENDEMIC PLANTS *Ferula violacea Korovin*

**Saidbeg Satorov, Sulkhiy N Mavlonazarova, Salomuddin J Usufi and Nilufar Eshonboboeva**
*Medical-Social Institute of Tajikistan, Tajikistan*

## Abstract:

Now, potential antiviral agents are either quite toxic or their activity is low. In this situation, drugs that are effective against many viruses and have a number of other properties will have an undeniable advantage, which will allow combining etiotropic and pathogenetic treatment. Therefore, substances of plant origin are considerable interest, since some of them, being relatively low toxic, have a wide spectrum of biological activity, exhibiting antiviral, antimicrobial, immunomodulating and other properties. Tajikistan is a region where about 640 varieties of endemic plant species grow. From the 37 species of the genus *Ferula* 6 species growing here belong to local endemic kinds, the properties of which still remain unexplored. In this regard, we were tasked to study the possible antiviral effect of the endemic species *Ferula violacea Korovin*. To determine the virus-inhibiting activity, influenza virus strains with different antigenic formulas were taken: A/Almaty/8/98 (H3N2) and A/Vladivostok/2/09 (H1N1). It has been established that the extract obtained from the root of this species *Ferula* is capable of suppressing 50% of the reproduction of influenza viruses with different antigenic in a given concentration range. When compared with the commercial drug «Tamiflu» extract of this species *Ferula* showed a more pronounced antiviral activity.

## Biography

Saidbeg Satorov pay special attention to the antiviral, antibacterial and antifungal activity of endemic plants growing on the territory of his country. The main fields of his researches are to study characteristics of pathogens microorganisms circulating in Tajikistan and their spectrum of antibiotic resistance. He have published more than 100 scientific articles in international journals dedicated on typhoid fever, anthrax, staphylococcal and streptococcal infections, helicobacteriosis. His articles are widely cited by researchers from various countries. Besides that, his hobby is to play chess and travel to different countries and get to know their culture.

# *In silico* SCREENING OF SOME COMPOUNDS DERIVED FROM THE DESERT MEDICINAL PLANT *Rhazya stricta* FOR THE POTENTIAL TREATMENT OF COVID 19

**Naseebh N Baeshen, Nabih A Baeshen, Abdulaziz O Albeshri, Roba Attar, Alaa Karkashan, Basma Abbas, Thamer A Bouback, Abdullah A Aljaddawi, Mohammed Y Refai, Hayam S Abdelkader, Abdullah Al Tamim, Abdullah Alowaifeer, Firoz Ahmed and Mohammed N Baeshen**
*University of Jeddah, Saudi Arabia*

## Abstract:

The latest coronavirus pandemic (SARS-CoV-2) poses an exceptional threat to human health and society worldwide. The coronavirus (SARS-CoV-2) spike (S) protein, which is required for viral–host cell penetration, might be considered a promising and suitable target for treatment. In this study, we utilized the nonalkaloid fraction of the medicinal plant *Rhazya stricta* to computationally investigate its antiviral activity against SARS-CoV-2. Molecular docking and molecular dynamics simulations were the main tools used to examine the binding interactions of the compounds isolated by HPLC analysis. Ceftazidime was utilized as a reference control, which showed high potency against the SARS-CoV-2 receptor binding domain (RBD) in an *in vitro* study. The five compounds (CID:1, CID:2, CID:3, CID:4, and CID:5) exhibited remarkable binding affinities (CID:1, -8.9; CID:2, -8.7; and CID:3, 4, and 5, -8.5 kcal/mol) compared to the control compound (-6.2 kcal/mol). MD simulations over a period of 200 ns further corroborated those certain interactions occurred with the five compounds, and the nonalkaloidal compounds retained their positions within the RBD active site. CID:2, CID:4, and CID:5 demonstrated high stability and less variance, while CID:1 and CID:3 were less stable than ceftazidime. The average number of hydrogen bonds formed per timeframe by CID:1, CID:2, CID:3, and CID:5 (0.914, 0.451, 1.566, and 1.755, respectively) were greater than that formed by ceftazidime (0.317). The total binding free energy calculations revealed that the five compounds interacted more strongly within RBD residues (CID:1=-68.8, CID:2=-71.6, CID:3=-74.9, CID:4=-75.4, CID:5=-60.9 kJ/mol) than ceftazidime (-34.5 kJ/mol). The drug-like properties of the selected compounds were relatively similar to those of ceftazidime, and the toxicity predictions categorized these compounds into less toxic classes. Structural similarity and functional group analyses suggested that the presence of more H-acceptor atoms, electronegative atoms, acidic oxygen groups, and nitrogen atoms in amide or aromatic groups were common among the compounds with the lowest binding affinities. In conclusion, this *in silico* work predicts for the first time the potential of using five *R. stricta* nonalkaloid compounds as a treatment strategy to control SARS-CoV-2 viral entry.

## Biography

Naseebh Nabih Baeshen is an Assistant Professor in the Department of Biological Sciences, Faculty of Science and Arts at the University of Jeddah, Saudi Arabia, where she has been since 2020. In 2015, I was awarded my PhD in Molecular Medicine- Molecular Virology from the University of Essex, United Kingdom. I am currently teaching Virology, Microbiology, Immunology, Cancer Biology, and Medical Microbiology. Highly motivated researcher and my research interests span both Laboratories and healthcare. Much of my work has been on improving the understanding, design, and performance of molecular approaches, mainly centered on the molecular biology of medically important viruses which can cause a number of human diseases, including respiratory infections, aseptic meningitis, and heart disease. All the work done in my research area is concerned with improving the understanding of interactions between viruses and their hosts and how viruses replicate and cause disease, which is intended to provide insights that may facilitate the design of effective vaccines or antivirus agents, as well as developing viruses as potential anti-cancer agents.

# NEW PHENYLENEDIBORONIC ACID DERIVATIVES – DIRECT ANTIBACTERIAL AND BETA-LACTAMASE INHIBITORY ACTIVITY

**Agnieszka E Laudy[1], Joanna Krajewska[1], Stefan Tyski[2], Krzysztof Durka[3] and Sergiusz Luliński[3]**

[1]*Medical University of Warsaw, Poland*
[2]*National Medicines Institute, Poland*
[3]*Warsaw University of Technology, Poland*

## Abstract:

European Medicines Agency approved Vabomere (cyclic boronic acid pharmacophore) containing vaborbactam (new beta-lactamase inhibitor) with meropenem for treatment. The aim of our study was to investigate the direct antibacterial activity and the beta-lactamase inhibition (BLI) ability of the six new 1,3-phenylenediboronic acid and seven 1,4- phenylenediboronic acid derivatives. Direct antibacterial activity against Gram-positive (n=7) and Gram-negative (n=12) strains was examined by the disc-diffusion test, MIC and MBC (minimal bactericidal concentration) determination assays according to EUCAST. For Gram-negative rods, MICs of new agents in the presence of the efflux pumps inhibitor Phe-Arg-β-naphthylamide (PAβN) were also determined. The ability of new compounds to inhibit beta-lactamases (like KPC, AmpC, ESBL and MBL) was examined against 8 reference strains by disc tests, microdilution test, and by checkerboard assays. The fractional inhibitory concentration index (FICI) was calculated for combination of the tested agent with meropenem. Interestingly, for the tested 1,4-phenylenediboronic acid and its derivatives very promising BLI-activity was observed at concentration of 16 mg/L in combination with ceftazidime, meropenem and imipenem, excluding ertapenem. The carbapenem MICs were reduced 4-8-fold in the case of the KPC-2-, KPC-3-producing strains. While a 4-8-fold reduction in the MIC of ceftazidime was obtained with the AmpC producing strains. Checkerboard assay revealed synergistic activity with meropenem against KPC-producing *Eschericha coli* and *Klebsiella pneumoniae* (FICI=<0.11). Unlike 1,4-phenylenediboronic acid, 1,3-phenylenediboronic acid and its derivatives showed selective activity only against cephalosporinase-producing strains (MICs of ceftazidime were reduced 4-8-fold at the concentration 16 mg/L of tested agents). Besides, 1,3-phenylenediboronic acid and 1,4-phenylenediboronic acid were no active against Gram-negative rods. However, they showed direct moderate activity against Gram-positive bacteria. 1,4-phenylenediboronic acid and its derivatives possess promising BLI activity against KPC-2 and KPC-3 carbapenemases, cephalosporinases (AmpC and CMY-2) and can be a potential antibacterial drug source.

Funded by the National Science Centre (Poland) within the project DEC-UMO-2018/31/B/ST5/00210.

## Biography

Agnieszka E. Laudy is the leading pharmaceutical microbiologist with a great experience in scientific research, evaluation and teaching in Medical University of Warsaw. Her main scientific interests are the investigation of the mechanisms of bacterial resistance to drugs and the search for new compounds with antibacterial activity. She discovered 3 new genes encoding ESBL enzymes, deposited in NCBI GenBank. Her scientific achievements include about 40 published scientific papers, with a total IF over 80. Her Hirsch index is 13. She received two scholarships in Technical University of Vienna. She is also a member of the Presidium of Main Board of Polish Society of Microbiologists.

# BIOLOGICAL AND MOLECULAR CHARACTERIZATION OF SARS-COV-2 VIRUS ISOLATES FROM CUBAN PATIENTS WITH COVID-19

**Enrique Noa Romero[1], Juliet Enríquez Puertas[1], Liuber Yans Machado Zaldívar[1], Dayamí Martín Alfonso[1], Madelin Blanco de Armas[1], Viviana Falcón Cama[2], Nibaldo Gonzáles Sosa[1], Marta Dubed Echevarría[1], Gretel Susana Pérez Bartutis[1], Danay Carrillo Valdes[1], Mireida Rodríguez Acosta[1], Neisi Valdez de Calzadilla[1], María Teresa Pérez Guevara[1] and Otto Cruz Sui[1]**

[1]*National AIDS Research Laboratory, Cuba*
[2]*Genetic and Biotechnology Engineering Center, Cuba*

## Abstract:

The continued emergence of SARS-CoV-2 variants raises concerns about their global health implications, both in terms of possible increased transmissibility and lethality, and reduced vaccine efficacy. This paper presents the biological and molecular characterization of Cuban isolates of SARS-CoV-2. The virus was isolated in Vero E6 cells and virus replication was confirmed by real time RT-PCR; ELISA to quantify SARS-CoV-2 protein N antigen and by electron microscopy. The replication kinetics of the isolates in Vero E6 cells were estimated, using a multiplicity of infection of 0.01. The viral RNA was purified from cell culture supernatant and the S gene of SARS-CoV-2 was amplified using RT-nested PCR. The purified PCR product was sequenced and the data generated was used for the identification and subsequent molecular characterization of the genetic variants of the virus using the Coronavirus Typing Tool and SARS-CoV-2 Program (www.covdb.stanford.edu). Threshold cycling levels in RT-PCRrt in the culture supernatant were associated with morphological changes in Vero E6 cells and quantification of antigen to N protein in the supernatant. Viral particles with a diameter between 80 and 100 nm were observed by electron microscopy, which corroborated the isolation of the SARS-CoV-2 virus from the nasopharyngeal exudate of Cuban patients with COVID-19. The predominant variants in the Cuban SARS-CoV-2 isolates studied were Delta B.1.617.2 and Omicron BA1.21K (33%), followed by D614G (21%), Alpha B.1.1.7 (8%) and Beta B 1,351 (4%). The maximum replication of all the variants was achieved between 72 and 96 hours of infection, with the exception of Omicron BA1.21K, which was between 96 and 120 hours. The biological and molecular characterization of the isolates has made it possible to establish a collection of SARS-CoV-2 variants, used in the evaluation of vaccines and biomolecules for the treatment of COVID-19.

## Biography

Enrique Noa Romero has extensive experience and expertise in work in human virology. Developing tools to deal with emerging and re-emerging diseases; standardization of methodologies for the purification of viral antigens for the development of diagnostic means; *in vitro* antiviral effectiveness of synthetic or natural products that meet the requirements for human use; study of the biological-molecular characteristics and variability of the strains of human retroviruses (HIV-1, HIV-2 and HTLV-I) circulating in Cuba. He led the group of Cuban researchers who isolated the SARS-CoV-2 virus for the first time in Cuba; as well as the biological and molecular characterization of the circulating SARS-CoV-2 variants in Cuba. In the fight against COVID-19, he has participated in the standardization and validation of the microneutralization assay for the determination of neutralizing antibodies against SARS-CoV-2; the researcher responsible for our center for the study of neutralizing antibodies in the subjects involved in the clinical trials of Cuban vaccines against COVID-19; development and evaluation of an ELISA system for capturing the N protein of SARS CoV-2 and *in vitro* and *in vivo* evaluation of the anti-SARS-CoV-2 activity of natural products and biomolecules.

# ADEQUATE CORRELATION BETWEEN THE NEUTRALIZATION ASSAY AND THE UMELISA SARS-COV-2 ANTI RBD

**Otto Cruz Sui[1], Juliet María Enriquez Puertas[1], María Teresa Pérez Guevara[1], Marta Dubed Echevarría[1], Dayamí Martín Alfonso[1], Nibaldo Luis González Sosa[1], Gretel Susana Pérez Bartutis[1], Mireida Rodríguez Acosta[1], Yanet Climent Ruiz[2], Dagmar García Rivera[2], Dionne Casillas Casanova[3], Gilda Lemus Pérez[3] and Enrique Noa Romero[1]**

*[1]National AIDS Research Laboratory, Cuba*
*[2]Finlay Vaccine Institute, Cuba*
*[3]Genetic and Biotechnology Engineering Center, Cuba*

## Abstract:

Since the beginning of the SARS-CoV-2 pandemic, researchers have had a specific interest in determining and quantifying neutralizing antibody titers. The main serological tests developed are based on enzyme-linked immunosorbent assays (ELISA), these tests cannot discriminate between neutralizing and non-neutralizing antibodies. It is known that only a small subset of specific antibodies against the virus is capable of neutralizing its infectivity. To determine the correlation between the total antibody titers (IgG) and the neutralizing antibodies, 783 sera from patients immunized with the Cuban vaccines against SARS-CoV-2 were evaluated with the Umelisa SARS-CoV-2 anti RBD system (Immunoassay Center, Cuba) and the standardized microneutralization method at the National AIDS Research Laboratory. Neutralization with live virus was also correlated with molecular neutralization based on blockade of ACE2-RBD binding. The analysis of the results used Spearman's correlation coefficient and they were processed using the Graphpad Prism version 5.0 program for Windows. The correlation between neutralizing antibody titers and IgG antibodies was highly significant ($p<0.0001$), with a correlation coefficient of 0.8524 (confidence interval 0.8314 to 0.8710). Similarly, the results of the correlation between the microneutralization assay and molecular neutralization demonstrated a strong association ($p<0.0001$) between the assays, with a value of $r=0.8589$ (confidence interval 0.8294 to 0.8836). The total IgG titers against SARS-CoV-2 using Umelisa SARS-CoV-2 anti RBD make it possible to estimate the neutralizing capacity present in the serum of vaccinated people. The microneutralization assay has adequate sensitivity for the detection of neutralizing antibodies against SARS-CoV-2 in serum samples from individuals immunized with the Cuban vaccines against SARS-CoV-2 with different IgG antibody titers.

## Biography

Otto Cruz Sui, PhD, Senior researcher. He has vast experience in the field of diagnostic means for the detection of infectious agents; standardization of methodologies for the purification of viral antigens for the development of diagnostic means; he has participated in the serological and molecular diagnosis of human retroviruses in the Cuban population and he has collaborated with other countries in clarifying epidemiological events. He formed the group of researchers that carried out the isolation and characterization of the circulating variants of SARS-CoV-2 in Cuba; he has participated in the standardization and validation of the microneutralization assay for the determination of neutralizing antibodies against SARS-CoV-2; development and evaluation of an ELISA system for capturing the N protein of SARS CoV-2 and *in vitro* and *in vivo* evaluation of the anti-SARS-CoV-2 activity of natural products and biomolecules.

# Virtual Presentations

# Keynote Presentations

# ANALYTICS ON THE IMPACT OF CLIMATE IN THE TRANSMISSION OF VECTOR BORNE DISEASES

**Daphne Lopez**
*Vellore Institute of Technology, India*

## Abstract:

**Background:** Dengue Fever (DF), an outbreak prone viral infection is transmitted by Aedes mosquitoes, which is mostly found in tropical and sub-tropical climatic regions. Some infection can result in Dengue Haemorrhagic Fever (DHF), also known as severe dengue which can be fatal. DF and DHF are caused by four serotypes of dengue virus (DENV). Infection with one serotype can provide lifelong immunity to that virus but not to the other serotype viruses. Recent global epidemic infection requires us to monitor disease spread continuously. Vector-borne diseases are more prone to cause epidemics and are challenging to control once the disease spreads. It is necessary to periodically monitor the status of the Dengue incidence in a locality. Climatic factors significantly influence the mosquito population's survival and breeding rate that causes Dengue Infection. A deep learning technique to better capture the correlation between climatic parameters and monthly dengue incidence for the districts of Tamil Nadu.

**Objective:** To find the correlation between temperature, relative humidity, weekly surface rainfall for at least a period of 10 years and dengue incidences using deep learning models. A Long Short Term Memory (LSTM) model can be used to predict dengue incidences.

**Outcome:** Model that predicts dengue incidences based on the varied climate parameters for a future time step. This predictive analytics can help in the prevention and control of the infection.

**Methods:** A deep learning model to predict the monthly dengue incidence is built for the districts of Tamil Nadu, India.The LSTM model is extensively studied to capture the correlation between climatic parameters and dengue incidence. A comparative study of the LSTM model with machine learning methods and different LSTM models such as Stacked LSTM, Bidirectional LSTM, and Bidirectional Stacked LSTM.

**Results:** It is observed that rainfall has a direct impact on the spread of dengue. Other parameters like Mosquito Larval index and Vegetation Index can also be included as a part of the input and the model can be trained.

**Conclusion:** This trained model can be rolled out of other similar diseases like Zika and Chikungunya with Transfer Learning.

## Biography

Daphne Lopez, her research interests span both Data Mining, Big Data Analytics and Scheduling in Cloud computing. Much of her work has been on improving the understanding and application of analytics in various domains. In the health arena, she has worked on characterizing the transmission of H1N1 based on spatial temporal factors. She has explored the hot spots and identified the mobility of the patients and applied spatial graph clustering to predict the patterns. She has received funds from ICMR for analysing the H1N1 transmission. Currently her focus is on the analysis of changing climate big data and its impact on public health. She has worked on change detection algorithms and has explored the implications of the climate changes on dengue incidences. In addition she has made contributions to the modelling of diseases and also analysis on social media data.

# WHY IS SARS-COV-2 INFECTION JUST THE TIP OF AN ICEBERG?

**Huang Wei Ling**
*Medical Acupuncture and Pain Management Clinic, Brazil*

## Abstract:

**Introduction:** SARS-CoV-2 infection is a contagious disease that can cause a severe acute respiratory syndrome and caused more than 6 million deaths since the beginning of 2022. The purpose of this study is to demonstrate that patients with SARS-CoV-2 infection has energy deficiency in the five internal massive organs (Liver, Heart, Spleen, Lungs and Kidney) that are responsible for the production of internal energy for our health that represents our immune system.

**Methods:** In research that I did in my clinic in Brazil analyzing 1000 patients internal five massive organs energy measuring the energy of the chakras' energy centers, from 2015 to 2020.

**Results:** I concluded that 90% of all my patients were in the lowest level of energy and all patients that are acquiring SARS-CoV-2 infection has in the back ground this energy deficiency alteration that are predisposing them to acquire this kind of infection. The treatment of this energy deficiency condition (caused by chronic exposition to electromagnetic waves of cell phone and computers), using highly diluted medications according to the theory Constitutional Homeopathy of the Five Elements Based on Traditional Chinese Medicine will increase the immune system of the patient and will fight against the invasion of this virus in the patient's body (that is causing this infection due to low Zheng-Qi, or energy of the Kidney or second chakra).

Conclusion of this study is that SARS-CoV-2 infection is only the tip of the iceberg and the necessity of treating the cause of reduced immune system is still not treated until today because Western medicine's reasoning is only looking at the virus itself but not focusing on the cause, that is invisible by the naked eyes, that are the energy alterations in the human body, leading to a weakness state of our immune system and this is the point that we need to treat that the majority of physicians still not treating ( that is the part under the ocean that we cannot see by our naked eyes).

## Biography

Huang Wei Ling, born in Taiwan, raised and graduated in medicine in Brazil, specialist in infectious and parasitic diseases, a General Practitioner and Parenteral and Enteral Medical Nutrition Therapist. Once in charge of the Hospital Infection Control Service of the City of Franca's General Hospital, she was responsible for the control of all prescribed antimicrobial medication and received an award for the best paper presented at the Brazilian Hospital Infection Control Congress in 1998. Since 1997, she works with the approach and treatment of all chronic diseases in a holistic way, with treatment guided through the teachings of Traditional Chinese Medicine and Hippocrates. Researcher in the University of São Paulo, in the Ophthalmology department from 2012 to 2013.Author of the theory Constitutional Homeopathy of the Five Elements Based on Traditional Chinese Medicine. Author of more than 100 publications about treatment of variety of diseases rebalancing the internal energy using Hippocrates thoughts.

# BIOFABRICATION OF TITANIUM OXIDE NANOPARTICLES FROM *Ochradenus arabicus* TO TREAT BIOFILM BASED DIABETIC FOOT INFECTIONS CAUSED BY DRUG RESISTANT *Staphylococcus aureus* AND *Pseudomonas aeruginosa:* POTENTIAL ROLE AS NOVEL ANTIPATHOGENIC DRUG

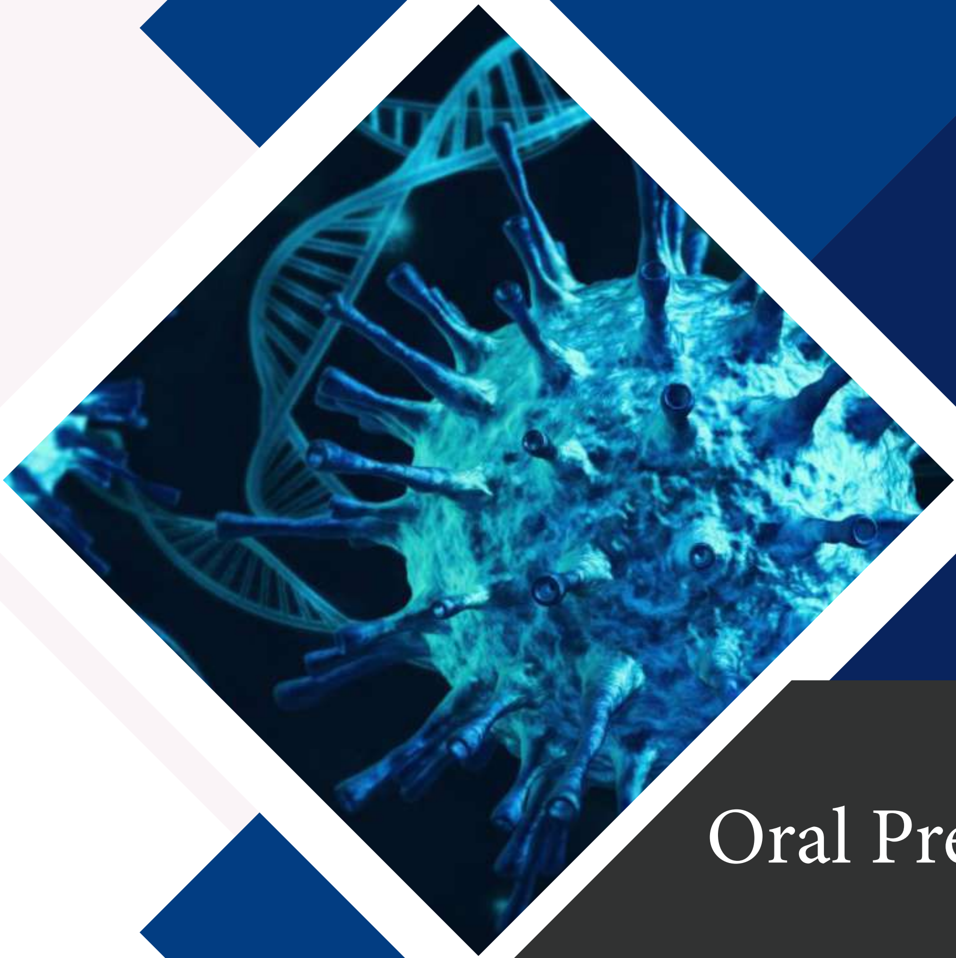
**Mohammad Zubair**
*University of Tabuk, Saudi Arabia*

## Abstract:

Diabetes and its related complications are responsible for severe morbidity and deaths round the globe. Diabetic foot infections (DFIs) is a severe and dreadful complication of diabetes mellitus. DFI/DFUs are colonized with numerous pathogenic, multi-drug resistant microorganisms and progression in colonization of these microorganism leads to biofilm establishment making treatment challenging. There is an indispensable requirement for alternative approaches to combat this threat. In the present assignment, titanium oxide nanoparticles (TiO2¬-NPs) were fabricated from the leaf extract of *Ochradenus arabicus* and inhibition of biofilm and related functions was examined against multi-drug resistant strains of *P. aeruginosa* and methicillin resistant S. aureus (MRSA) isolated from foot ulcers. Bio-fabricated $TiO_2$-NPs reduced biofilm formation in the selected strains by 22%-70% at tested sub-MICs. Significant reduction in alginate and severely impaired motility of *P. aeruginosa* strains was also observed. Key functions like cell surface hydrophobicity and EPS production that contribute in the attachment and maintenance of biofilm, respectively, were also inhibited considerably in test strains at sub-MICs. Statistically significant reduction (51%-63%) in the pre-formed biofilms of all strains was also recorded. Interaction of bacterial cell and $TiO_2$-NPs resulted in increased levels of ROS and this could be the plausible the reason for the biofilm inhibitory action of NPs. These NPs could be exploited in the current treatment strategies to combat the threat of biofilm based drug resistant diabetic foot infections and facilitate wound healing.

## Biography

Mohammad Zubair core area of research is the Extended Spectrum beta Lactamase gene (CTX, TEM & SHV), pro and anti-inflammatory cytokines and healing proteins, and its clinical correlations since the development of my acumen in the area of foot infections in diabetic patients. He had received several awards among which, the most prestigious was "Marvil Levin" which was conferred by American Diabetes Association of the USA in 2012 and recently awarded the Presidents awards for research at the University of Tabuk along with many awards and recognitions. He had published more than 55 research articles in International journals that explore different aspects of diabetic foot ulcer. His work has been widely cited and accepted at various International conferences. Besides this, his hobbies are traveling to new places and know their culture.



# Oral Presentations

# UTILITY OF A SYNDROMIC PNEUMONIA MOLECULAR DIAGNOSTIC ASSAY FOR ANTIMICROBIAL STEWARDSHIP: *ALLY* OR ADVERSARY?

**Nazlee Samodien, Mene van der Westhuyzen; Clinton Moodley and Adrian Brink**
*University of Cape Town, South Africa*

## Abstract:

Determining the aetiology of lower respiratory tract infections (LRTIs) is notoriously difficult. Culture-based methods are laborious and time-consuming. Molecular diagnostics can overcome these limitations but the view that they) incontrovertibly detect pneumonic pathogens and can invariably lead to appropriate AMS interventions is debatable. This laboratory study assessed the utility of the BioFire® FilmArray® Pneumonia Panel plus assay (FA-PP) and potential effects on AMS in a low resource setting. Routine respiratory samples collected from adult patients at Groote Schuur Hospital, Cape Town or referring facilities with clinically suspected LRTI or with a concomitant blood culture were included. The results of the culture and FA-PP were compared and pharmacy data was analyzed to determine the appropriateness of antibiotic prescriptions retrospectively.

Majority of cultured bacteria correlated with a FA-PP bin of 107.The FA-PP compared to culture was significantly more sensitive for pathogen detection (86,6% *versus* 17,9%); demonstrated a combined 100% positive percent agreement and 88% negative percent agreement; and detected significantly more additional typical bacteria. The FA-PP detected bacterial-viral combinations (27%) and 3 *Legionella pneumophila* bacteria. Upon correlation of FA-PP results with pharmacy data (n=69); 75% could have qualified for potential antibiotic changes. The FA-PP semi-quantitative reporting does not describe the relationship between the different bin values and diagnostic interpretation (colonizers *versus* pathogens) which may lead to over-diagnosis and over-treatment. Multiple bacterial and viral co-detection complicated interpretation. The detection of *Legionella via* FA-PP was clinically beneficial. The AMS impact derived from the pharmacy results are dubitable due to the assay's higher sensitivity and the lack of both clinical data and an appropriate gold standard.

Our study highlights the potential impact of introducing rapid molecular assays in routine care in settings such ours, but nonetheless underscores the interpretive challenges associated with novel rapid tests.

## Biography

Nazlee Samodien is a senior clinical microbiologist at the National Health Laboratory Services based at Groote Schuur Academic Hospital. Her expertise is in guiding management of complex infections in critical care patients; infection prevention and control; and antimicrobial stewardship. She is passionate about education and serves as an examiner on the College of Medicine (South Africa) board and is also a senior lecturer with extensive teaching experience and an expert in curriculum development and assessment. The primary focus of her current research is in molecular genotyping of multi-drug-resistant Gram-negative organisms. She is dedicated to providing quality microbiology services, optimizing patient management and motivating students to excel in science fields.

# COVID-19 AND MICROCIRCULATORY THROMBOSIS

**Aristotle G Koutsiaris**
*University of Thessaly, Greece*

## Abstract:

With a total death count of 6.8 million [WHO] we are now [Feb 2023] close to the end of the public health emergency due to the COVID-19 infectious disease. The disease is caused by an RNA beta coronavirus (SARS-CoV-2) which binds to the Angiotensin Converting Enzyme 2 (ACE2) endothelial receptor with the help of the TransMembrane serine protease type 2 (TMPRSS2).

The injured endothelium has a central role in the progress of the COVID-19 disease and as one of the three components of the Virchow's triad, it is the cause of extending thrombotic microangiopathy. Microthrombotic mechanisms that were proposed, are degradation of endothelial junctional proteins and glycocalyx, endothelial cell derived microvesicles, endothelial exocytosis, and immunothrombosis with NETs.

Regardless of the endothelial mechanism, COVID-19 leads to altered microvascular hemodynamics and extensive microthrombosis and that was the reason clinical doctors proposed antithrombotic strategies. However, it was not shown whether antithrombotics reduce microthrombosis and an unknown coagulation factor was recently proposed. This presentation will focus on the latest COVID-19 related microthrombotic and microfluidic *in vivo* data, mainly from imaging techniques, in correlation to antithrombotic strategies.

## Biography

Aristotle G. Koutsiaris is currently an Assistant Professor in the Department of Medicine, School of Health Sciences, University of Thessaly, Biopolis, Larissa, Greece. His postgraduate work was on the application of optical imaging techniques on microvessels *in-vitro* and *in-vivo* and since then he has worked and taught at several academic institutions. His research work on biofluid dynamics, hemodynamics, microcirculation, biomedical imaging, and bio-microscopy, both *in-vitro* and *in-vivo* (in animals and humans) includes many papers in international scientific journals with a good scientific impact.

# "MUCOVID-21" STUDY OF MUCORMYCOSIS IN TERTIARY CARE CENTRE DURING COVID-19 PANDEMIC

**Sumeet Kumar, Rupal Choudhary and VP Pandey**
*Mahatma Gandhi Memorial Medical College and Maharaja Yashwantrao and Associated Hospitals, India*

## Abstract:

**Background:** Mucormycosis has been reported in several Indian states with the second wave of COVID-19 from January 2021 onwards. This prospective study was conducted with the objective of defining the contribution or association of various known and many suspected factors in the incidence of this disease during the ongoing pandemic.

**Method:** The study included 464 adults with Mucormycosis. Basic demographic data were collected. Patient history of COVID infection, its severity, duration of treatment, and oxygen use was taken to assess the association. History of use of antibiotics, steroids, antivirals, biologicals, and other complementary treatments was sought. History of diabetes and other comorbidities was noted. Patients were investigated for mucor confirmation using a nasal swab KOH mount, nasal endoscopy with biopsy, and radiological investigations were done to assess the extent.

**Results:** Out of 464 patients, 175 were known diabetics, and 157 were treated with steroids during COVID infection. Out of 287 post-COVID patients, 125 (44%) had rhino-Mucormycosis (RM), 102 (35%) had rhino-oculo-Mucormycosis (ROM) and 60 (21%) had rhino-oculo-cerebral- Mucormycosis (ROCM). 162 did not have a history of COVID, of which 93 (57%) had RM, 48 (30%) had ROM and 21 (13%) had ROCM.

**Conclusion:** This study has showed that COVID was not the only factor contributing to mucor, rather other factors such as diabetes, steroid use etc. were also contributory. Many patients who were suffering from Mucormycosis did not have a history of COVID. Advanced age, ROCM, and ICU admission were associated with increased mortality.

## Biography

Sumeet Kumar is currently working as an M.D General Medicine Doctor in Mahatma Gandhi Medical College & Associated Maharana Yashwantrao Hospital, Indore, Madhya Pradesh, India. His Paper Titled " MuCovid-21" Study of Mucormycosis in a Tertiary Care Centre during Covid-19 Pandemic has been published in Royal College of Physician, Edinburgh in the year 2021, December. Currently this Article has been accredited as one of the "Best Clinical Investigation" reviewed from Fellow of Royal College of Physician Edinburgh, Journal editorial staff for the year 2021-2022.

# FOURIER TRANSFORM INFRARED SPECTROSCOPY USED IN VIRUSES' DETECTION

**Andrei A. Bunaciu**
*AAB_IR Research Company, Romania*

## Abstract:

Recently, there have been an increasing number of reports of hitherto unknown viruses emerging as well as previously recognized viruses that had been under check reappearing. It should be remembered that 75% of newly emerging diseases in people are zoonotic, or brought on by infections that are spread from animals to people. The biochemical analysis gives essential information for the healthcare of patients. This evaluation is performed with the help of several connected disciplines and is the final result is the reunion of all the data elements. Nowadays, the chemical analysis and microbiological evaluation are the most important steps in a complete clinical analysis. Infrared spectroscopy is an analytical technique more and more used for the characterization of complex biological matrix, for studying all the modifications appearing in the human body and so to detect earlier changes that can generate diseases. Given the growing number of samples that need to be analyzed as soon as possible, there is an urgent need to develop fast and cost-effective methods for viruses' diagnosis analysis. This presentation reviews some applications of this vibrational spectroscopic technique for viruses' analysis recently published.

## Biography

Andrei A. Bunaciu, graduated the Politehnica University of Bucharest in 1979. He received the Ph.D. degree from the Politehnica University of Bucharest, Faculty of Chemistry, Department of Analytical Chemistry in the field of ion-selective membrane electrodes applied in pharmaceutical analysis in 1990. After several years as Senior Researcher in the Institute of Chemical and Pharmaceutical Research and Romanian Intelligence Service, he was also Senior Researcher in Vibrational Spectroscopy Department at SCIENT - Research Center for Instrumental Analysis, Bucharest. Now he is the C.E.O. of AAB_IR research company, www.aab-ir.ro. His research interests concern molecular recognition of pharmaceutical and biological compounds, using infrared spectroscopy techniques. He is the author/co-author of more that 95 publications in biomedical, pharmaceutical and food analysis, using different analytical techniques. He is the author/co-author of a book VIBRATIONAL SPECTROSCOPY APPLICATIONS IN BIOMEDICAL, PHARMACEUTICAL AND FOOD SCIENCES, A.A. Bunaciu, H.Y. Aboul-Enein and V.D. Hoang, published in 2020 by Elsevier, Inc. and two chapters: VIBRATIONAL SPECTROSCOPY APPLICATIONS IN DRUG-ANALYSIS, A.A. Bunaciu, H.Y. Aboul-Enein, in Encyclopedia of Spectroscopy and Spectrometry, 3rd Edition, Lindon, J.C., Tranter, G.E. and Koppenaal, D.W. (eds.), Oxford; Elsevier, 2017, vol. 4, pp. 575-581, and respectively RECENT APPLICATIONS OF INFRARED SPECTROSCOPY IN BIOMEDICAL ANALYSIS, A.A. Bunaciu, H.Y. Aboul-Enein, in FTIR Spectroscopy: Advances in Research and Applications, edited by Adriana S. Franca and Leandro S. Oliveira, Nova Publishers, NY, USA, 2022, pp. 575-581.

# THE PLACE OF OMEGA 3 FATTY ACIDS IN OPTICAL AND CARDIAC HEALTH

**Ibezim Emmanuel Chinedum**
*University Of Nigeria Nsukka, Nigeria*

## Abstract:

The omega 3 fatty acids are obtainable in the diet and also in human plasma and tissues. They are a group of polyunsaturated fatty acids that are important for a number of functions in the body. Two omega-3 fatty acids: Eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA) are found in seafood, such as fatty fish (e.g., salmon, tuna, and trout) and shellfish (e.g., crab, mussels, and oysters). A different kind of omega-3, called alpha-linolenic acid (ALA), is found in other foods, including some vegetable oils (e.g., canola and soy). Omega-3s are also available as dietary supplements; for example, fish oil supplements contain EPA and DHA, and flaxseed oil supplements contain ALA. Of these, DHA is the most abundant fatty acid in plasma, as well as in brain and retinal cell membranes. Omega 3 fatty acids have been found very useful in heart health, treatment of eye conditions, infant development, treatment of rheumatoid arthritis, brain function development and treatment of cancers. In the heart, they are reported to regulate heart beat thereby helping in the treatment of cardiac arrhythmias, cardiac arrest, lowering of blood pressure, ease inflammation and reduce the incidence of atherosclerosis. DHA is in the eye's retina, so a diet rich in this type of omega-3 can improve eye health and help prevent degenerative conditions such as muscular degeneration. Research suggests that EPA can also improve eye health to a lesser degree, but the reasons are, as yet, unknown. DHA plays important roles in the functioning of the eye. Researchers are actively investigating the possible benefits of DHA and other omega-3 fatty acids in preventing or treating a variety of eye-related conditions. There is also strong evidence of the usefulness of Omega 3 fatty acids in the treatment of age-related eye diseases (AREDs) and age-related maculopathy (ARM).

## Biography

Emmanuel C. Ibezim is a Fellow of the Pharmaceutical Society of Nigeria (PSN), Fellow of the Nigeria Academy of Pharmacy, Fellow of the Third World Academy of Sciences and Fellow of Institute of Industrial Administration. He is the emeritus National Chairman of Nigeria Association of Pharmacists in Academia (NAPA), one time Board member of World Association of Medical Editors, Board member of University of Nigeria College of Medicine and a current Board member of the University of Nigeria Agricultural Board. He is the current Chairman of the University of Nigeria Nsukka (UNN) Drug Manufacturing Firm. He has received several awards of recognition, including Award of Excellence by PSN Enugu State, Medical International Award by Institute of Industrial Administration, Young Professor Award by Pharmaceutical Society of Nigeria Enugu State, Award of Excellence by National Fellowship of Christian Pharmacy Students, UNN Best of Dean of the Year 2016, Gold Mentor Award of the Young Pharmacists Group of PSN, Mention in Marqui's Who is Who in American Science and Technology, Mention in Outstanding Scientists of the 21st Century, Biographee in 2002 International Directory of Distinguished Leadership, USA, Research Fellowship Awards to CDRI India (twice), IMA, Brazil (thrice), INIFTA Argentina, FIP Travel Award to Capetown SA, TETFUND IBR/Book Grant/Travel Awards, Legacy Award by SCM of Nigeria, UNN VCs Research Leadership Award, Outstanding Achievement Award by ISPOR, Excellence Award by Pharmacy UNN, Excellence Award by PANS and a host of others. He is a facilitator of several academic exchange programs of UNN with University of Toledo, Mercer University and Texas State University, all in USA. Professor Ibezim is a Jerusalem Pilgrim.

# *Canine brucellosis* AND MALE DOG INFERTILITY

**Baharak Akhtardanesh, Elham Mohammadi, Morteza Aghamiri, Zahra Asadi, Maziar Jajermi and Saba Yousefi**
*Shahid Bahonar University of Kerman, Iran*

## Abstract:

*Brucella canis* is the most common cause of Brucellosis in dogs. Other species that cause brucellosis in dogs include *B.abortus*, *B.melitensis* and *B.swiss*. In infected males, the normal morphology of sperm is changed and sometimes orchitis, epididymitis and scrotal edema and irreversible infertility may occur. The prolonged bacteremia and persistence of infection in the prostate gland in male dogs were reported and *Brucella spp* shed in their semen and urine in large quantities, causing risk of transmission to female dogs in sexual contact and zoonotic risk for people who handle dogs in breeding kennels or owners who prepare their pets from infected kennels. In this cross-sectional study, 40 male dogs with breeding disorders, aged 1 to 8 years were selected from several Kennels. After complete clinical examinations and under physical restraint, semen, blood and urine samples were collected. Confirmation of *Brucella* contamination was done the using conventional PCR method with IS711-specific primers. Real time PCR with UFI and URI primers for detecting *B. abortus* and *B. mellitensis* and BCAN B0548 primer for *B. canis* contamination were used in positive samples. The infection rate in semen, blood, and urine samples were 30%, 10% and 27.5% respectively. In the positive semen samples 15% were *B.millitensis*, and 12.5% were *B.abortus*, and *B. canis* . Out of positive blood samples 10% were *B.abortus* and 5 % were *B. canis*. In the positive urine samples *B.abortus, B.millitensis* and *B. canis* infection rate were 12.5%. In positive urine and semen samples, mix infection (*B.canis* –*B.abortus*) and (*B.canis* - *B.melitensis*) were detected. In the Positive blood samples only mix *B.abortus* and *B. canis* infection was recorded. Based on this finding, canine brucellosis must be considered as an emerging zoonotic disease in Iran. Therefore, identifying the infected dogs by screening methods is of particular importance in kennels.

## Biography

Baharak Akhtardanesh is a Professor of the Small animal internal medicine at the Shahid Bahonar University of Kerman where she has been a veterinary medicine faculty member since 2005. Her research interests lie in the area of Veterinary Infectious Diseases, Small animal internal medicine, Zoonosis, Vector-Borne Diseases, and Exotic animal and laboratory animal science. She has collaborated actively with researchers in several other disciplines of public health in research committees and published about 70 international research articles in these research fields.

# SEROPREVALENCE OF HBV AND HCV IN HIV PATIENTS AND IMMUNE RESPONSE AFTER 24 MONTHS OF HAART IN HIV/HBV OR HIV/HCV CO-INFECTIONS

**Ndifontiayong Adamu Ndongho**
*Dschang University, Cameroon*

## Abstract:

Hepatitis B (HBV) and C (HCV) are two among other forms of infections for which co-infection in HIV has been associated with alteration of the immune response, increased risk of progression to liver diseases and increased risk of hepatotoxicity associated to antiretroviral therapy. This study was aim to establish the prevalence of hepatitis B surface antigen (HBsAg) and hepatitis C antibody (HCVAb) among HIV patients, treatment outcomes and possible risk factors in Kumba Health, in the South West Region of Cameroon.

We performed a systematic screening using Rapid Diagnostic Test, for HBsAg and HCVAb among 299 HIV patients enrolled at the treatment centers in Kumba Health District with all positives for HBV or HCV confirmed by the ELISA and results analyzed using SPSS version 20. Out of the 299 participants, 36 (12.0%) were positive for HBV and 12 (4%) for HCV by both RDT and ELISA, out of which 52 HIV patients, 36 HIV/HBV and 12 HIV/HCV patients were involved in the prospective cohort study for 24 months which permitted monitored the immune response (CD4 counts and viral load test), as well as variation of biochemical parameters (ALAT/ASAT, albumin, bilirubine, creatinine) and weights of the studied participants. There were positive variations in all the biomarkers and immune response measurement which differed among the different groups and so this result could be used for health decisions regarding co-infecteds.

## Biography

Ndifontiayong Adamu Ndongho has completed his PhD at the age of 33 years from Dschang University and is a Senior Public Health Administrator from the National School of Administration and Magistracy Yaounde. He is the Chief of Bureau Health, Focal Point Disease Surveillance in the South West Region of Cameroon. He is a Frontline field Epidemiologist and an expert in Incidence and Risk management. He has published articles in International Journals, a speaker in International Conferences and a Reviewer.

# PROFILING OF VIRUSES AIDS THE DEVELOPMENT OF EFFICIENT MANAGEMENT STRATEGIES

**Suja Aarattuthodi, Lester Khoo, Brian Bosworth and Ganesh Kumar**
*Mississippi State University, USA*

## Abstract:

Catfish industry with an economic impact of $1.9 billion per year and 74% contribution to the finfish production is the largest sector of the U.S. aquaculture. Infectious agents can severely impact catfish production. Catfish viruses such as channel catfish virus (CCV) and blue catfish alloherpesvirus (BCAHV) are problematic during the hatchery and nursery phases of catfish culture. Viruses are dynamic entities that constantly evolve and adapt according to the surrounding environment, available resources, and hosts potentially leading to expansion in host range, host switch, and increase in virulence. Profiling catfish viruses will facilitate development of efficient pathogen-targeted management strategies. The external and internal clinical signs of infection, histopathological alterations, and cytopathic effects on cell cultures caused by these viruses are similar. While CCV is more pathogenic to channel catfish fingerlings, BCAHV caused significant mortality in blue catfish. Younger catfish are more vulnerable to viral infections. Crowding of fish and increased viral loads significantly increased viral infectivity and associated mortalities. Development of disinfection protocols, vaccines, and establishment of new catfish cell lines will aid with the management of these viruses. Both *in vitro* and *in vivo* experiments indicated the inactivation of CCV in the presence of a commercial disinfectant. An attenuated CCV vaccine was developed by serial passage of the wildtype virus in catfish cell lines. This attenuated vaccine was administered to channel and hybrid catfish fingerlings via immersion. Thirty days post immunization, the immunized and non-immunized fish were exposed to wildtype CCV. Results indicated that the vaccine significantly improved the survival of immunized channel and hybrid catfish compared to the non-immunized group confirming the protective immunity conferred by the attenuated virus vaccine. Further studies are underway to evaluate the efficacy of the vaccine.

## Biography

Suja Aarattuthodi is an Assistant Research Professor at the Thad Cochran National Warmwater Aquaculture Center, Mississippi State University. Her research interests include characterization (phenotypic and genotypic) of fish pathogens, host-pathogen interactions, development and evaluation of vaccines against fish pathogens, development of fish cell lines and screening of antivirals etc.

# PENICILLIN SUSCEPTIBLE *Staphylococcus aureus*: INTER-RATER AGREEMENT IN INTERPRETING THE PENICILLIN ZONE EDGE TEST

**Lee-Ann Sampson**
*National Health Laboratory, South Africa*

## Abstract:

**Background:** The penicillin zone edge test is a method used to detect the enzyme penicillinase in Staphylococcus aureus. Experience at the Groote Schuur Hospital, Microbiology laboratory, has found the test to be difficult to interpret because of its subjectivity, and the test was discontinued. In this study we aim to prove the value and liability of the penicillin zone edge test in the laboratory.

**Methods:** We prospectively reviewed and compared the results of 6 technologists, of different years of experience and confidence levels, who analysed the penicillin zone edge tests of 20 susceptible Staphylococcus aureus isolates. The inter-rater agreement between technologists were calculated using the Kappa statistic score. The Kappa value and P-value was calculated for all technologists and by technologist experience and was repeated for high and low confidence calls.

**Results:** The kappa was at an overall low, although, by observation the level of agreement was expected to be high. One would suspect a phenomenon known as the paradoxical effect to have taken place, which means that even if technologists agree nearly most of the time, the kappa result remains low. An alternative method was proposed in readings where we would have to calculate a new coefficient, $AC_1$, as the conditional probability that two randomly selected observers will agree, given that no agreement will occur by chance. Using this method, $AC_1$ will resist the 'paradoxical' effect of kappa.

**Conclusion:** A moderate to almost perfect agreement was met between technologist and a possible reimplementation of the penicillin zone edge test could be considered.

## Biography

Lee-Ann has her BHSc in Medical Laboratory Science. Her passion for Microbiology can be shown in her work done and the way she uplifted herself in the field since 2012-She started off as a general worker making Diagnostic media and today, through part time studying and learning, she is a qualified Medical laboratory scientist specializing in Microbiology at a top rated Academic laboratory based at Groote Schuur Hospital, Cape Town, South Africa. She is constantly seeking for improvements for the laboratory as well as for patient care- as shown in her project presented. Her passion for research was truly enhanced in this project after going through many stumble blocks and figuring everything out at the end-it surely ignited some fire.

# EVALUATION OF ANTIBACTERIAL POTENTIAL OF ENDOPHYTIC FUNGI AND GC-MS METABOLIC PROFILING OF *Talaromyces assiutensis*

**Hafiza Farhat, Shahid Ullah**
*Gomal University D.I Khan, Pakistan*

## Abstract:

Endophytic fungi live inside plant tissues but do not cause any disease. Several reports have now revealed that they have great influence on host. In this study, the beneficial role of endophytic fungi is highlighted and explored. Endophytic fungi were isolated from healthy wild as well as cultivated plants and were identified as *Aspergillus terreus*, *Curvularia lunata*, *C. hawaiiensis*, *Macrophomina phaseolina*, *Fusarium solani*, *Talaromyces assiutensis*, and *T. trachyspermus*. The endophytic fungi initially identified morphologically and also confirmed by using 18S rRNA gene sequencing. *In vitro*, the isolated fungi evaluated for antibacterial activity and were tested against common laboratory bacteria (*Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Salmonella typhimurium*, *Bacillus subtilis* and *Escherichia coli*), showed significant activity. Culture filtrates of *Talaromyces assiutensis* showed strong antibacterial potential and are further used to check the presence of metabolites by GC–MS analysis. Several new compounds were isolated from *T. assiutensis* by Gas Chromatography and Mass Spectrometry technique. The major bioactive compounds identified from n-hexane fraction of *T. assiutensis* are Coumarin, 3,4-dihydro-6-methoxy- 4,4-dimethyl, 1-Monolinoleoylglycerol trimethylsilyl ether, 1,2-Propanediol, 3-(octadecyloxy), Ethyl iso-allocholate, and 1H-Pyrazole, which possess antioxidant, antitumor, antibacterial, anticancer, and antimicrobial properties. These findings will lead to further in-depth research toward the potential use of these endophytic fungi for their possible use in agriculture and drug formation.

## Biography

Hafiza Farhat did Ph.D on Antibiotic producing endophytic fungi associated with healthy plants and received Ph.D degree from university of Karachi. Now she is serving in well renowned and Public Sector University (Gomal University D.I Khan) of Pakistan as an Assistant Professor. She have research articles in high impact factor journal in national and international journals. She attended so many conference and workshop as a speaker. She is also a gold medalist as she achieved two gold medals in University level by getting first position in M.Sc.

# THE NEUTROPHIL TO LYMPHOCYTE RATIO IN POSTSTROKE INFECTION: A SYSTEMATIC REVIEW AND META-ANALYSIS

**Brandon Lucke-Wold**
*University of Florida, USA*

## Abstract:

Ischemic and hemorrhagic strokes have multiple downstream consequences for patients. One of the most critical is poststroke infection (PSI). The goal of this systematic review and meta-analysis was to critically evaluate the literature regarding the use of the neutrophil to lymphocyte ratio (NLR) as a reliable means to detect early PSI development, particularly poststroke pneumonia (PSP) development to help clinicians institute early interventions and improve outcomes. The following were the inclusion criteria: (1) cross-sectional, case-control, and cohort studies; (2) studies comparing NLR data from PSI or PSP patients to controls; and (3) studies with a control group of stroke patients without infection. There was not any language or publication preference. The Newcastle-Ottawa Scale was used by two writers to assess the quality of the included studies. We assessed the certainty of the associations with GRADE methods. Web of Science, PubMed, and Scopus were searched, and 25 studies were included in the qualitative review. Among them, 15 studies were included in the meta-analysis. Standardized mean difference (SMD) was reported with a 95% confidence interval (CI) for the NLR levels. Patients with PSI had significantly higher NLR levels than stroke patients without infection (SMD = 1.08; CI 95% = 0.78-1.39, P value < 0.001). In addition, the NLR levels of the stroke patients with pneumonia were significantly higher than those without pneumonia (SMD = 0.98; CI 95% = 0.81-1.14, P value < 0.001). However, data extracted from the qualitative review suggested that NLR could not predict urinary tract infection, sepsis, or ventriculitis in stroke patients. Our study indicated that NLR could be recommended as an inexpensive biomarker for predicting infection, particularly pneumonia, in stroke patients. It can help clinicians institute early interventions that can reduce PSI and improve outcomes.

# COVID 19 IN PATIENTS WITH NEUROLOGICAL DISEASES

**Andreea Cristina Stoian[1], Carmen Albu[1], Ramona Denise Mălin[2], Alexandra Poenaru[2], Florentina Dumitrescu[1], L. Giubelan[1] and Livia Dragonu[1]**
[1]*University of Medicine and Pharmacy from Craiova, Romania*
[2]*Neurological Hospital Diseses from Craiova, Romania*

## Abstract:

**Objectives:** Epidemiological and Clinical Analysis of patients (Px) with neurological diseases and COVID 19.

**Method:** Retrospective study in Clinical Hospital of Neuropsychiatry from Craiova, in period 01/03/2021-31/12/2022, in 2 groups of Px: group A-274 Px with COVID 19 and favorable evolution and group B-67 Px death with COVID 19 in which clinical and epidemiological data were analyzed. The statistical analysis used the Epi Info program, the threshold (p) being statistically significant at values ≤ 0.05 and the regression coefficient ($R^2$).

**Results:** Group A *versus* group B: F/M-131 Px (47.81%)/143 Px (52.18%) *vs* 32 Px (47.76%)/35Px(52.23%) %); ($p<0.05$); average age=69 ± 9.8 years (28-89 years) *vs* 77.23 ± 12.6 years (28-89 years), mean= 68 years *vs* 76 de years ($p<0,0001$), seasonal distribution: 146 Px (42,82%) in period 01/10/2021-31/12/2021 ($R^2=0,398$). The highest death rate was found in period 01/10/2021-31/12/2021- 26 Px (38. 81%) of total death ($R^2=0.076$). In group A 173 Px (74.25%) *vs* 2 Px (3.7%) in group B ($p<0.05$). was vaccinated anti SARS CoV2. “Late presenters” (more 7 days from onset of disease) was 119 Px (43.75%) from group A *vs* 43 Px (67.17%) from group B. Neurological manifestations at the onset of COVID was found in 173 Px from group A *vs* 41 Px from group B ($p<0.05$). Each Px was presented ≥ 3 comorbidities. The forms of SARS-CoV2 infection were: mild (41 Px-14.97%), moderate (136 Px-49.63%), severe (97 Px-35.41 %); Antiviral treatment was administered at 295 Px (86.51% of total Px with COVID 19) so: 252 Px (73.91%) from group A *vs* 40 Px (59.71%) from group B: Favipiravir in 82 Px and Remdesivir in 176 Px ($p<0.05$).

**Conclusion:** At Px with neurological disease and COVID 19, most cases were present in males, with peaks of seasonal incidence; the most common were moderate and severe forms of the disease and the high risk of death. Unfavorable development has been associated with: male, immunosenescence, absence of SARS CoV2 vaccination, multiple comorbidities and severe neurological manifestations of onset. Antiviral therapy was associated with favorable evolution

# THE ESSENTIAL ROLES OF METABOLIC REPROGRAMMING AND GENETIC VARIATION IN THE DEVELOPMENT OF ANTIMICROBIAL RESISTANCE IN *Helicobacter pylori*

**Anis Rageh Al-Maleki, Naim Aysraf Rosli, Loke Mun Fai and Jamuna Vedivelu**
*Universiti Malaya, Malaysia*

## Abstract:

**Introduction:** Clarithromycin is used to treat Helicobacter pylori infections that could lead to gastritis, peptic ulcer disease, and gastric cancer. One of the most prevalent causes of treatment failure is the emergence of antibiotic-resistant H. pylori infection. An important part of antimicrobial resistance mechanisms is played by bacterial genetic variation and metabolic processes such as energy production, bacterial growth, cell wall construction, and cell-cell communication. Identification of microbial genetic and metabolites variations may lead to discovery of novel antimicrobial drug targets and treatments.

**Aim:** This study aims to determine the H. pylori genetic and metabolomic reprogramming and compensatory mutations that associated to the development of antibiotic resistance in clarithromycin-induced resistant H. pylori strain.

**Method:** Four H. pylori strains were induced to become resistant against clarithromycin by exposure to gradually higher concentration of clarithromycin in vitro. Genomic profile of sensitive pre-resistant and resistant strains was analysed by whole genome sequencing approach using Illumina NGS technology. Moreover, the bacterial metabolites were isolated using the Bligh and Dyer technique and analysed using liquid chromatography-mass spectrometry (QTOF-LCMS). The MassHunter Qualitative Analysis (MHQ) and Mass Profiler Professional (MPP) tools were used to process and analyse the data.

**Result:** There were 113 distinct single nucleotide variants (SNVs) and 286 unique insertions and deletions (InDels) changes discovered among the induced-resistant H. pylori strains. Among the induced-resistant H. pylori strains, highly polymorphism in cag1, cag4, fliR, obgE, tlpA, vacA, and rsmH were detected, which are known virulence genes that may help in bacterial survival, indicating that those mutations may be associated with the emergence of resistant H. pylori. Enhanced biofilm formation was significantly detected among induced strains comparing to wild type. Furthermore, highly polymorphism also detected among several genes associated with biofilm production. Moreover, several metabolites (L-leucine, Pyridoxone [Vitamine B6], D-Mannitol, Sphinganine, Indoleacrylic acid, and Dulcitol) were significantly (p-value $<0.05$) upregulated in induced-resistant H. pylori strains comparing to sensitive. These metabolites correlated with bacterial survival and may constitute a potential antibiotic mechanism.

**Conclusion:** We suggest that clarithromycin resistance development is associated with enhanced virulence and survival of H. pylori. Moreover, metabolomics technologies offer great potential to unravel metabolic underpinnings of antibiotic drug action and resistance. Understanding the underlying metabolome variations between clarithromycin-sensitive H. pylori strains and clarithromycin-resistance H. pylori strains may be a promising technique for developing novel antibiotic candidates.

# POLYCYSTIC OVARY SYNDROME FEATURE EXTRACTION USING DESIGN OF EXPERIMENTS

**Kavita Pandey**
*Jaypee Institute of Information Technology, India*

## Abstract:

All over the world, Polycystic ovary syndrome (PCOS) is the most common syndrome found in women. In India, earlier one in every ten women had PCOS but nowadays, one in every five women has PCOS. Actually, it is not a disease but it's a syndrome as it may lead to several other diseases like diabetes, high blood pressure, irregular periods, etc. PCOS symptoms vary according to age like in teenagers, PCOS may be detected by irregular periods and in middle age, PCOS may be detected by infertility, cancer in the uterus, risk of miscarriages, etc. In the modern era, PCOS identification is not easy as it is dependent on various parameters. Here, the objective is to find the most important parameters for identifying the PCOS with the Design of experiments (DOE) analysis tool. The question "Can we identify the PCOS with less number of parameters" needs to be answered. The 2k-p fractional factorial design was utilized as it can take a large number of inputs and gives the response in a fewer number of experiments. PCOS dataset of 541 instances and 7 attributes were taken to implement DOE in which 7 attributes are reduced to 4 attributes. The percentage of variation of reduced attributes, Follicle No. (r), FSH/ LH, Follicle No. (l), Skin Darkening has been obtained as 28.44%, 21.36%, 15.29% and 15.29% respectively through 2k-p fractional factorial design method. DOE response was validated using ANOVA and Minitab statistical software. Pareto chart reference line indicates the effectiveness of Follicle No. (r), FSH/ LH, Follicle No. (l) and Skin Darkening. This analysis can help doctors to diagnose PCOS and researchers to save time by disposing of irrelevant parameters when performing experiments for PCOS diagnosis-related studies in future.

## Biography

Kavita Pandey is currently working as an Assistant Professor (Senior Grade) in Jaypee Institute of Information Technology (JIIT), Noida. She has more than 18 years of academic experience. She received her B.Tech. in Computer Science and Engineering from M.D. University in 2002 and M.Tech. (CS) from Banasthali Vidyapeeth University in year 2003. She has obtained her Ph.D. (CS) from JIIT, Noida, India in January, 2017. Presently, she is guiding two Ph.D. students. She has mentored 15 M.Tech. thesis / industrial projects and 56 + undergraduate projects. She is an editor of a book named as "Artificial Intelligence, Machine Learning and Mental Health in Pandemics: A Computational Approach", Elsevier. Her research interests include Soft Computing, Machine Learning, Vehicular Ad hoc Networks, Internet of Things and Optimization Techniques. She has published 50+ articles in International journals and conferences including Wiley, IEEE, Springer, Inderscience, etc. She worked as a guest editor of special issue, "Advances in Computational Intelligence and Applications" in International Journal of Information Retrieval Research (IJIRR), IGI Global, ESCI, Web of Science. She is working as an Academic Editor on the Editorial Board of International Journal of Distributed Sensor Networks, Hindawi. She worked as a reviewer in many international journals of renowned publishers including Elsevier, Inderscience, IEEE Access, etc. She is an active TPC member of many conferences such as REDSET, IC3, UPCON, TEAMC, ICTCS and many more. She is also a senior member of IEEE society.

# PREVALENCE, BACTERIAL PROFILES AND FACTORS ASSOCIATED WITH SURGICAL SITE INFECTION AMONG POST-OPERATIVE MOTHERS AT KAWEMPE NATIONAL REFERRAL HOSPITAL, UGANDA

**Muyingo Yusuf, Nakijoba Jawuhala, Olwee Isaac Eluma, Hassan Muhammad, Angwiunzi Alfred Koma, And Rogers Kalyetsi**
*Kiwoko Hospital, Mulago Hospital, Uganda*

## Abstract:

Surgical site infections (SSI) pose a global threat of morbidity and mortality in patients undergoing all types of operations and account for a fifth of all healthcare-associated infections and about 12% of maternal deaths in developing countries Uganda inclusive, Ideally cesarean section is a sterile procedure where no infections are expected post operatively aseptic techniques and sterile instruments are used. Post operatively, antibiotics are administered and the wound is cleaned with a disinfectant under aseptic techniques to prevent surgical wound infection. The mother as well is given nutritious foods post operatively with plenty of vitamin C which promotes quick wound healing. Despite all the above endeavors to prevent wound infection, it has been noted that post cesarean wound infection is still a problem in Kawempe National Hospital.

In 2012, the rate of wound infection after cesarean section in Mulago hospital was 7.03% in 2012, 20.4% in 2013, and 85% of SSI in 2020 with 58.5% gram-negative and 41.5% gram-positive bacteria. *S. aureus* and *Enterococci* species, and *Klebsiella*, *E. coli* and Citrobacter were dominant gram-positives and gram negatives respectively. Due to this outrageous increased number of mothers failing to heal-off their surgical site, and Its not clear why these mothers end up with sepsis post operatively; therefore the study is focused on determining the commonest pathogens causing sepsis, their antimicrobial susceptibility and the associated factors.

Across-sectional study, with 202 participant using purposive sampling(non-probability selection) will be conducted within the period of two months 2023. Swabs will be inoculated on microbial agar plates, incubated in carbondioxide at 37°C for 24-48 h and examined macroscopically for potential pathogens. Gram reaction will be done to enable suitable biochemical tests of the pathogens.

Meuller Hinton agar plates will be uniformly seeded with a suspension of fresh isolates of pathogens, Antimicrobial discs of the right potency will then aseptically be placed, incubated at 37°C for 18-24 h. Zones of inhibitions will be measured in millimeters using a ruler and interpreted according to the inhibition zone sizes as sensitive, intermediate and resistant against the standard chart.

## Biography

Muyingo Yusuf is a medical laboratory profession with passion to uphold the role of every laboratory professional in the health sector in Uganda and abroad. He is currently the General secretary of Uganda medical laboratory technology association, Working as a quality officer at Kiwoko hospital, Deputy chairperson secretariat on the previously concluded Africa cancer test and treat initiative conference held at Hotel Africana.

He has a working experience of so far 10 years in the medical laboratory health sector, completing his bachelors degree in medical laboratory science at Mbarara University, holds advanced diplomas in Six Sigma, Workplace Safety And Health, Quality Management from Alison, Advanced Microbiology from Saylor Academy, and Advanced Fungal Microscopy from University of Manchester(UK).

Has interested him self contributing in research, evaluation, teaching and administration both in hospital and education institutions thus attaining an enrolment for Master degree in Public Health/Microbiology at Atlantic International University starting July 2023.

# BIOTECHNOLOGICAL EXPLORATIONS OF PHYTO-DRUGS, SAPONIN-POLYBROMOPHENOL OF *Cassia fistula* BARK AND TEPENTINE-GLYCOSIDES OF *Suregada multiflora* ROOT AGAINST MDR BACTERIAL INFECTIONS

**Asit Kumar Chakraborty**
*Vidyasagar University, India*

## Abstract:

Presently, *Escherichia coli, Salmonella enterica, Acinetobacter baumannii, Pseudomonas aeguginosa, Enterococcus faecium* and *Klebsilla pneumoniae* mediated infections were not cured by conventional antibiotics like ampicillin, streptomycin, chloramphenicol, erythromycin and ciprofloxacin due to presence multiple large and small MDR plasmids with >10 mdr (*amp, bla, cat, str, aac, aph, aad*) genes and drug efflux genes (tetA/B/C, acrAB-TolC, mexAB-OprM) in those pathogens. MDR genes inactivate antibiotics through phosphorylation, acetylation, adenylation or antibiotic cleavage. Chromosomal genes mutations (rpoB, gyrA/B) in Mycobacteriaum tuberculosis were reported for drug resistance to conventional anti-tuberculosis drugs. Thus, development of new antibiotics is urgently needed. Plants secret anti-metabolites to retard growth of soil and water bacteria and are ideal source of new antibiotics. We selected few antibacterial phyto-drugs from 80 ethanol extracts. The *Cassia fistula* bark saponin polybromophenol compound (CU1) inhibited (IC50=20-30 µg/ml) RNA polymerase from *Escherichia coli* as well as *Mycobacterium tuberculosis* as compared to refampicin. Similarly, well cultivated *Suregada multiflora* root extract was found exceptionally active (18 fold than bark) against MDR bacteria and TLC-purified NU2 glycoside inhibited *E. coli* DNA topoisomerase I at $10^{-20}$ µg/ml and RNA polymerase to some lesser extent at >20µg/ml. Ethanol extracts of Jatropha gossipifolia root, *Shorea robusta* inner bark, and Trapa bispinota fruit peel also have good MDR antibacterial activities but need further evaluation. Phyto-chemical in each extract was abundant and gave a distinct band on preparative TLC (20 cm x 15 cm) needed for large quantity purification. MDR-bacteria were easily isolated from 100 µl of Ganga River water, rain water, chicken meat extract, milk and human hair extract on 10 cm LB-Agar plus ampicillin plate. The imipenem resistant bacteria were isolated from 10 ml Ganga River water to grow over night with 5 µg/ml imipenem and then single colony was purified from 1µl of overnight culture plated on10 cm LB-Agar plus 20 µg/ml imipenem. A mixture of TLC-purified active chemicals cured MDR human nail infections. In rat model, such active chemicals (CU1, CU2, NU2, JU2) eliminated systemic *E. coli* KT-1_mdr infection (>85%) where ampicillin failed to do so. NU2 and CU1 did not killed Molly fishes *in vitro* at 20-50µg/ml and also have no effects on cultured HeLa cells in DMEM medium. We think antibiotic void will increase due to few reasons: (1) mdr genes are accumulated in large conjugative plasmids with many IS elements; (2) the spread of mdr genes in bacteria is increasing at ~5%/year and (3) mdr genes protect gut microbiota from antibiotics. Thus, phyto-drugs discovery is logistic and demanding. We proved that MDR-CURE Phyto-Drug is useful to tackle multi-drug resistant infections.

**Audience will learn:** The lecture will be very informative on abundance in MDR bacteria in Ganga river water as well as in chicken meat and milk as well as its present status on mdr enzymes that inactivate antibiotics. A details purification and characterization of phyto-drugs through MASS, HPLC, NMR, FTIR will be focused. Toxicological study using HeLa cells and molly fishes will be discussed. Further, few human clinical trials on MDR nail infections will be reported.

## Biography

Asit Kumar Chakraborty was performed his PhD at CSIR-Indian Institute of Chemical Biology, Kolkata and awarded PhD degree in 1990 from Calcutta University. He did postdoctoral work at University of California at Berkeley and visiting scientist at Johns Hopkins University School of Medicine. He was Associate Professor of Biochemistry at OIST, Department of Biotechnology, Vidyasagar University and now retired. He published more than 60 papers in reputed journals.

# EVALUATION OF NEMATICIDAL POTENTIAL OF ENDOPHYTIC FUNGI ASSOCIATED WITH HEALTHY PLANTS AND GC-MS METABOLIC PROFILING OF *FUSARIUM SOLANI*

**Hafiza Farhat, Shahid Ullah**
*Gomal University D.I Khan, Pakistan*

## Abstract:

Endophytic fungi are now recognized as an excellent source of widely occurring natural products. Fungi are wonderful producers of natural products, mostly secondary metabolites. The vital use of these fungi may provide benefit to current demand for novel biomolecules in agriculture, medical and pharmaceutical industries. In this study, endophytic fungi *Aspergillus terreus*, *Cephalosporium sp*., *Chaetomium sp*., *Curvularia lunata*, *Curvularia hawaiiensis*, *Macrophomina phaseolina*, *Fusarium solani*, *Talaromyces assiutensis* and *Talaromyces trachyspermus* isolated from healthy plants and evaluated for nematicidal activity against Meloidogyne javanica, a root-knot nematode. *In vitro* culture filtrates of these fungi showed strong nematicidal activity by killing juveniles of nematode to varying degree, where *F. solani* caused 100% mortality after 48 hours. n- Hexane fraction of culture filtrate and n-hexane extract of mycelium of *F. solani* were subjected to GC-MS analysis, resulted in the identification of several compounds and some are not reported before from this fungus. Metabolites from endophytic *F. solani* could be used in the development of antimicrobial agents that can be used in medicine or agrochemicals. The use of fungal based products offers a unique opportunity to discover novel therapeutic agents to combat various infectious agents and agricultural pests.

## Biography

Hafiza Farhat did Ph.D on Antibiotic producing endophytic fungi associated with healthy plants and received Ph.D degree from university of Karachi. Now she is working in well renowned university (Gomal University D.I Khan) of Pakistan as an Assistant Professor. She have research articles in high impact factor journal in national and international journals. She attended so many conference and workshop as a speaker.

# DETECTION OF ADHESIVE SURFACE PROTEINS IN MRSA ISOLATES OBTAINED FROM KARACHI, PAKISTAN

**Uroosa Ejaz, Muhammad Sohail and Fakhur Uddin**

*Shaheed Zulfikar Ali Bhutto Institute of Science and Technology, Pakistan*

## Abstract:

*Staphylococcus aureus* is one of the most important human pathogen that causes a wide range of infections. These isolates asymptomatically colonize on surfaces of healthy individuals, and thus the carriers can spread these infectious pathogens. The emergence of methicillin-resistant *S. aureus* (MRSA) strains is an increasing public health challenge associated with high mortality and morbidity. In order to carry out epidemiological studies of MRSA strains several typing methods are available. There are some reports of molecular analysis and typing of MRSA strains from all over the world, although there is limited data regarding major MRSA clones circulating in our region. Therefore, MRSA isolates from hospital of Karachi were collected and screened for gene analysis. A total of 36 MRSA isolated were collected. Detection of the mecA and several adhesive surface proteins genes including *clfA* (encoding clumping factors A, B); *fnb* A, B (encoding finronectin binding proteins A, B); *fib* (encoding fibrinogen binding protein); *eno* (encoding laminin binding protein); *cna* (encoding collagen binding protein); *fem A* (encoding a protein precursor involved in peptidoglycan biosynthesis); and *bbp* (encoding bone sialo-protein binding protein), was performed by PCR. A relatively high diversity was found in MRSA genotypes. Isolates of *S. aureus* express a myriad of adhesive surface proteins that play important role in colonization of the bacteria on nasal and skin surfaces, beginning the process of pathogenesis. In addition, the high prevalence of MSCRAMMs genes in MRSA isolates demonstrates the high potential of these strains for pathogenicity. The high prevalence of these genes is important for future plans in vaccine designation.

## Biography

Uroosa Ejaz is a highly motivated researcher with a MPhil in Microbiology and over 06 years of research experience. She has published 18 research articles in well reputed International Journals and also wrote 05 book chapters sponsored by Springer and Elsevier. She has work experience from Agha Khan University and Hospital, Patel Hospital, Bahria University and University of Karachi. She also worked as a research assistant in HEC funded NRPU project. Currently, she is serving as a Lecturer at SZABIST and she is also a PhD scholar in University of Karachi, Pakistan.

# NEONATAL SEPTIC ARTHRITIS – ANALYSIS FROM A NOSOCOMIAL OUTBREAK IN AN NICU

**Nachappa Sivanesan Uthraraj, Srushti Sahukar, Meghana Prakash Hiriyur Prakash, Siddharth Virani, Gowdar Guruprasad, Jai Relwani**

*East Kent Hospital University Foundation trust, United Kingdom*

## Abstract:

Septic arthritis of the neonates as part of a nosocomial outbreak is not a common condition. 16 joints of 14 neonates affected by this condition were profiled over a 3 month period. *Pseudomonas aeruginosa* was found to the predominant organism overall. The risk factors were analyzed. The course in the hospital including the diagnostic modalities, microbiological profiling, and treatment instituted (including surgery and adjunctive therapy with arthrotomy and antibiotics), immediate outcomes and the one year follow up were analyzed. The hip joint was the most commonly involved joint. The majority of the patients were pre-mature and all the neonates had low birth weight. The most effective treatment regimen was found to be arthrotomy surgery with adjunctive antibiotic therapy as per the local guidelines.

## Biography

Nachappa Sivanesan Uthraraj graduated in Medicine in India with an honors (distinction) in Anatomy. He then went on to pursue his clinical training in Trauma and Orthopaedic surgery, successfully defending his thesis and earning a masters from the Rajiv Gandhi University of Health Sciences, Karnataka, India. After taking up various roles including formal teaching and quality improvement, he was inducted as a member into the Royal College of Surgeons of Edinburgh. This was followed by various roles including, as a clinical research fellow, registrar and medical education fellow in the United Kingdom. He currently works as a medical education fellow and is faculty at the Royal College of Surgeons of England for the Basic Surgical Skills course. He is faculty for the MRCS preparatory course, conducted in collaboration with the Cardiff University. He holds a PG certificate in Medical Education and has designed courses delivered to the student body of the Cardiff University and the Federation of Obstetrics and Gynaecological Society of India. Apart from this he has numerous first author and collaborative publications and presentations to his credit. Outside work he is keen racer and holds a British Motorsports Karting License. He also enjoys running, sailing and playing tennis.

# STUDY OF STRESS LEVEL AMONG THE UNIVERSITY STUDENTS IN THE KINGDOM OF SAUDI ARABIA DURING AND AFTER LOCKDOWN

**Bader Naif M Alsubaie, Waad Ali M Alkaabneh, Nada Sulaiman E Alatawi, Ruby Naif Al Subaie, Saif Mohmmed Alomrany, Mohammad Zubair**

*MBBS Students of Faculty of Medicine, University of Tabuk, Saudi Arabia*

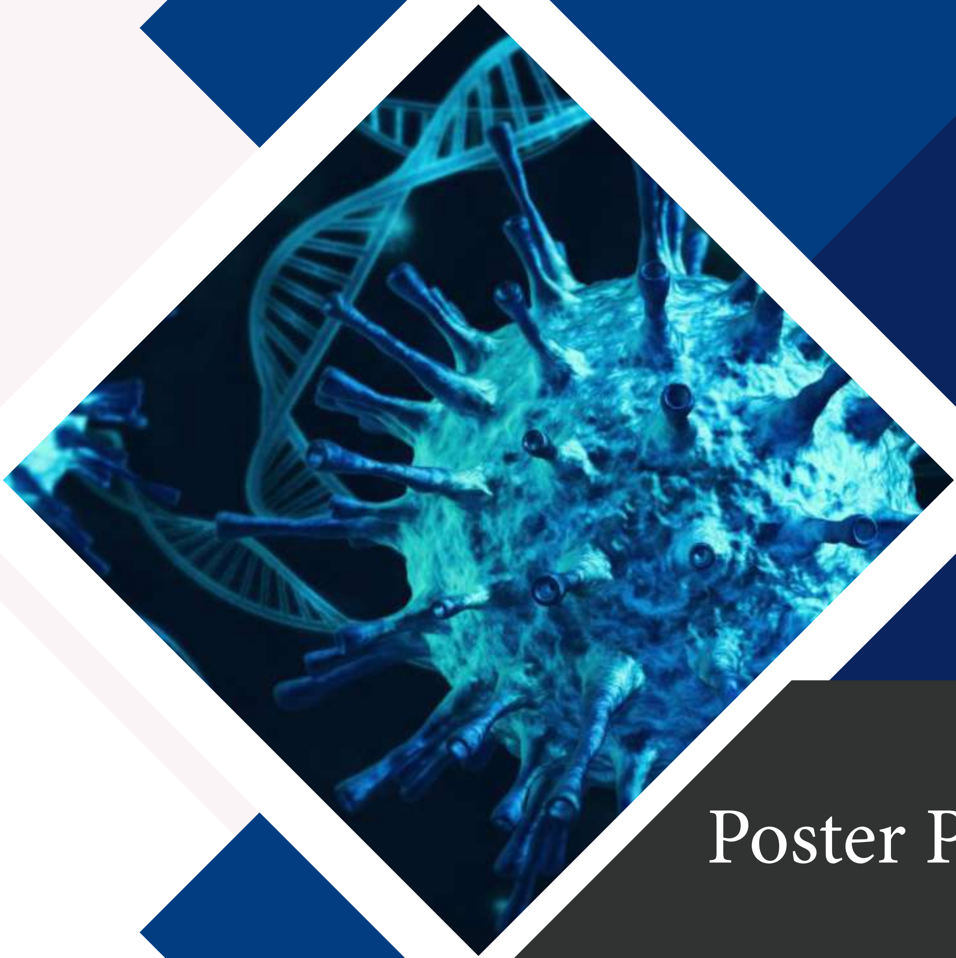
## Abstract:

**Background:** COVID-19 is the new coronavirus and most cases appeared in the Chinese city, Wuhan. At the end of December 2019 in the form of acute pneumonia. Older people, and people with pre-existing medical conditions (such as obesity, diabetes, and heart disease) appear to be more vulnerable to becoming severely ill with the virus. However, there are a lot of studies have shown a misconception regarding COVID-19 among different communities. This study was conducted in 13 provinces in the kingdom of Saudi Arabia in the year 2021 to measure the level of awareness, knowledge, and behaviors toward physical activity.

**Methods:** A cross-sectional study was conducted in 13 provinces in the kingdom of Saudi Arabia in the year 2021, during a period of 30 days. Nine hundred and one Saudi and non-Saudi students from Saudi universities who are doing bachelor's were included; using an electronic questionnaire. Data entry and analysis were performed using Microsoft Excel

**Results:** The prevalence of physical inactivity among participants is very high. The commonest reason for not using walking permission during the pandemic is fear of catching an infection. We found very high significance between males and females regarding physical activity rate before the pandemic and males will have a double chance to have their disease complicated. Regarding the effect 31% reported that their life is affected by stress and fear of catching an infection.

**Conclusion:** From this study, we conclude that stress analysis within the kingdom incorporates students from all 13 provinces. We found that organizing awareness campaigns and community programs by various organizations and health associates institutions was beneficial is relieving the stress levels during and after the pandemic.



# Poster Presentations

# ERDHEIM-CHESTER DISEASE: AN INCIDENTAL FINDING IN AN ASYMPTOMATIC 69-YEAR OLD

**Hema Merai, Adams L[1] Trotter C[1], Karachaliou Prasinou A[1], Ramsay M[2] and Campbell H[2]**

*National Health Service, UK*
*[1]Disease Dynamics Unit, University of Cambridge, UK*
*[2]UK Health Security Agency, UK*

## Abstract:

**Introduction:** In 2018 GSK announced their decision to cease the manufacture and supply of Hib/MenC combination vaccine Menitorix®. Therefore, changes to the UK immunisation programme need to be considered. The quadrivalent MenACWY vaccine is likely to be the most sustainable long-term option and is already used as part of the teenage immunisation programme. MenW and MenC cases may be controlled indirectly from the teenage MenACWY programme, however since meningococcal disease occurs more frequently in the first 24 months of life vaccination at 3 months or 12 months should also be considered.

**Aims:** To estimate the potential number of MenACWY cases prevented in one cohort born in 2025 from MenACWY vaccine given at 3-month or 12-month of age.

**Method:** Carriage data from two large UK studies was used to recalibrate a carriage-by-age prevalence curve and estimate the proportion of meningococcal carriage due to different serogroups. We then used a transmission model to estimate the indirect effects of the teenage MenACWY programme before adding the direct effects of MenACWY immunisation at either 3 or 12-months. Given the observed falls in cases of meningococcal disease during the pandemic and the reductions in the average number of contacts we also simulate the transmission model for periods of Covid-19 lockdown.

**Results:** We show that carriage prevalence of MenACWY is well controlled by the teenage vaccination programme. Using the pandemic assumptions and maintained high vaccine uptake we predict that MenACWY carriage prevalence will be <1% by 2025. In all scenarios, we predict that very few cases would be prevented by the addition of an infant/toddler MenACWY programme. Although adding the MenACWY dose at 3-months consistently results in a larger number of cases prevented. Assuming maintained teenage vaccination uptake, for one cohort born in 2025 we predict a maximum of 22 cases prevented (assuming 5 years protection for all the vaccinations we account for, no pandemic assumptions). Therefore, provided teenage uptake remains high and the infant 4CMenB programme is maintained we predict very few cases will be prevented from an infant/toddler MenACWY dose.

## Biography

Hema Merai, a Clinical Radiology Registrar, is in the final year of her specialty training. After practising as breast surgical trainee, she pursued her passion for breast imaging and completed an MSc in 'The Impact of Breast MRI on Invasive Lobular Cancer Management and its Correlation with Pathological Tumour Size – A 10-Year Study'. This led her to shift her focus to breast radiology and specialise in Northwick Park Hospital in London, U.K. With a keen interest in infectious diseases of the breast, she has published a paper titled 'Mammary Tuberculosis in the Young: A Case Report and Literature Review'.

# PREVALENCE OF COLISTIN RESISTANCE AMONGST GRAM-NEGATIVE BACTERIA AT GROOTE SCHUUR ACADEMIC HOSPITAL IN SOUTH AFRICA: RETROSPECTIVE STUDY AND LITERATURE REVIEW

**Nazlee Samodien, Zingisa Sinyeke and Kruger Marais**
*University of Cape Town, South Africa*

## Abstract:

Antimicrobial resistance is a global public health threat that is associated with considerable morbidity and mortality. The carbapenem class of antibiotics has long served as the last line of defence against extended-spectrum β-lactamase producing Gram-negative bacteria. Since the emergence and rise of carbapenem resistant Enterobacterales, carbapenems are less efficacious and the antimicrobial colistin has been increasingly used as salvage therapy to treat multi-drug-resistant Gram negative organisms.

There is a dearth of African data on colistin resistance rates. This retrospective laboratory based study included culture and antimicrobial susceptibility (AST) results for 668 clinical isolates from Groote Schuur Hospital, Cape Town over a 3 year period (2019–2021).  Colistin minimum inhibitory concentrations (MIC) were determined by the gold standard which is traditional broth microdilution testing as recommended by the Clinical Laboratory Standard Institute. The prevalence and trends of colistin resistance was analysed for most common, multi-drug-resistant clinical isolates namely *Klebsiella species, Acinetobacter baumannii* and *Pseudomonas aeruginosa.* Statistical analysis showed a trend towards higher MIC for *Klebsiella spp*. and *Acinetobacter baumannii* but this was not statistically significant. For *P. aeruginosa,* there was a statistically significant ($P<0.0001$) increase in MIC. The absolute rate of colistin resistant isolates increased from 3% in 2019 to 18% in 2020 to 61% in 2021. *P. aeruginosa* had the highest rates of colistin resistance (36%) as per CLSI 2021 interpretive criterion.

Low-to-middle socioeconomic countries like South Africa face catastrophic patient treatment failures if colistin resistance continues to increase. The true prevalence of colistin resistance in South Africa is likely underestimated due to the lack of access to BMD which is not routinely available at diagnostic laboratories. Unlike higher income countries, many of the novel agents targeting multi-drug-resistant pathogens are not currently available therefore efforts to curb resistance need to be escalated.

## Biography

Nazlee Samodien is a senior clinical microbiologist at the National Health Laboratory Services based at Groote Schuur Academic Hospital. Her expertise is in guiding management of complex infections in critical care patients; infection prevention and control; and antimicrobial stewardship. She is passionate about education and serves as an examiner on the College of Medicine (South Africa) board and is also a senior lecturer with extensive teaching experience and an expert in curriculum development and assessment.  The primary focus of her current research is in molecular genotyping of multi-drug-resistant Gram-negative organisms. She is dedicated to providing quality microbiology services, optimizing patient management and motivating students to excel in science fields.

# THE CO-COLONIZATION OF FUNGAL AND SARS-COV-2 IN MINI BAL SAMPLES OF THE HOSPITALIZED CHILDREN IN ONE YEAR

**Fatemeh Fallah, Abdollah Karimi, Ensieh Lotfali, Leila Azimi and Saeedeh Yaghoubi**
*University of Medical Sciences, Iran*

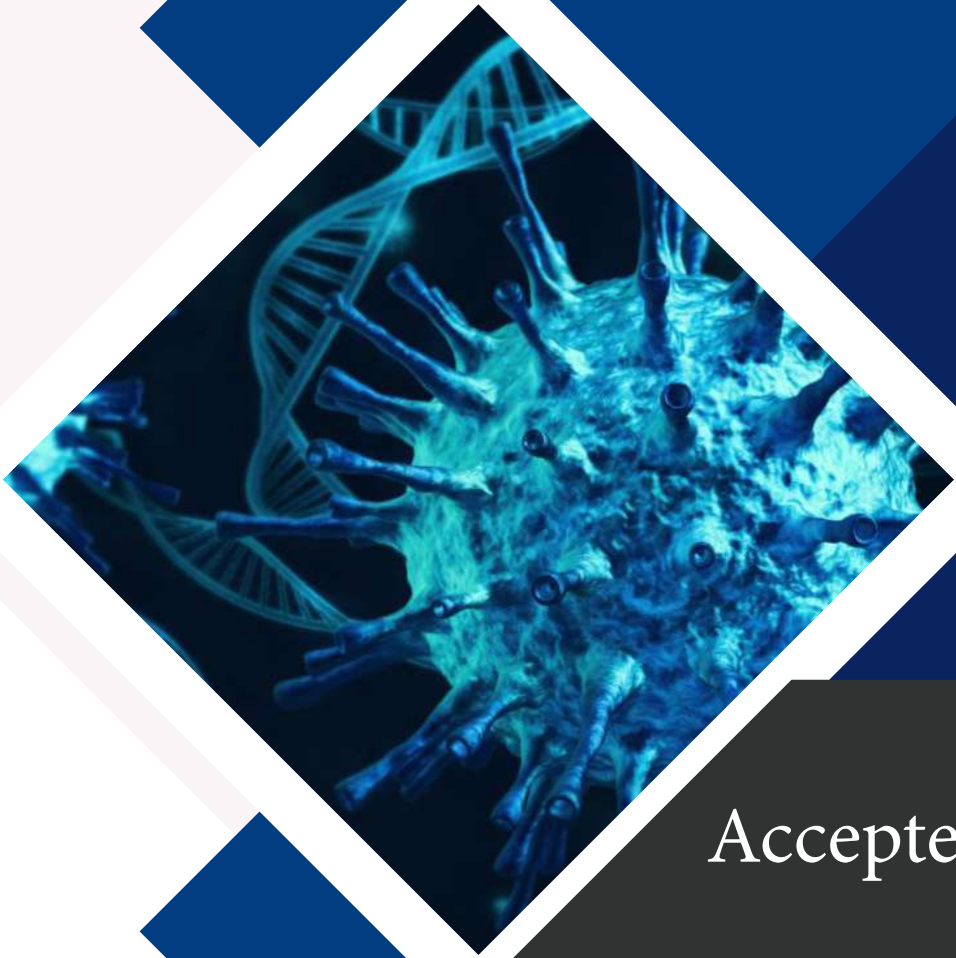
## Abstract:

**Background and Objectives:** The coronavirus disease 2019 (COVID-19) has become a worldwide issue due to its high prevalence and rapid transmission. Fungal infections have been detected in COVID-19 patients, leading to increased morbidity and mortality. This study aimed to isolate *Aspergillus species* (spp.) and *Mucor spp*. on mini-bronchoalveolar lavage (BAL) samples obtained from children with COVID-19 hospitalized in an Iranian children's hospital.

**Methods:** Demographic characteristics, such as age, gender, symptoms, previous history of COVID-19, and underlying disease were recorded for 100 children infected with COVID-19 and admitted to the ICU from April 2021 to February 2022. Fungal DNA was extracted from miniBAL samples taken from children. Nested PCR was made with two sets of primers for *Aspergillus* and *Mucor*.

**Results:** Out of 100 children with COVID-19, all samples were negative for *Aspergillus spp*.; however, 12 cases were positive for *Mucor* spp. Among 12 patients, fever, shortness of breath, cough, and decreased level of consciousness were reported in 11%, 13%, 16%, and 20%, respectively. The majority of cases (40%) suffered from heart diseases, followed by underlying malignancy (33%). All positive cases taken steroids and antibiotics had significantly higher chest CT scan scores and spent more time under a ventilator.

**Conclusion:** The co-colonization of COVID-19 with *Mucor* spp. was observed among 12% of children hospitalized in a COVID-19 ICU. When dealing with paediatric COVID-19 patients, clinicians should consider the differential diagnosis of fungal coinfections and have a low threshold to begin treatment. Moreover, it is highly advisable to take prophylactic measures, such as the proper use of corticosteroids and even shortening the intubation time.



# Accepted Abstracts

# THE EFFECT OF ASCORBIC ACID AND NICOTINAMIDE ON PANTON–VALENTINE LEUKOCIDIN CYTOTOXICITY AN *ex vivo* STUDY

**Abdullah AlSaleh**

*Arabian Gulf University, Bahrain*

## Abstract:

**Background:** Panton–Valentine Leukocidin sustains a strong cytotoxic activity, targeting immune cells and, consequently, perforating the plasma membrane and inducing cell death. The present study is aimed to examine the individual effect of ascorbic acid and nicotinamide on PVL cytotoxicity *ex vivo*, as well as their effect on granulocytes viability when treated with PVL.

**Materials and Methods:** The PVL cytotoxicity assay was performed in triplicates using the commercial Cytotoxicity Detection Kit PLUS (LDH). LDH release was measured to determine cell damage and cell viability was measured via flow cytometry.

**Results and Discussion:** A clear reduction in PVL cytotoxicity was demonstrated ($p < 0.001$). Treatment with ascorbic acid at 5 mg/mL has shown a 3-fold reduction in PVL cytotoxicity; likewise, nicotinamide illustrated a 4-fold reduction in PVL cytotoxicity. Moreover, granulocytes' viability after PVL treatment was maintained when incubated with 5 mg/mL of ascorbic acid and nicotinamide.

**Conclusion:** our findings illustrated that ascorbic acid and nicotinamide exhibit an inhibitory effect on PVL cytotoxicity and promote cell viability, as the cytotoxic effect of the toxin is postulated to be neutralized by antioxidant incubation. Further investigations are needed to assess whether these antioxidants may be viable options in PVL cytotoxicity attenuation in PVL-associated diseases.

# STUDY OF STRESS LEVEL AMONG THE UNIVERSITY STUDENTS IN THE KINGDOM OF SAUDI ARABIA DURING AND AFTER LOCKDOWN

**Bader Naif M Alsubaie, Waad Ali M Alkaabneh, Nada Sulaiman E Alatawi, Ruby Naif Al Subaie, Saif Mohmmed Alomrany and Mohammad Zubair**
*University of Tabuk, Saudi Arabia*

## Abstract:

**Background:** COVID-19 is the new coronavirus and most cases appeared in the Chinese city, Wuhan. At the end of December 2019 in the form of acute pneumonia. Older people, and people with pre-existing medical conditions (such as obesity, diabetes, heart disease) appear to be more vulnerable to becoming severely ill with the virus. However, there are a lot of studies have shown a misconception regarding COVID-19 among different communities. This study was conducted in 13 provinces in the kingdom of Saudi Arabia in the year 2021 to measure the level of awareness, knowledge, and behaviors toward physical activity.

**Methods:** A cross-sectional study was conducted in 13 provinces in the kingdom of Saudi Arabia in the year 2021, during a period of 30 days. Nine hundred and one Saudi and non-Saudi students from Saudi universities who are doing bachelor's were included; using an electronic questionnaire. Data entry and analysis were performed using Microsoft Excel.

**Results:** The prevalence of physical inactivity among participants is very high. The commonest reason for not using walking permission during the pandemic is fear of catching an infection. We found very high significance between males and females regarding physical activity rate before the pandemic and males will have a double chance to have their disease complicated. Regarding the effect 31% reported that their life is affected by stress and fear of catching an infection.

**Conclusion:** From this study, we conclude that stress analysis within the kingdom incorporates students from all 13 provinces. We found that organizing awareness campaigns and community programs by various organizations and health associates institutions was beneficial is relieving the stress levels during and after the pandemic.

# FAECAL MICROBIAL TRANSPLANTATION TO REDUCE RADIATION-INDUCED COLONIC EPITHELIAL DAMAGES: APPLICATION TO PELVIC RADIATION DISEASE

**Alexandra Sémont[1], Mallia Geiger[1], Oscar Gitton-Quent[2], Mathieu Almeida[2], Jean-Marc Chatel[2], Joël Doré[2] and Fabien Milliat[1]**

*[1]Institut de Radioprotection et de Sûreté Nucléaire, France*
*[2]Université Paris-Saclay, France*

## Abstract:

**Introduction:** Radiotherapy accounts for 60% of pelvic area cancer therapeutic strategies. Irradiation consequences in tissues surrounding the tumour can appear several years after radiotherapy. This has been described in 2010 as a new pathology: the "Pelvic Radiation Disease" (PRD). PRD can significantly affect the quality of life of patients. Late side effects may evolve though chronic inflammation/excessive scarring resulting in gut fibrosis, with important associated morbidities such as dysmotility and malabsorption, but also fistulae and perforations for the most severe grades. Patients need frequent hospitalizations. The PRD prevalence is higher than that of inflammatory bowel diseases (IBD). No curative therapies are available. Our ambition at the IRSN Institute is to develop innovative therapeutic strategies to decrease radiotherapy-induced intestinal complications. Recent experimental data showed that gut microbiome-metabolome crosstalk play a crucial role in substantial protection against radiation-induced toxicity. Indeed, our aim is to demonstrate using adapted preclinical model that irradiation leads to modifications of the intestinal ecosystem which in fine is responsible for the evolution of lesions.

**Results:** First, we developed a new animal model in which rats were subjected to pelvic irradiation using fractioned doses to mimic radiotherapy procedure. In this model, radiation induced similar histological alterations of the mucosa than those observed in patients beneficing of pelvic radiotherapy and developing complications. We showed increasing colorectal epithelial disorders (moderate epithelial atypia or severe epithelial ulceration) with escalating doses of irradiation. In this model, we then analysed temporal dynamic of (i) dysbiosis assessing faecal microbiota taxonomical and functional composition by shotgun metagenomic sequencing (ii) metabolome using MS-based analytical methods

**Discussion:** Using relevant preclinical models and complementary multi-omic approaches, this work provides new insights into the dynamics of the colonic ecosystem in response to radiation. The use of high throughput data generation is an added value and a very strong originality of this project. All the data set will be next integrated to build a mathematical model of intestinal alternative ecosystem states. This step will guide the identification of combined and optimal therapeutic options targeting microbiota and/or immune system to limit tissue toxicity and improve its regeneration.

**Conclusion:** This work supports the development of new therapeutic strategy acting on the microbiota for the reduction of radiation-induced intestinal toxicity.

# SIDE EFFECTS AFTER FIRST AND SECOND DOSE OF PFIZER-BIONTECH COVID-19 VACCINE IN UAE

**Balsam Qubais Saeed, Ahmed Omar Adrees, Rula Al-Shahrabi, Zainab Mansour Alkokhardi and Kholod Hussain Haj Hussain**
*University of Sharjah, United Arab Emirates*

## Abstract:

**Objectives:** The mRNA technology was used to manufacture the Pfizer vaccine; side effects of Pfizer–BioNTech COVID-19 vaccine among the general population is still unassuming. The aim of this study to is to reveal the potential side effects after taking the vaccine, and associated risk factors.

**Methods:** A cross-sectional survey-based study was carried out from April to September 2021, using an online questionnaire to collect the data from individuals, side effects of the vaccine were reported after the first and second doses of vaccine.

**Results:** The most common side effects of post 1st dose (≤ 39 years *vs* >39 years) were pain at the vaccination site, fatigue, severe pain at the vaccination site, and fever, while pain at the vaccination site, fever, fatigue, headache, muscle pain, and lethargy, were the most side effects follow 2nd dose of vaccination in both groups.

Among female's *vs* males, side effects were more common in Females in both doses. The most common reactions of 1st dose were fatigue, fever, tenderness, lethargy, and muscle pain while, in 2nd dose were fever, fatigue, headache, severe injection site pain, muscle pain, and lethargy. None of the cases were required intensive hospitalization. 4.2% of both ages did visit clinics for minor management

**Conclusion:** Pfizer–BioNTech COVID-19 vaccine was associated with a higher prevalence of local side effects in both genders and all age groups. The genders- and age-based differences warrant further rigorous investigation and standardized methodology.

# INTRACELLULAR DELIVERY OF NUCLEAR LOCALIZATION SEQUENCES BY INHALATION SUPPRESSES IMMUNE CELL INFILTRATION AND DAMAGE TO LUNG STRUCTURE

**Dasom Shin, Dongho Kim and Jieun Kim**
*Cellivery Therapeutics, Inc., South Korea*

## Abstract:

Community-acquired pneumonia (CAP) is a respiratory infection caused by a variety of bacteria and viruses. Pneumonia increases the influx of inflammatory cells such as neutrophils into the lungs due to excessive secretion of pro-inflammatory cytokines, which destroys the bronchi and alveoli and eventually leads to death. The over-expression of cytokines/chemokines and neutrophil activation are promoted by the nuclear translocation of inflammation-associated transcription factors (IATFs) such as NF-κB, STAT1/3, NFAT, and AP-1. Therefore, it is important to regulate cytokines by blocking nuclear translocation of IATFs. To inhibit activation of IATFs, an improved cell-permeable nuclear import inhibitor (iCP-NI) was conducted by fusing a nuclear localization sequence (NLS) of NF-κB with hydrophobic cell-penetrating peptide (CPP), namely advanced macromolecule transduction domain (aMTD). In addition, for the effective treatment of inflammatory pulmonary respiratory diseases, iCP-NI has been developed as a more accessible and patient-friendly formulation. To demonstrate the effectiveness of iCP-NI, an acute pneumonitis animal model was developed by intratracheal injection of Poly I:C and LPS. As a result, iCP-NI showed inhibitory efficacy by decreasing cytokines such as TNF-α, IL-6, MCP-1 and IFN-γ in bronchoalveolar lavage fluid. Also, it was observed that the infiltration of immune cells in the lung was significantly suppressed, and lung tissue damage was suppressed. At the *in vitro* level, iCP-NI It suppressed pro-inflammatory cytokine/chemokine expression and reduced the expression of MPO associated with neutrophil activity. In addition, it was shown to inhibit NETosis by down-regulating IATFs translocation. These results demonstrated that iCP-NI inhalant can downregulation inflammation and inhibit lung tissue damage by inhibiting immune cells infiltrating the lungs.

# EFFECTS OF BIOFILMS AND LATENT UTERINE INFECTIONS ON FERTILITY OF MARES, HOW TO DETECT AND TREAT

**David Hoadley-Trundell**
*Savoch Oaks Farm, USA*

## Abstract:

There are four main bacterial species considered pathogenic in the mare's uterus: *Streptococcus equi spp. zooepidemicus, Klebsiella pneumoniae, Pseudomonas aeruginosa* and *Escherichia coli*. Isolation of any of these species should be considered clinically relevant. Up to 60% of barren mares culture positive for one of the above bacterial species. Mare's that appear refractory to routine antimicrobial treatment in cases of infectious endometritis, can be frustrating for the attending clinician. It is now established in our equine patients that biofilm production of these bacteria within the endometrium may lead to the refractory nature to traditional antimicrobial treatment. Several treatments have been proposed for treatment of biofilms in the mare, including N-acetylcysteine, hydrogen peroxide, and chelating agents. Antibiotics are most effective when bacteria are in a planktonic state, therefore when they are in a biofilm state traditional antimicrobials tend to have little to no effect on resolving infection. There have been some advances in causing latent biofilm bacteria to "re-awaken" into their planktonic state, making them more susceptible to antimicrobials. Having a thorough understanding of when latent infections or biofilms may be present in our mare population is important to increase the fertility efficacy of those mares affected. Selecting the most appropriate treatment, and in particular the correct antimicrobial, is essential for proper antimicrobial stewardship and successful treatment.

# COVID-19 IN SÃO TOMÉ AND PRÍNCIPE - ACTIVE CASE SEARCH AND CONTACT TRACING/MULTI RISK APPROACH

**Deodato Xavier Dias da Costa Neto**
*Ministry of Health, São Tomé and Príncipe*

## Abstract:

During the period from 6th of April 2020 to 20th of June 2021, it was laboratory confirmed the existence of Covid-19 in the Democratic Republic of São Tomé and Príncipe. The case definition and the suspected case notification were made. According the context of the increasing hospitalisations, the epidemiology surveillance team, used the forms of active case search and contact tracing providing: advices on the signs, symptoms, transmission and the need for a change in the behavior; definition of the laboratory confirmated and suspected cases; the effective treatment (prophylactic and symptomatic) and timely isolations with case monitoring, which helped to reduce and bring under control the infection's transmission, alongside with the vaccination campaign. The COVID-19 epidemic registered a number of 2365 confirmed cases, being extremely contagious with a number of 37 deaths, attack rate of 1102 for 100 thousand habitants and a 1.6% of lethality rate, for which, we could conclude that these status associated with the high vulnerability from the part of the communities and due to the climate factor issues. Also there were 6664 contacts indentified all across the country for which within 9 of them showed evidences of symptoms. It is also very important to highlight, that during the active case search and contact tracing investigation process beside the vaccination campaign, we also emphasized on the probability of there being any other related diseases in action, for example: malaria; poliomyelitis, measles (multi-risk study approach), and on the matter of campaign actions to control vaccination in children under five years old.

# ANTIFUNGAL EFFECT OF DIVERSE PROPOLIS COMPOUNDS ON THE PROTECTIVE IMMUNITY IN A MURINE MODEL OF INFECTION BY PARACOCCIDIOIDOMYCOSIS

**Eva Burger, Lauana Aparecida Santos, Julia de Castro Dutra, Enrico Picoli Marinho, Rinaldo Poncio Mendes and José Henrique Fernandes Faraldo**
*Universidade Federal de Alfenas, Brazil*

## Abstract:

Paracoccidioidomycosis is a severe systemic mycosis, endemic in Latin America. The disease presents different clinical forms and its incidence is higher in male adults at the productive age, preferentially involved in agricultural activities. The real prevalence of this disease is unknown as compulsory notification is not required, but it is known that it affects immunocompetent subjects. Therapy with antifungals is difficult, presents serious collateral effects and requires long-term treatment, therefore inducing the patients to abandon the therapy. Research to develop new antifungals is scarce so the introduction of complementary therapies to reduce the time of therapy is highly desirable. Propolis is a natural resin-like product produced by bees from plant parts. Its chemical composition, color and structure are dependent on several aspects, which involve geographic factors, locations, climate, pollination area, vegetation and available local flora. Propolis is generally classified according to its color in Brazil. Green propolis is rich in prenilatephenolic and phenolic compounds, bown propolis contains mainly phenolic acids and diterpenes and red propolis contains mainly isoflavones and benzophanes. Propolis is used in folk and traditional medicine as an antibacterial, antiviral and antifungal agent but the support by scientific literature is scarce. There is only one report in the literature that *P. brasiliensis* was affected by unspecific Propolis. In mycoses, as in general, neutrophils play a dual role, being responsible for an initial antifungal activity during the innate immune response and also by secreting cytokines that elicit an effective protective acquired immune response. However, in par coccidioidomycosis patients, neutrophils function was shown to be impaired, and studies aiming to reverse this neutrophils malfunctioning are incipient. We employed an experimental model established by our group that allows the direct interaction of either type of Propolis, neutrophils and other cells from the innate immune system with the fungus *Paracoccidioides brasiliensis*, in a close *in vivo* environment. We observed that neither of the Propolis samples was cytotoxic, but all showed direct antifungal activity at the different time-points analyzed, reducing the number of viable fungi, as well as marked stimulatory effect on the PMNs at the air pouch, as verified by the production of oxidative metabolites and mitochondrial activity. Our results strongly suggest, for the first time in the literature, that all Propolis types studied show two protective mechanisms in experimental paracoccidioidomycosis: activating the neutrophils recruited to the site of infection and by exerting direct antifungal activity and thus controlling the fungus *Paracoccidioides brasiliensis*.

# MORTALITY FROM CHRONIC HEPATITIS C IN BRAZIL: ANALYSIS OF THE MULTIPLE CAUSES OF DEATH IN THE PERIOD 2000 TO 2019

**Gerusa Maria Figueiredo and Larissa Festa**
*University of Sao Paulo, Brazil*

## Abstract:

**Introduction:** Chronic hepatitis C (CHC) is the leading cause of death among viral hepatitis in Brazil. The relevance of working with multiple causes of death (basic cause and associated causes) constitutes a breakthrough in the analysis of mortality statistics.

**Objective:** To describe deaths from chronic hepatitis C, as the underlying cause and multiple causes of death, and to analyze the temporal and spatial distribution of these deaths in Brazil, from 2000 to 2019.

**Material and Methods:** This is an ecological study, with data from the Mortality Information System (SIM). All analyzes will be performed comparing mortality rates for CHC as the underlying cause of death and as multiple causes of death. Descriptive analysis of deaths from CHC will be performed, according to sociodemographic aspects, by Pearson's chi-square test or Fisher's exact test. For the time series analysis, CHC mortality rates will be calculated by macro-region, and the temporal trend will be analyzed by Prais-Winsten regression. The spatial distribution by states of Brazil of mortality rates by CHC will be carried out, over 5-year periods from 2000 to 2019.

**Preliminary Results:** The database consisted of 30,748 deaths from CHC in any line of the death certificate, 25,394 (82.58%) deaths with CHC as the underlying cause of death and 5,354 (17.41%) from CHC as associated causes of death, so that the sum of the underlying cause and associated causes results in multiple causes of death. It is expected that this study of the analysis of mortality rates due to hepatitis C considering the multiple causes of death demonstrates that there is a probable underestimation of the mortality of this condition in Brazil, a factor that has not been evaluated to date. The fall in the staggered mortality rate by 2030 is one of the goals of the Sustainable Development Goals.

# VOLUNTEER WORKING DURING COVID-19 IN JORDANIAN COMMUNITY: ADVANTAGES AND CHALLENGES

**Huda A. Alhajjaj and Hana H. Al Nabulsi**
*University of Jordan, Jordan*

## Abstract:

This study deals with the crisis volunteering during the lockdown period of the COVID-19 pandemic in Jordan. This study aims to identify the skills that volunteers acquire during voluntary work. Moreover, it aims to identify whether there are significant differences for volunteer difficulties and advantages regarding gender, age, and education level. Researchers employed a quantitative method, using a questionnaire to achieve the goals of this study. The sample was 121 voluntary people (females and males) during the pandemic in a Jordanian community. The results of this study have shown that volunteering during the COVID-19 pandemic has had a positive impact on volunteers during this period in terms of acquiring a variety of skills. Furthermore, there were numerous difficulties faced by volunteers, and there were no statistically significant differences in the level of skills acquired by volunteers as a result of their participation in volunteering.

# CHARACTERISTICS OF HEPATITIS B VIRUS GENOTYPE AND SUB-GENOTYPE IN HEPATOCELLULAR PATIENTS IN VIETNAM

**Karen Kieu Nguyen, Phat Tan Ho, Mario GiosuèBalzanelli, Pietro Distratis, Rita Lazzaro, Duy Khanh Tran, Tri Minh Bui, Thinh Tien Nguyen, Son Truong Pham, Huy Song Dinh Nguyen, Vinh Thanh Tran, Toan Trong Ho Gianna Dipalma Francesco Inchingolo Camelia Quek, Huong Thien Pham, Ciro Gargiulo Isacco, Luigi Santacroce and Van Hung Pham**

*Aldo Moro University, Italy*

## Abstract:

Untreated chronic hepatitis B virus (HBV) infection can lead to chronic liver disease and may progress to cirrhosis or hepatocellular carcinoma (HCC). HBV infection has been prevalent in Vietnam, but there is little information available on the genotypes, sub-genotypes, and mutations of HBV in patients with HBV-related HCC confirmed by histopathological diagnosis. We studied the molecular characteristics of HBV and its genetic variants in Vietnamese HCC patients after liver tumor resection. We conducted a descriptive cross-sectional study on 107 HBV-related HCC hospi- talized patients from October 2018 to April 2019. The specimens collected included EDTA anticoag- ulant blood and liver tissues. Extracted HBV DNA was subjected to whole genome sequencing by the Sanger method. We discovered 62 individuals (57.9%) with genotype B and 45 patients (42.1%) with genotype C, with only sub-genotypes B4 and C1. Among the mutations, the double mutation, A1762T-G1764A, had the most significant frequency (73/107 samples; 68.2%) and was higher in gen- otype C than in genotype B ($p < 0.001$). The most common genotypes found in HCC patients in this investigation were B and C, with sub-genotypes B4 and C1 for each. The prevalence of genotype B4 was greater in HBV-infected Vietnamese HCC patients.

# POST-COVID-19 SYNDROME: INSIGHTS INTO A NOVEL POST-INFECTIOUS SYSTEMIC INFLAMMATORY DISORDER

**Marilena Stoian**
*Carol Davila University of Medicine Bucharest Romania, Romania*

## Abstract:

Coronavirus disease 2019 (COVID-19) is currently considered a complex systemic infectious and inflammatory disease, determined by the infection with severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2), and the cause of one of the most important epidemiological phenomena in the last century – the COVID-19 pandemic. This infectious-inflammatory disease may generate a wide range of clinical manifestations and biological modifications, explained both by the ubiquitous nature of the SARS-CoV-2 receptors, represented by the *angiotensin-converting enzyme-2* (ACE-2), and by the host's violent immune and proinflammatory reaction to the viral infection. These manifestations include immunological disturbances, which, according to certain clinical findings, may persist post-infection, in the form of a presumed systemic inflammatory entity, defined by several clinical concepts with a common pathological significance: post-COVID-19 multisystem (or systemic) inflammatory syndrome, post-COVID-19 syndrome or long-COVID. Although the pathophysiological mechanisms of post-COVID-19 syndrome are elusive at the present moment, there are currently several studies that describe a systemic inflammatory or autoimmune phenomenon following the remission of the COVID-19 infection in some patients, which suggests the existence of molecular and cellular immune abnormalities, most probably due to the host's prior violent immune response to the viral infection, in the form of three overlapping entities: secondary hemophagocytic lymphohistiocytosis (HLH), *macrophage activation syndrome* (MAS) and *cytokine release syndrome* (CRS). Thus, this is reminiscent of different classic autoimmune diseases, in which various infections possess important roles as risk factors in the development of the autoimmune process.

# EPIDEMIOLOGY OF *Clostridioides difficile* INFECTION AT A TERTIARY CARE FACILITY IN SAUDI ARABIA: RESULTS OF PROSPECTIVE SURVEILLANCE

**Nabiha Bouafia, Naoufel Kaabia, Hanadi Al Basha, Dalal Bukhari, Lina Sallam, Aisha Al Qahtani, Amal Al Aidaroos and Abdulrahman Odayani**
*Prince Sultan Medical Military City, Saudi Arabia*

## Abstract:

**Introduction:** A significant increase in the *Clostridioides difficile* infection (CDI) rate has been reported globally, but there remains a paucity of data in Saudi Arabia. Hence, this study aimed to determine the incidence rate of CDI and the frequency of their known risk factors

**Methods:** Prospective hospital-based surveillance for CDI, according to the CDC criteria was conducted from July2019 to March 2022 for all patients aged more than 1 year in Prince Sultan Military Medical City, Saudi Arabia. Duplicated CDI cases and outpatients were excluded.

**Results:** 139 cases of CDI were diagnosed during the survey among 130 patients admitted in the hospital. Majority of cases were incident (n =130; 93.5%) and almost three quarters (n=102; 73.4%) were Hospital onset CDI with a density incidence rate of 1.61per 10,000 patients day (PD), the highest rates were noted in ICU (3 per10,000 PD) and Immunocompromised wards (2.72 per 10000 PD). The most prevalent risk factor for CDI was the use of acid-reducing drugs (72.6%). Vancomycin (48%) and ciprofloxacin (25%) were the most frequent antibiotics prescribed in patients with CDI. CDI complications were identified in 5.7% of cases with a reported 28-day mortality rate of 3.8%.

**Conclusion:** In our hospital, HO-CDI incidence rate is low comparing with high-income countries. National multi centric surveillance is needed to evaluate the real burden of CDI in Saudi Arabia.

# DETECTION OF ANTIBIOTIC RESISTANT NOSOCOMIAL PATHOGENS FOUND IN THE HOSPITAL ENVIRONMENT OF BANGLADESH

**Anika Bushra, Talukder Nazmus Safin and Fahim Kabir Monjurul**
*Brac University, Bangladesh*

## Abstract:

Nowadays nosocomial infection is a very vital issue. In the socio-economic background of Bangladesh, the safety management of hospitals is a less focused topic. Every year, thousands of people get infected and die because of the unhygienic environment of hospitals. The Centre for Disease Control and prevention (CDC) stated that there are around 1.7 million (approximately 10%) hospital associated infections from all types of pathogens. Nosocomial pathogens are responsible for the most of the infections that occur in hospital environments. Among all the pathogens, the presence of *Acinetobacter baumannii* is not clear yet. This is a challenge for us to discover the presence and identify its antibiotic resistance. Nosocomial pathogens usually infect urinary tract (40%), surgical sites (19%), respiratory tracts (15%), skin (8%), septicemia (6%) and other sites like gastroenteritis (12%). By vector transmission and droplet transmission, the pathogens transmit to the body. Our targeted organisms in this research were, *Escherichia coli*, *Klebsiella pneumoniae*, *Salmonella typhi* and *Staphylococcus aureus* . However, the only way to reduce the transmission rate is to follow the safety protocols properly and to be aware of hygiene.

**Methods and materials:** Non-clinical samples (surface and air) were taken from different wards and areas of Shaheed Suhrawardy Medical College and Hospital, Dhaka. Surface samples were taken by cotton swabs dipped in 9% NaCl and air samples were taken by selective media petri plates and buffer peptone water. To determine the antibiotic susceptibility test *Kirby-Bauer* method was applied. PCR and gel electrophoresis were also applied after extracting the DNA of the targeted organisms.

**Result:** By performing the experiment, it is found that from the 4 batches of sample total 206 isolates were found where 23% of E.coli, 16% of Klebsiella pneumonie, 15.04% Staphylococcus aureus, 7% Salmonella typhie, 22% of other organisms and most importantly 15% of Acinetobacter baumanii was found. Organisms were highly multidrug resistant.

# CHANGING THE DIAGNOSTIC PARADIGM OF BACTERIAL IDENTIFICATION THROUGH PRECISION TAXONOMY

**Nur A Hasan**
*University of Maryland, USA*

## Abstract:

Accurate microbial identification is critical for rational choice of treatment and proper management of a disease. Several different phenotypic, proteotypic and genotypic methodologies are available today for identifying unknown isolates. Among them, matrix-assisted laser desorption-ionization time of flight mass spectrometry (MALDI-TOF MS) has been widely used in clinical laboratories because of its simplicity, reduced cost, and rapid turnaround time. While it is effective in identifying frequently observed species, for less frequently observed species its performance is limited due to lack of such spectra coverage in their database. The 16S rRNA gene-based identification is considered the most powerful and accurate tool as its database is extensively larger than that of MALDI-TOF, however it also has limitation in distinguishing closely related species. Whole genome-based identifications are, therefore, preferred as it opens up the opportunity in analyzing the entire genetic make-up of an organism to inform accurate identification. We, therefore, developed TrueBacTM ID, a platform for accurate and definitive bacterial identification using sequence data.

The system provides definitive species identification for clinical and other industrial applications. The database contains expert-curated and taxonomy-validated genome and gene sequences of Type- and Reference-strains and comprise over 21,529 species/sub-species. The system also characterizes isolate for carriage of antibiotic resistance and virulence genes and offers rapid sub-typing to aid molecular epidemiology. Performance has been validated in laboratory and clinical settings, where TrueBacTM ID accurately identified all isolates (94% at species level) that could not be identified using commercial MALDI-TOF MS systems. Additional benchmarking with datasets derived from an Intensive Care Unit of an US hospital demonstrates successful identification of >1,200 bacterial strains with unprecedented accuracy and precision. TrueBacID system offers a paradigm shift in clinical microbiology with its most accurate and definitive identification of known, novel and emerging pathogens, along with comprehensive sub-typing or lineage information.

# SYSTEMATIC REVIEW AND META-ANALYSIS OF INTEGRATED STUDIES ON *Salmonella* AND *Campylobacter* PREVALENCE, SEROVAR, AND PHENOTYPING AND GENETIC OF ANTIMICROBIAL RESISTANCE IN THE MIDDLE EAST—A ONE HEALTH PERSPECTIVE

**Said Abukhattab, Haneen Taweel, Arein Awad, Lisa Crump, Pascale Vonaesch, Jakob Zinsstag, Jan Hattendorf and Niveen ME Abu-Rmeileh**
*Swiss Tropical and Public Health Institute, Switzerland*

## Abstract:

**Background:** *Campylobacter and Salmonella* are the leading causes of foodborne diseases worldwide. Recently, antimicrobial resistance (AMR) has become one of the most critical challenges for public health and food safety. To investigate and detect infections commonly transmitted from animals, food, and the environment to humans, a surveillance–response system integrating human and animal health, the environment, and food production components (iSRS), called a One Health approach, would be optimal.

**Objective:** We aimed to identify existing integrated One Health studies on foodborne illnesses in the Middle East and to determine the prevalence, serovars, and antimicrobial resistance phenotypes and genotypes of *Salmonella and Campylobacter* strains among humans and food-producing animals.

**Methods:** The databases Web of Science, Scopus, and PubMed were searched for literature published from January 2010 until September 2021. Studies meeting inclusion criteria were included and assessed for risk of bias. To assess the temporal and spatial relationship between resistant strains from humans and animals, a statistical random-effects model meta-analysis was performed.

**Results:** 41 out of 1610 studies that investigated *Campylobacter* and non-typhoid *Salmonella* (NTS) in the Middle East were included. The NTS prevalence rates among human and food-producing animals were 9% and 13%, respectively. The *Campylobacter* prevalence rates were 22% in humans and 30% in food-producing animals. The most-reported NTS serovars were *Salmonella Enteritidis* and *Salmonella Typhimurium*, while *Campylobacter jejuni* and *Campylobacter coli* were the most prevalent species of *Campylobacter*. NTS isolates were highly resistant to erythromycin, amoxicillin, tetracycline, and ampicillin. *C. jejuni* isolates showed high resistance against amoxicillin, trimethoprim–sulfamethoxazole, nalidixic acid, azithromycin, chloramphenicol, ampicillin, tetracycline, and ciprofloxacin. The most prevalent Antimicrobial Resistance Genes (ARGs) in isolates from humans included tetO (85%), Class 1 Integrons (81%), blaOXA-61 (53%), and cmeB (51%), whereas in food-producing animals, the genes were tetO (77%), Class 1 integrons (69%), blaOXA-61 (35%), and cmeB (35%). The One Health approach was not rigorously applied in the Middle East countries. Furthermore, there was an uneven distribution in the reported data between the countries.

**Conclusion:** More studies using a simultaneous approach targeting human, animal health, the environment, and food production components along with a solid epidemiological study design are needed to better understand the drivers for the emergence and spread of foodborne pathogens and AMR in the Middle East.

# MOTHER TO CHILD TRANSMISSION RATE OF HEPATITIS B AFTER TENOFOVIR DISOPROXIL FUMARATE IMPLEMENTATION

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## Abstract:

Hepatitis B is a global issue, especially in underdeveloped nations. Hepatitis B affects almost 8% of Asians. HBV is transmitted from mothers to toddlers in Thailand. 90% of HBV-infected babies develop hepatocellular cancer. Since 2017, Thai national guidelines propose Tenofovir disoproxil fumarate for mothers with high viral loads or HBeAg positivity (TDF). MTCT in Thailand was studied. Retrospective analysis used medical data of Thai children delivered to mothers with HBV infection (positive HBsAg) between 1 January 2018 and 31 December 2020, after tenofovir disoproxil fumarate was implemented (TDF). Multivariable binary regression was used to compute transmission rate and identify MTCT risk factors. There were 342 infants born from positive HBsAg mothers during the study period, and all of mothers were 14 to 44 years old of age (median 30). There were 42.40% (145) of infants born to mothers who received TDF as well as 28.36% (97/342) had HBeAg positive mothers. 55.17 % of mothers who received TDF greater than or equal to four weeks before delivery. At birth, all infants received the hepatitis B vaccine, and 94% also received hepatitis B immune globulin (HBIG) for 5.56% (19 infants) who did not receive hepatitis B immune globulin (HBIG). The overall MTCT incidence rate is 0.88 % (3/342; 95%CI, 0.1-2.5) the MTCT rate among TDF mothers is 0.69% (1/145) and no association between risk factors and MTCT among mothers HBsAg positive. However, 15.7 % (3/19) of those who were infected and did not get HBIG. TDF-treated HBsAg-positive women reduced mother-to-child transmission (0.69 *versus* 1.02). TDF relative risk is 0.679 (95%CI, 0.062–7.539) in infected newborns, and treatment effectiveness is 32%. HBIG-treated newborns showed no MTC. For pregnant women with HBV, TDF costs 500 baht (16 USD) every four weeks. This study advises giving newborns HBIG and HBV.

# NATURAL FOCAL INFECTIOUS DISEASES DISTRIBUTION IN THE RUSSIAN FAR EAST

**Svetlana Malkhazova, Fedor Korennoy, Dmitry Orlov and Natalia Shartova**
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## Abstract:

The international public health has faced a problem of the rapid transformation of existing ranges of environmental diseases and emergence of new disease outbreaks, which is stipulated by increasing population mobility and trade by animal- and plant originated products as well as by environmental and climatic changes. One of the most dangerous territories for these diseases is the Far Eastern Federal District. We here present a medical-geographical approach to the study of some environmental infectious diseases at the regional and local level in the Far Eastern area of Russia for 2000-2020.

Thematic maps reflecting the epidemiological situation and the dynamic features of natural focal infectious diseases distribution were created using various cartographic techniques. A group of methods based on data aggregation using a “space-time cube” were tested to identify hot spots and trends, as well as spatial differences in the epidemic patterns of the study diseases in the Trans-Baikal Territory, Amur Region and Khabarovsk Krai of Russia. The results of a comparative geographical analysis revealed significant spatial heterogeneity in the distribution and incidence rates due to the geographical specifics of the regions. Existing segregation in diseases distribution across state border can be attributed to the hydrographic boundaries (the Amur River), as a barrier for hosts and vectors. Significantly different population density, different level of economic development, including the intensity of farming, as well as a climate change and land cover change over the study period were found to be additional influencing factors.

The research was performed according to the Development program of the Interdisciplinary Scientific and Educational School of M.V.Lomonosov Moscow State University “Future Planet and Global Environmental Change”.

# VALIDATION OF THE MEP PATHWAY'S [Fe-S] CLUSTER ENZYMES AS DRUG TARGETS IN MYCOBACTERIA

**Tumelo Maila**
*Stellenbosch University, South Africa*

## Abstract:

Tuberculosis (TB) still remains a global health burden with an estimated 1.5 million mortalities in 2020. Despite the availability of the current drug regimens aimed at eradication of TB, the cases of drug-resistant TB continue to increase, reflecting the urgent need for development of new drugs with novel mechanisms of action. In a quest to find new drug targets, we used CRISPR interference (CRISPRi) technology to investigate the vulnerability of IspG and IspH, the two [Fe-S] cluster-dependent enzymes found in the methylerythritol phosphate (MEP) pathway, which display a high level of homology amongst mycobacterial species. Activation of the CRISPRi system through addition of anhydrotetracycline (ATc) resulted in over 96 % gene knockdown for both genes, which led to strong growth inhibition in *Mycobacterium smegmatis*. The intracellular gene depletion led to severe growth impairment of the hypomorphs, thereby confirming the essentiality of both gene products in standard growth medium. Vulnerability of IspG and IspH was also sustained in growth medium supplemented with different carbon sources, with partial growth rescue only observed on IspG and IspH hypomorphs when alanine and succinate were used as the sole carbon sources, respectively. Extensive clumping was observed in the liquid cultures of the IspG hypomorph and subsequent scanning electron microscopy (SEM) revealed severe morphological aberration marked by large number of particles on the surfaces of the mutant cells. Notably, the IspG and IspH hypomorphs were hypersensitive to nitric oxide, a potent natural oxidant produced by activated human immune system. Furthermore, both hypomorphs were highly sensitive to the sub-lethal concentration of ethambutol and tunicamycin. This suggests that potential inhibitors of either enzyme could be used to improve the efficacy of the standard TB treatment regimen. Overall, the study provided the evidence conforming IspG and IspH as a vulnerable target that can be prioritized for development of inhibitor molecules, whose effectiveness could be enhanced by host activated immune systems.

# A PROSPECTIVE STUDY ON THE TRANSMISSION DYNAMICS OF CORONA VIRUS DISEASE (2019) (COVID-19) AMONG HOUSEHOLD CONTACTS IN DELHI, INDIA

**Warisha Mariam**
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## Abstract:

**Background:** Close settings such as households having fixed populations provide opportunities for tracking the viral transmission patterns of emerging respiratory infections. This study was conducted to gain an understanding of the transmission dynamics of COVID-19 among the household contacts of laboratory-confirmed cases of COVID-19, as well as to have an insight into the information on key clinical, epidemiological and virological characteristics of COVID-9 infection.

**Materials and Methods:** This was a prospective case ascertained study conducted among the household contacts of laboratory-confirmed COVID-19 cases residing in the Central and North East districts of Delhi between December 28, 2020 and June 28, 2021. The 'household contact' was defined as any person who has resided in the same household as a confirmed COVID-19 primary case. Baseline data collection and sample collection for RT PCR and serology from the primary case and the contacts were done on day one of visit and then they were followed up on days 7, 14 and 28 for development of symptoms, antigen testing from nasopharyngeal samples and blood specimen for antibody presence. Also, a daily symptom diary was maintained for all the primary cases and contacts for 28 days from enrolment both by the study participants and the project field investigators.

**Results:** A total of 109 primary cases and their 202 household contacts were included in the study analysis. The secondary attack rate (SAR) estimated was 13.86% (9.71%,19.39%) and the secondary infection rate was 33.16% (26.97%, 40.00%). The serial interval and basic reproduction number (R0) within household were estimated to be 3.6 ± 5.73 days and 1.26.[95% C.I. 1.21-1.31] respectively. The proportion of secondary cases being symptomatic and asymptomatic was 24 (34.78%) and 45 (65.22%) respectively. On univariate analysis, the significant predictors/risk factors of the infection were location of household in Central district (SAR= 20% [13.75,28.16]) *vs* North East District (SAR= 4.87% [1.83-12.35]) p= 0.002, sharing of utensils (SAR= 42.85% [14.26-77.11], p=0.02), and using the room to sleep where case has been isolated (SAR= 25% [12.97-42.71], p=0.047). Other socio-demographic factors like sex, sharing of toilet, presence of comorbidity was not significantly associated. It was also observed that only one in 89 cases needed hospitalisation among the total cases in household (1.1%) in both the districts.

**Conclusion:** The transmission dynamics was observed to be higher among the household contacts. Therefore, it is needed that the primary case and their contacts maintain COVID-19 appropriate behaviour within the household to interrupt the transmission of infection. Strengthening of testing capacity and early identification of primary case through active and passive surveillance will help to break the transmission chain at household level as well as prevent the spread in community.

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Note

# Forthcoming Events

International Conference on **Biomaterials and Biodevices**
September 25-26, 2023 | Paris, France

2nd International Conference on **Neurology and Brain Disorders**
November 2-3, 2023 | London, UK

Internarional Conference on **Hematology and Blood Disorders**
November 6-7, 2023 | Paris, France

European Conference on **Human Genetics**
November 6-7, 2023 | Paris, France

International Conference on **Gynecology and Obstetrics**
November 6-7, 2023 | Dubai, UAE

International Conference on **Biomedical Science and Engineering**
November 6-8, 2023 | Dubai, UAE

International Conferce on **Clinical Case Reports**
November 8-9, 2023 | Dubai, UAE

2nd International Conference on **Materials Science & Engineering**
November 8-9, 2023 | Dubai, UAE

2nd European Congress on **Chemistry and Applied Sciences**
November 9-10, 2023 | Paris, France

2nd International Conference on **Catalysis & Chemical Engineering**
November 9-10, 2023 | Paris, France

European Congress on **Renewable Energy and Sustainable Development**
November 16-17, 2023 | Rome, Italy

European Congress on **Biopolymers and Bioplastics**
November 16-17, 2023 | Rome, Italy

2nd International Conference on **Nanomaterials and Nanotechnology**
November 20-21, 2023 | Vienna, Austria

2nd European Congress on **Microbiology**
November 20-21, 2023 | Vienna, Austria

2nd International Conference on **Infectious Diseases**
November 20-21, 2023 | Vienna, Austria

2nd International Conference on **Addiction & Psychiatry**
November 20-21, 2023 | Vienna, Austria