IRIS Scientific Group

INFECTIOUS DISEASES CONGRESS 2026

23 April, 2026
Online Event

BOOK OF ABSTRACTS

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Keynote Speakers



Alexey Severtsev

Pirogov Russian National Research Medical University, Russian Federation



Mehmet Yavuz

Firat University, Turkey



Sergey Suchkov

HUN-REN Wigner RCP, Hungary



Welcome Message

Dear Colleagues, Partners and Friends,

On behalf of the Organizing Committee, it is my genuine pleasure to address this Welcome Message to the **Infectious Diseases Congress (IDC 2026)** which is scheduled to perform in Paris as an academic, scientific, artistic and intellectual Capital of the World.

Infectious diseasesrepresent an old paradigm but the upgraded future in the development of OMICS-based and IT-driven innovations to the development of next-generation diagnostic, predictive, prognostic, therapeutic, preventive and prophylactic toolsin ***Personalized and Precision Medicine (PPM).***In this context, this Event would stimulate an enhanced understanding to surmount the obstacles to the creation of effective personalized drugs as well as precision diagnostic tools to protect against pathogens, and would disclose clinically relevant biomarkers of predictive diagnostics, protection, prevention and treatment, and vaccine response heterogeneity.

From practical strategies to translational research, the unique transdisciplinary Program reflects the realities the profiled experts face every day. And you'll be surrounded by peers across precise diagnostics, predictive and prognostic protocols, preventive, prophylactic and therapeutic manipulations of the next-step generations, - from informatics to regulatory strategy - that can reshape what's possible in your mind and experience.

The diverse Program of the Eventunlocking the secrecy of the Biodesign-driven innovations in infectious disease predictive diagnosis, prevention, treatment and rehabilitation, reaches into the far corners of the infectious disease landscape with the aim of show-casing the latest cutting-edge studies and breakthroughs to improve human health globally and to shape policy and practice for years to come. In reality, the Program covers a comprehensive array of topics, from novel microbial diagnostics and innovative antimicrobial therapies to insights into emerging infectious diseases

and updated infection prevention and control protocols. On the other hand, the Program will also highlight the challenges and innovations addressing the impact of global phenomena such as pandemics, post-pandemic realities, geopolitical changes, personalized vaccinomics, antimicrobial resistance, quality of care and other critical issues.

This prestigious Event brings together the brightest minds in infectious disease research, design-driven biotech and translational applications, clinical practice, and public health to address some of the most pressing challenges facing our world today.This Conferenece aims to foster interdisciplinary discussions and innovative approaches to some of the most pressing global health challenges posed by infectious diseases today. Moreover, thisConference aims to explore new frontiers together and serve as a unique opportunity to share knowledge, discuss revolutionary ideas and, above all, build the future of infectious diseases together. In this context, this Grand Event serves as a platform for basic and clinical researchers, biodesigners and bioengineers, practitioners, healthcare administrators, medical insurance expertsto come together and share insights into the latest advancements in the area of infectious diseases.

We are thrilled to extend our warmest invitation to you to join us at the Infectious Diseases Congress, a premier Event which is held during April 23-25, 2026 at Paris, France.We look forward to welcoming you to Infectious Diseases Congress (IDC 2026), as we come together to explore the future of vaccines and their impact on global health

Dr Sergey Suchkov, MD, PhD

Professor in Medicine and Immunology,

Vice-Director for Research and Development of

the Centro de Estudios de la Fotosíntesis Humana, Aguascalientes, México Member, New York Academy of Sciences, USA

Member, The Russian Academy of Natural Sciences (RANS), Russia

Member: EPMA (European Association for Predictive, Preventive and Personalized Medicine), Brussels, EU

Member, ISPM (International Society for Personalized Medicine), Japan

Member, PMC (Personalized Medicine Coalition), Washington, USA

Member, AMEE (Association for Medical Education in Europe), Dundee, Scotland

Member, ACS (American Chemical Society), Washington, DC, USA

Member, AHA (American Heart Association), Dallas, TX, USA

Member, ARVO (The Association in Research in Vision & Ophthalmology),

Rockville, MD, USA

Member, ISER (International Society for Eye Research), Anchorage, AK USA

Secretary General, United Cultural Convention (UCC), Cambridge, UK



Welcome Message

Mehmet Yavuz is a Full Professor in the Mathematics and Computer Department at Necmettin Erbakan University where he have been a faculty member since 2012. He have been affiliated with Kyrgyz -Turkiye Manas University since 2025 March. He obtained my B.Sc. in Mathematics (2009) at the Bulent Ecevit University, my M.Sc. (2012) and Ph.D. (2016) degrees in Applied Mathematics at the Balikesir University in Turkey. In December 2012, he joined the Necmettin Erbakan University, Turkey as a lecturer. He worked at the same university as an Assistant Professor in 2018-2019, Associate Professor in 2019-2025. As of September 2025, he became a Full Professor in Applied Mathematics at the same university. He also joined the University of Exeter (U.K.) in September 2019 as a post-doctoral researcher under supervision Prof. Dr. Stuart Townley in the Department of Mathematics on the Penryn Campus. His research interests lie in the area of fractional calculus and applications, optimal control, adaptive and robust control, chaos and bifurcation analysis, dynamical systems, biological models, financial mathematics and numerical methods, ranging from theory to design to implementation. Also, he have been collaborating actively with researchers in several other disciplines and he would be pleased to study with those who are willing to make collaborations in these research fields.

Mehmet Yavuz
Necmettin Erbakan University, Turkey

ABOUT US

Iris Scientific Group

Iris Scientific Group is started to fulfill the requirements and to seek after aggregate objectives of the scientific community particularly focusing in the field of Science and technology to support the efforts to exchange knowledge and ideas which encourage the cooperation between the researchers, scientists, academicians and analysts of interdisciplinary research or same field.

We are expert in conducting conferences, workshops, seminars, and meetings with the peerless and inspired speakers all around the world. We are here to provide you and your association with the opportunities to connect with others, explain your research and make your unique identity in front of others. Our conferences and workshops are known as the sea of learning where we help you to swim and learn everything you want.

In a very short period, Iris Scientific Group became successful in developing a unique platform for experts, budding researchers and professionals from different universities, countries, research institutions, hospitals, companies and industries. Here we provide an opportunity to easily discuss and socialize their techniques of research, goals, facts, latest science discoveries and news.

BOOK OF ABSTRACTS

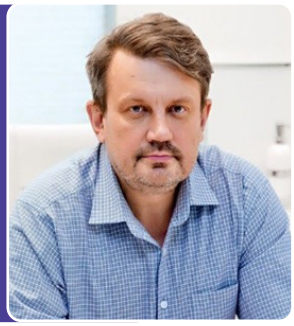


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KEYNOTE SESSIONS



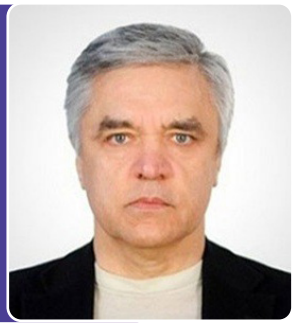
Alexey Severtsev
Pirogov Russian National Research Medical University, Russian Federation

Surgery: Sepsis in severe acute pancreatitis

Severe acute pancreatitis (SAP) has many similarities with sepsis syndrome and septic shock. The hemodynamic features are virtually indistinguishable in each of these conditions. Septic complications of SAP are usually late manifestations, although sterile pancreatic necrosis is observed early in acute pancreatitis.
In patients with SAP, it is extremely important to understand possible septic complications, methods of their diagnosis and treatment. The overall mortality of patients with SAP is about 20%. Secondary pancreatic infection and sepsis develop in 40-70% of patients with 80% mortality. Pancreatic infection is caused by bacterial/ fungal contamination of pancreatic necrosis. Infection is usually recorded in the second (25%) to fourth (70%) weeks of the disease. The frequency of secondary infection and sepsis correlates with the degree of pancreatic necrosis. Sepsis and sepsis-related multiple organ failure are the cause of mortality in approximately 50% of patients. Prevention of infection and sepsis by systemic antibiotics is considered the mainstay of therapy for SAP. However, the effect of antibiotic prophylaxis has not yet been proven.
Patients with SAP at the stage of purulent-septic complications are a heterogeneous group, but from the point of view of the pathogenesis of the disease, they have a significant number of common features. Similar features between SAP at the stage of purulent-septic complications and sepsis make SAP an excellent model for studying the general pathogenesis of sepsis.

Biography:

Alexey Severtsev (Russian: Алексей Николаевич Северцев) – a Russian doctor of medicine sciences, Head and the professor in the surgical department of the medical faculty in Pirogov Russian National Research Medical University.Visiting professor in the University of California, Los Angeles (UCLA) (1991-1992); Surgeon in the King Faisal Specialist Hospital and Research Centre (Riyadh, the Kingdom of Saudi Arabia) (1993); 1998-2002 – The head of the surgical department in the Clinical Hospital No.1 of the Medical Centre UD of the President of the Russian Federation; 2002-2010 – The chief surgeon of the hospital and the head of department of surgery in the Central Clinical Hospital No.1 of JSC "Russian Railways"; 2003-until now – A professor of surgery department (from 2023: Head) of medical faculty in Pirogov Russian National Research Medical University;



Sergey Suchkov[1-6*], Holland Cheng[12], Noel Rose[15,16]

[1]N.D. Zelinskii Institute for Organic Chemistry of the Russian Academy of Sciences, Moscow, Russia
[2]InMedStar, Russia
[3]China Hong Kong Innovation International Business Association, Hong Kong
[4]New York Academy of Sciences, USA
[5]EPMA (European Association for Predictive, Preventive and Personalized Medicine), Brussels, EU
[6]ISPM (International Society for Personalized Medicine), Japan
[7]PMC (Personalized Medicine Coalition), Washington, USA
[8]AMEE (Association for Medical Education in Europe), Centre for Medical Education, Dundee, Scotland
[9]ACS (American Chemical Society), Washington, DC, USA
[10]AHA (American Heart Association), Dallas, TX, USA
[11]ARVO (The Association in Research in Vision & Ophthalmology), Rockville, MD, USA
[12]ISER (International Society for Eye Research), Anchorage, AK USA
[13]The Russian Academy of Natural Sciences, Moscow, Russia
[14]T College of Biological Sciences, UC Davis, CA, USA
[15]Center for Autoimmune Disease Research, John Hopkins University, Baltimore, MD, USA
[16]Harvard Medical School, Boston, MA, USA

Personalized and Precision Medicine (PPM) as a unique healthcare model *via* design-inspired & biotech-driven translational applications to secure the infectious disease prevention, human healthcare control and biosafety concerns

A new and upgraded approach to the diseased states and wellness,and to re-shape tomorrow's healthcarewhilst doing it today, resulted in a new global trend in the healthcare services, namely, ***Personalized and Precision Medicine (PPM).***PPMas a Unique Entity demonstrating an integrationof Fundamental, Healthcare & Life Sciences, ***Biodesign-driven BioTech, Translational ART***and***IT Armamentarium***, is based on the new developmental strategy driven by ***Biomarkers***- and ***Biotargeting***-related biomachines. It would be extremely useful to integrate data harvesting from different databanks for applications such as pre-early predictive diagnostics, precise prognostication and personalization of further treatment to provide more tailored measures for the diseases bodies and persons-at-risk resulting in improved outcomes and more cost effective use of the latest health care resources.

PPM as being the Grand Challenge to forecast, to predict and to prevent is rooted in a big and a new SCIENCE generated by the achievements of (i) ***Systems & Synthetic Biology***; (ii) ***Biodesign-driven Translational applications*** and ***Biotech-driven Biomanufacturing***; (iii) ***Bioindustry*** and ***Biomarketing*** of the next step generation. The latter, being a Grand Brick laid into the frame of National Bioeconomy, says and confirms that the efficiency and efficacy of the Bioeconomy are determined and dictated by the innovative trends,generated by fresh knowledge and their transfer into the scientific, bioindustrial and social areas to maintain the national stability and extensive development of the country.

The core strategic tool to operate the transdisciplinary approach is rooted in a unique tandem consisting of (i) ***integrated platforms of Fundamental Sciences (Basics) and innovative OMICs biotechnologies*** on one hand, and (ii) the algorithms of ***Bioinformatics***, on the other one.

The importance of PPM in the healthcare management is well-documented. Advances in genomics and computing are transforming the capacity for the characterization of biological systems, and researchers are now poised for a precision-focused transformation in the way they prepare for, and respond to, infectious diseases. But still, very little is known about the role of ***precision genomics*** and ***immunogenetics*** in susceptibility or resistance to infectious diseases. Despite being a forerunner, PPM is not yet routinely applied in infectious patient care.

Meanwhile, new technologies are supporting the rapid identification of infective agents and targeted approaches based on the genetic resistance of pathogens to antibiotics. For instance, recent technological advances have enabled the development of antimicrobials that can selectively target a gene, a cellular process, or a microbe of choice. These strategies bring us a step

closer to developing personalized therapies that exclusively remove disease-causing infectious agents. This information can lead to revising the data banks that can be used for personalized predicting diseases, improving PPM-driven treatment, personalized prevention strategies specific to infectious pathogens.

PPM-driven management of infectious diseases plays a critical role in trust for government, health-care organizations, science, and pharma. The improvement in biomedical technologies, availability of large clinical and OMICS data and appropriate application of applied bioinformatics-related algorithms may allow precision in vaccines and public health and restore trust. For this scope, the next step education is a crucial step for the successful implementation of PPM in the clinic, and with this part, we would like to encourage learning about PPM and the impact in the communicable (including infectious) disease field. Infectious disease management essentially consists in identifying the microbial cause(s) of an infection, initiating if necessary antimicrobial therapy, and controlling host reactions to infection. In canonical (PPM-ignored) clinical microbiology, the turnaround time of the diagnostic cycle (>24 hours) often leads to unnecessary suffering and deaths; approaches to relieve this burden include rapid diagnostic procedures and more efficient transmission or interpretation of molecular microbiology results. The implementation of point-of-care testing for infectious diseases will require acceptance by medical authorities, new technological and communication platforms, as well as reimbursement practices such that time- and life-saving procedures become available to the largest number of patients.

PPM has indeed arrived for the diagnosis of infectious diseases. More than that, it has arrived for all in the areas of clinical microbiology, molecular epidemiology and many other areas. With the current capabilities, cost, and speed of sequencing technologies, the field has finally reached a point where rapid genomic surveillance and analysis can start to become a standard part of the response to infectious disease outbreaks. Just as broadscale human genome sequencing revolutionized the treatment of many non-communicable diseases, pathogen genome data are poised to drive a similar revolution in the response to infectious diseases.

Healthcare is undergoing a transformation, and it is imperative to leverage new technologies to support the advent of PPM. This is the reason for developing global scientific, clinical, social, and educational projects in the area of PPM and TraMedto elicit the content of the new trend. The latter would provide a unique platform for dialogue and collaboration among thought stakeholders in government, academia, industry, foundations, and disease and patient advocacy with an interest in improving the system of healthcare delivery on one hand and drug discovery, development, and translation, on the other one, whilst educating the policy community about issues where biomedical science and policy intersect.

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 and was awarded with MD. In 1985, Suchkov maintained his PhD as a PhD student of the I.M. Sechenov Moscow Medical Academy and Institute of Medical Enzymology. In 2001, Suchkov maintained his Doctor Degree at the National Institute of Immunology, Russia. From 1989 through 1995, Dr Suchkov was being a Head of the Lab of Clinical Immunology, Helmholtz Eye Research Institute in Moscow. From 1995 through 2004 - a Chair of the Dept for Clinical Immunology, Moscow Clinical Research Institute (MONIKI). In 1993-1996, Dr Suchkov was a Secretary-in-Chief of the Editorial Board, Biomedical Science, an international journal published jointly by the USSR Academy of Sciences and the Royal Society of Chemistry, UK.

At present, Dr Sergey Suchkov, MD, PhD, is:

- Research and Development Director, National Center for Human Photosynthesis, Aguascalientes, México
- Senior Scientific Advisor, InMedStar, Russia-UAE
- Member, The Russian Academy of Natural Sciences, Moscow, Russia
- Member, New York Academy of Sciences, USA

Dr Suchkov is a member of the:

- American Chemical Society (ACS), USA;
- American Heart Association (AHA), USA;
- European Association for Medical Education (AMEE), Dundee, UK;
- EPMA (European Association for Predictive, Preventive and Personalized Medicine), Brussels, EU;
- ARVO (American Association for Research in Vision and Ophthalmology);
- ISER (International Society for Eye Research);
- Personalized Medicine Coalition (PMC), Washington, DC, USA



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ORAL SESSIONS



Aghapy Yermans Yakoup
Zewail City of Science and Technology, Egypt

Characterization, antibacterial, and cytotoxic activities of silver nanoparticles using the whole biofilm layer as a macromolecule in biosynthesis

Recently, multi-drug resistant (MDR) bacteria are responsible for a large number of infectious diseases that can be life-threatening. Globally, new approaches are targeted to solve this essential issue. This study aims to discover novel antibiotic alternatives by using the whole components of the biofilm layer as a macromolecule to synthesize silver nanoparticles (AgNPs) as a promising agent against MDR. In particular, the biosynthesized biofilm-AgNPs were characterized using UV-Vis spectroscopy, electron microscopes, Energy Dispersive X-ray (EDX), zeta sizer, and potential while their effect on bacterial strains, and normal cell lines was identified. Accordingly, biofilm-AgNPs have a lavender-colored solution, spherical shape, with a size range of 20–60 nm. Notably, they have inhibitory effects when used on various bacterial strains with concentrations ranging between 12.5 and 25 µg/mL. In addition, they have an effective synergistic effect when combined with phage ZCSE9 to inhibit and kill Salmonella enterica with a concentration of 3.1 µg/mL. In conclusion, this work presents a novel biosynthesis preparation of AgNPs using biofilm for antibacterial purposes to reduce the possible toxicity by reducing the MICs using phage ZCSE9.

Biography

Aghapy Yermans Yakoup is a graduate, batch 2023, with a biomedical sciences major (BMS) (medical sciences concentration) from Zewail City for Science, Technology, and Innovation. In addition, she have worked as a junior researcher assistant (jRA) in the Center for Microbiology and Phage Therapy (CMP) in Zewail City for Science, Technology, and Innovation from Fall 2021 until Summer 2023. She is working currently as an R&D specialist in Pharmaplast company. She is interested in finding new solutions to get rid of multi-drug-resistant bacteria and inventing new compounds that can be alternatives to antibiotics. Also, she is interested in the medical microbiology field. In the future, she is planning to enroll in a Ph.D. program that aims to find new applicable solutions for infectious diseases in different body systems like the nervous system and cardiovascular system.



PunamBedi- Sr. Professor, **Bhavna Gupta, Veenu Bhasin, Pushkar Gole

Department of Computer Science, University of Delhi, India Surbhi Rani- Ph. D. Scholar, Department of Computer Science, University of Delhi, India

Professor, Department of Computer Science, Keshav Mahavidyalaya College, University of Delhi, India

Associate Professor, Department of Computer Science, PGDAV College University of Delhi, India

Assistant Professor, Department of Computer Science, PGDAV College University of Delhi, India

EpiBrCan-Lite: A lightweight deep learning model for breast cancer subtype classification using epigenomic data

Early breast cancer subtypes classification improves the survival rate as it facilitates prognosis of the patient. In literature this problem was prominently solved by various Machine Learning and Deep Learning techniques. However, these studies have three major shortcomings: huge Trainable Weight Parameters (TWP), suffer from low performance and class imbalance problem. Our research proposed a lightweight model named EpiBrCan-Lite for classifying breast cancer subtypes using DNA methylation data. This model encompasses three blocks namely Data Encoding, TransGRU, and Classification blocks. In Data Encoding block, the input features are encoded into equal sized chunks and then passed down to TransGRU block which is a modified version of traditional Transformer Encoder (TE). In TransGRU block, MLP module of traditional TE is replaced by GRU module, consisting of two GRU layers to reduce TWP and capture the long-range dependencies of input feature data. Furthermore, outputof TransGRU block is passed to Classification block for classifying breast cancer into their subtypes. The proposed model is validated using Accuracy, Precision, Recall, F1-score, FPR, and FNR metrics on TCGA breast cancer dataset. This dataset suffers from the class imbalance problem which is mitigated using Synthetic Minority Oversampling Technique (SMOTE). Experimentation results demonstrate that EpiBrCan-Lite model attained 95.85 % accuracy, 95.96 % recall, 95.85 % precision, 95.90 % F1-score,1.03 % FPR, and 4.12 % FNR despite of utilizing only 1/1500 of TWP than other state-of-the-art models. EpiBrCan-Lite model is efficiently classifying breast cancer subtypes, and being lightweight, it is suitable to be deployed on low computational powered devices.

Biography

Bhavna Gupta is working as Professor in Department of Computer Science at Keshav Mahavidyalaya, University of Delhi. She brings over teaching experience of more than 25 years. She has contributed extensively to research through publications in Scopus-indexed international conferences and high-impact journals. Her research interests are in the followings domains : Artificial Intelligence, Multi Agent Systems, Recommender Systems, Machine Learning, Deep learning, Natural Language Processing, Sentiment Analysis, Healthcare Systems, Climatic Adversities, Fuzzy Systems, Collaborative Learning.



Feyera Gemeda Dima
Jimma University, Ethiopia

Global malaria challenge and its economic impact in ethiopia

Malaria remains a major public health challenge, particularly in sub-Saharan Africa, with significant economic consequences for endemic countries like Ethiopia. This study examines the global malaria burden, focusing on its prevalence, transmission dynamics, and economic impact in Ethiopia. Using a qualitative approach and secondary data from government reports, academic journals, and international health organizations, the research highlights Ethiopia's progress in malaria control alongside persistent challenges. Findings reveal that despite a decline in cases from 1.5 million in 2010 to around 1 million in 2019, malaria continues to impose a heavy economic burden. Direct healthcare costs account for approximately 20% of expenditures in endemic regions, while productivity losses exceed $200 million annually. The study underscores the need for sustained investment in prevention, vector control, and healthcare access, as well as addressing socioeconomic determinants such as poverty and education. A multifaceted approach is essential to reduce malaria's economic toll and support Ethiopia's broader development goals.

Keywords: Malaria, Economic Impact, Ethiopia, Healthcare Costs, Productivity Loss, Public Health Interventions.

Biography

Dr. Feyera Gemeda is an Associate Professor and Chief Scientist at Jimma University, specialized in infectious diseases, public health, and healthcare. With over 15 years of experience, he holds a PhD and three master's degrees in his field. Dr. Gemeda has led significant research teams, contributed to curriculum development, and served as an assessor for international grants. A recognized educator and mentor, he is dedicated to advancing global health through leadership, innovation, and impactful policy.

Hafiza Farhat
Assistant Professor, Gomal University D.I Khan, Pakistan

Bioactivity and mycochemical profile of mycelial extract of *talaromyces*species

Background: Infection is the second leading cause of death in patients with cancer. Loss of efficacy in antibiotics due to antibiotic resistance in bacteria is an urgent threat against the continuing success of cancer therapy.The advent of multidrug resistance among pathogenic bacteria is imperiling the worth of antibiotics, which have previously transformed medical sciences. The crisis of antimicrobial resistance has been ascribed to the misuse of these agents and due to unavailability of newer drugs attributable to exigent regulatory requirements and reduced financial inducements. Comprehensive efforts are needed to minimize the pace of resistance by studying emergent microorganisms, resistance mechanisms, and antimicrobial agents.

Objective: Drug development from microbial endophytes of *Talaromycesassiutensis*and *T. trachyspermus*

Methods: In this study, different plant sample were collected from different areas of agriculture lands in order to isolate endophytic fungi. The isolated fungi were test for antibacterial activity against common laboratory bacteria and also checked their antifungal activity against root rot fungi. Gas Chromatography and Mass Spectrometry analysis of mycelial extract of *Talaromycesassiutensis* and *T. trachyspermus*were also performed in order to characterize compound from them as they showed strong antimicrobial activity and antifungal activity.

Results: Endophytic fungi isolated from healthy plants have showed strong antibacterial activity against common laboratory bacteria (*Salmonella typhimurium, Pseudomonas aeruginosa,* and *E.coli, Bacillus subtilis* and *Staphylococcus aureus*) by forming the zone of inhibition. Theseendophytic fungialso showed strong potential against phytopathogensviz;*Macrophominaphaseolina, Fusariumoxysporum*, *F.solani*and*Rhizoctoniasolani*. GC-MS spectroscopy of mycelial extract of *Talaromycesassiutensis* and *T. trachyspermus*revealed the presence of several compounds and some of them are new from this source as confirmed by computer matching against National Institute of Standards and Technology, USA (NIST Mass Spectrometry Data Center (mainlib) and finally compared with Science finder.

Conclusion: Antibiotic stewardship is, therefore, much needed to ensure not only the appropriate use of antimicrobials but also the choice of antimicrobials and their duration of use.The problem of antimicrobial overuse extends beyond antibiotic resistance and includes fungal and viral resistance.

Biography

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



Manish Tripathi
All India Institute of Medical Sciences, India

Exploring a novel interaction between the human malaria parasite plasmodium vivax and reticulocyte protein

The global burden of malaria remains significant despite concerted elimination efforts, with Plasmodium vivax presenting unique challenges due to its distinctive biology and invasion mechanisms. Despite progress in understanding Plasmodium falciparum, the molecular interactions governing P. vivax infection remain relatively obscure, particularly regarding its exclusive preference for reticulocytes. This study illuminates a critical host-parasite interaction that advances our understanding of P. vivax pathogenesis and opens new avenues for therapeutic intervention. The research focuses on PvTRAg36.6, a member of the P. vivax-specific tryptophan-rich antigen family (Pv-fam-a). This protein represents an excellent candidate for investigation due to several key characteristics: it is consistently expressed during the merozoite stage, shows remarkable sequence conservation across geographically diverse parasite populations, and critically, elicits both cellular and humoral immune responses during natural infection. These properties suggest evolutionary importance and potential immunological relevance. Through meticulous biochemical analysis, we identified CD71 as the binding partner for PvTRAg36.6 on human reticulocytes. The investigation employed liquid chromatography-mass spectrometry (LC-MS) analysis of proteins recovered from pull-down assays, providing initial evidence of this interaction. The specificity of this receptor-ligand pairing was subsequently confirmed through multiple complementary approaches, including solid-phase binding assays and surface plasmon resonance (SPR), and Bio-layer interferometry establishing a robust foundation for the findings. Further characterization revealed that PvTRAg36.6 engages with CD71 through two discrete peptide regions. This molecular specificity suggests a highly evolved interaction that has been optimized throughout the parasite's evolutionary history. Functional assays demonstrated that this binding event plays a significant role in the invasion of reticulocytes by P. vivaxmerozoites, highlighting its biological relevance in the parasite's life cycle. The identification of CD71 as a receptor is particularly notable given its specific expression on reticulocytes. This aligns with P. vivax's strict tropism for these immature red blood cells and may partially explain this selective preference. The CD71 receptor is essential for iron uptake in developing erythroid cells and is progressively lost during red cell maturation, correlating with the window of susceptibility to P. vivax infection. The conservation of PvTRAg36.6 across parasite isolates suggests strong selective pressure to maintain this interaction, further emphasizing its importance for parasite survival and propagation. Unlike some other invasion ligands that show high variability to evade host immunity, the relative conservation of PvTRAg36.6 may indicate either limited immune pressure on this protein or critical functional constraints that prevent extensive sequence variation. From an immunological perspective, the documented humoral and cellular responses against PvTRAg36.6 during natural infection present promising opportunities for vaccine development. Targeting conserved epitopes involved in CD71 binding could potentially disrupt this critical invasion pathway. Additionally, the identification of the specific peptide regions mediating this interaction provides focused targets for the development of inhibitory antibodies or small molecule inhibitors. In conclusion, this study provides valuable insights into the molecular basis of P. vivax infection and highlights PvTRAg36.6 as a promising target for immunotherapeutic approaches. These findings advance our fundamental understanding of host-parasite biology while simultaneously offering practical directions for developing interventions against this persistent global health threat.

Biography

Manish Tripathi completed his post-graduation from All India Institute of Medical Sciences, New Delhi (2018), where he carried out his dissertation work in the Molecular Parasitology Laboratory. He is currently pursuing his Ph.D., with research focused on the characterization of parasite ligand–host receptor interactions in Plasmodium infection using a combination of proteomics-based approaches, in-silico techniques, and Plasmodium vivax culture systems. Through these approaches, he has successfully identified host receptors for Plasmodium vivax ligands and has published several research papers on host red cell–parasite interactions and malaria detection using aptamer-based diagnostic kits. In addition, his Ph.D. work extends to drug discovery, where he is actively involved in designing and screening potential drug molecules against P. falciparum and P. vivax. He has also authored two book chapters, reflecting his interest in malaria biology and therapeutic interventions.



Mariano Votta
Active Citizenship Network, Italy

Grassroots mobilisation: Leveraging civil society and community leadership to bridge gaps in vaccine coverage

The WHO has defined community engagement as “a process of developing relationships that enable stakeholders to work together to address health related issues and promote well being to achieve positive health impact and outcomes” and it underlines the “Community and civil society engagement” as a pillar of its “Global Action Plan for Healthy Lives and Well-being for All”.

On December 5, 2023, on the occasion ofthe adoption by the European Commission of the EU4Health 2024 work program to implement key health policy priorities within the European Health Union, Stella Kyriakides, European Commissioner for Health and Food Safety, said that "Civil society has a crucial role to play in reaching out to our citizens".

Recently, on the occasion of the G7 Ministers’ Meeting on Health held on 9/11 Oct. 2024 in Ancona (Italy), global leaders emphasis that “vaccination is an essential preventive measure and reiterate the crucial role of routine immunisation and campaigns”, higlihting “the importance of raising awareness and involving the general population by providing evidence-based information through campaigns aimed at citizens’ empowerment and increasing health literacy regarding prevention, research and care”. In concrete way, the aim of the presentation is to show how the so-called intermediated bodies of the society, when recognized as a stakeholder, can play an active role in support of public policy on vaccionation. Around this goal, the Vaccination Informal Platform (V.I.P.) for life-course immunization promotion, a collective of leaders of patient and citizen organizations across Europe promoted by Active Citizenship Network, has united with the desire to strengthen the exchange of experiences among the many expressions of active citizenship working to support public vaccination policies.The ultimate goal is to update a narrative that, when it comes to vaccination, almost never refers to the active role of Civil Society Organizations (CSOs) and Patient Advocacy Groups (PAGs), instead focusing mainly on hesitant or even hostile attitudes toward vaccines, which, though present, do not represent the whole picture. There are many of actors from the intermediated bodies of the society that can play a constructive role with institutional and non-institutional stakeholders, as well as act as a driving force for other organizations, and there are different typologies of initiatives to testify their activist on vaccination arena.

Biography:

Mariano Votta is responsible for EU Affairs at the Italian NGO Cittadinanzattiva and Director of its EU branch “Active Citizenship Network”.

Passionate about health & consumer issues, Mariano has 25 years of experience in advocacy, stakeholder engagement, communication, European Public Affairs & EU funded-projects.
Mariano holds a Degree in Political Science and two post-graduate master's degrees in European Public Relations and Corporate Social Responsibility. He is also a journalist with more than 50 publications in international peer-reviewed journals.

He led the political initiative to launch in 2015 at the EU Parliament the Interest Group "EU Patients' Rights & Cross-Border Healthcare," – now at its third mandate - endorsed by more than 100 organisations across Europe and dozens of Members of the European Parliament. In 2016 Mariano won the Efhre International University Excellence Awards on patients’ rights.



**Nia Muhammad, B.S, NIAID
Danielle Cunnigham, Ph.D., UNC
Todd Seaman, Ph.D., NIAID
Jennifer Webster-Cyriaque, Ph.D., DDS, NIDCR

Bacteria driven HPV outcomes in anogenital cancers

Cervical cancer remains a major global health burden and is the fourth most common cancer among women worldwide, with over 600,000 new cases and approximately 340,000 deaths each year. Persistent infection with high-risk human papillomavirus (HPV) is the primary etiologic factor in cervical and head and neck cancers, with HPV16 and HPV18 conferring the highest oncogenic risk. Although HPV is predominantly transmitted through sexual contact, additional transmission routes, including contaminated surfaces, shared personal items, and vertical transmission, have been reported. Following infection of cervical epithelial cells, high-risk HPV disrupts cellular replication and signaling pathways, enabling persistent infection and progression from precancerous lesions to invasive disease over years to decades.

Emerging evidence suggests that microbial co-infections may influence HPV persistence and disease severity. Building on prior work demonstrating synergistic interactions between oral pathogens and oncogenic viruses, we investigated whether oral and anogenital bacterial pathogens modulate HPV-driven carcinogenesis. The healthy cervicovaginal microbiome is typically dominated by Lactobacillus species that maintain a protective, low-diversity environment; disruption of this balance (dysbiosis) has been associated with increased susceptibility to infection and disease progression. Notably, oral bacterial genera such as Porphyromonas, Fusobacterium, and Prevotella are enriched in the cervicovaginal microbiome during cervical disease, suggesting potential cross-site microbial influences shaped by sexual behaviors.

In HPV16-positive cervical cancer cells, treatment with Porphyromonasgingivalis (Pg) resulted in a threefold increase in E6/E7 transcript levels compared to uninoculated controls. RNA-sequencing revealed increased expression of spliced E6/E7 transcripts and activation of oncogenic signaling pathways, including MAPK and NF-κB. Pg exposure induced global histone H3 acetylation, and increased H3K9 and H3K27 acetylation with up to a 90% enrichment of H3K9 acetylation occupancy at the HPV long control region (LCR) as determined by chromatin immunoprecipitation. Pharmacologic inhibition of p38 MAPK reduced histone acetylation and occupancy at the LCR and attenuated E6/E7 expression, implicating p38-mediated epigenetic regulation in bacteria-driven enhancement of HPV oncogene expression. Consistent with these findings, Pg and Fusobacterium nucleatum increased H3K9 acetylation in both HPV16-positive and -negative cells in a pathogen-specific, dose-dependent manner. These data suggest that bacterial metabolites may promote HPV persistence and pathogenesis, highlighting polymicrobial interactions as potential therapeutic targets in HPV-associated disease.

The audience take away from presentation:

- Will highlight polymicrobial interactions as potential therapeutic targets
- Other faculty could use to expand their own HPV-related research
- Consideration of bacterial co-infections as drivers of HPV pathogenesis

Biography:

Nia Muhammad is a Postbaccalaureate Intramural Research Training Award (IRTA) Fellow at the National Institutes of Health. She earned a Bachelor of Science in Chemistry with a concentration in Biochemistry from Stanford University. Her research focuses on host–microbe and virus–microbiome interactions, with an emphasis on understanding how bacterial pathogens influence viral persistence and cancer progression. Nia integrates molecular biology, epidemiology, and mass-spectrometry-based approaches to study HPV-associated disease. She is a Gates Millennium Scholar and is interested in pursuing a career in academic medicine centered on translational research, reproductive health, and health equity.



Rachel Wong Si Yin[2],**

Christen Zhu Kexin, M.Sc.[1], *

Jolene Oon, MB BCh BAO, MRCP, MHPE[3,5],

Sanjay De Mel, B.Sc, BM, MRCP, FRCPath[1], Clarice Choong, MBBS, MMED, MRCP, FRCPath[1], Yap Eng Soo, MBBS, M.Med, MRCP, FRCPath[4],

VisulaAbeysuriya, MBBS, HDip, MPHMPhil, Phd, FRSPH, FRSS[6],

Nesaretnam Barr Kumarakulasinghe, MBBS, MRCP, FAMS, M. Health Informatics[1]

National University Cancer Institute Singapore, Singapore

Yong Loo Lin School of Medicine, National University of Singapore, Singapore

Department of Medicine, Yong Loo Lin School of Medicine, National University of Singapore, Singapore

Department of Laboratory Medicine, National University Hospital, Singapore

Division of Infectious Diseases, Department of Medicine, National University Hospital, National University Health System, Singapore

Institute of Biochemistry, Molecular Biology and Biotechnology, University of Colombo, Sri Lanka

Supervised machine learning for predicting low-risk dengue: A clinical data-driven approach for appropriate and value-based healthcare

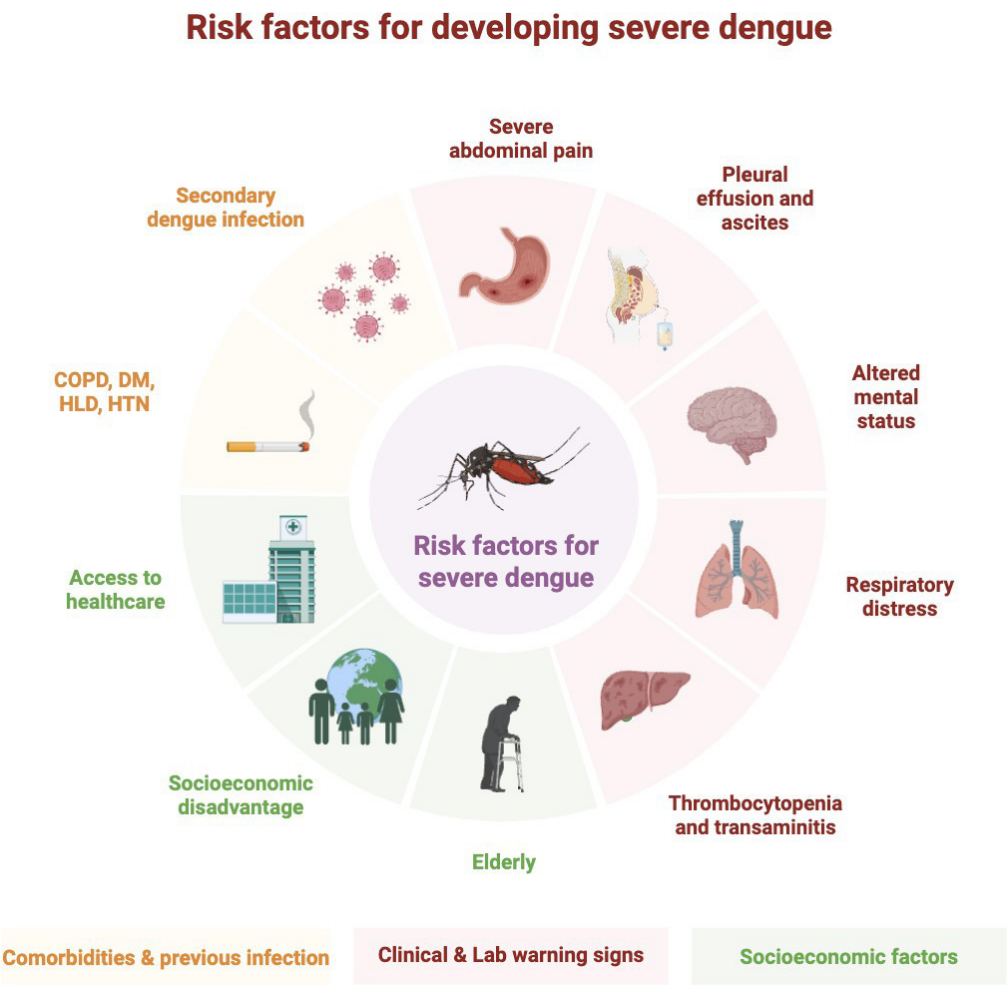
Background: Dengue fever represents the majority of dengue virus infections and is typically characterized by self-limiting febrile illness without progression to severe complications. Despite its benign course, accurate risk stratification remains critical to prevent unnecessary hospitalisations and to optimise resource allocation, especially in endemic regions. Existing clinical criteria help guide management decisions, but their utility varies across different healthcare settings and populations. This study aims to identify low-risk dengue patients suitable for outpatient management to reduce healthcare burden and support appropriate care placement.

Methods: Clinical and laboratory data comprising 35 features were collected from 530 dengue patients in Sri Lanka, classified per WHO criteria into 407 low-risk and 123 high-risk cases. Variables included age, sex, comorbidities, hypoalbuminaemia, haematocrit increase, and platelet count. Multiple machine learning models—including Logistic Regression, SVM, KNN, Random Forest, and XGBoost—were trained to predict low-risk patients. Model performance was assessed using AUC, F1 score, recall, precision.

Results: Following hyperparameter tuning and feature selection, 22 features1 (12 categorical and 10 continuous) were selected for model development. Among the evaluated models, the CatBoostClassifier achieved the best overall performance, with an AUC of 0.88 and an F1-score of 0.89, supported by balanced precision and recall values (both 0.89). The AdaBoostClassifier also demonstrated competitive performance, particularly with a strong F1-score (0.9) and a relatively high AUC 0.87, highlighting its effectiveness as an alternative approach.

Conclusion: Our findings highlight the potential of machine learning models —particularly the CatBoost algorithm in predicting low-risk dengue cases. By accurately identifying patients safe for outpatient management, this model can significantly optimize healthcare resource allocation and reduce the overall burden on the healthcare system. The next phases of this research will focus on external validation of our models using an independent patient dataset and prospective validation within a proposed clinical

1 Refer to image below titled "Risk Factors for Developing Severe Dengue workflow.

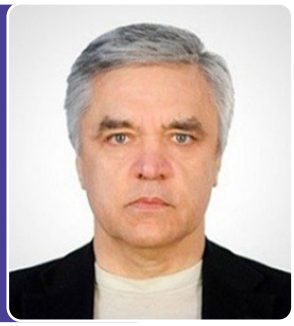


The audience take away from presentation:

- A practical understanding of how machine learning models can be applied to clinical decision-making in infectious diseases.
- Insights into a predictive tool that improves dengue triage accuracy, ensuring safer outpatient management.
- Evidence on how data-driven tools can reduce unnecessary hospitalizations, saving healthcare resources.
- Knowledge of how this approach can be adapted to other conditions beyond dengue, broadening its utility.
- A framework for integrating predictive analytics into routine hospital protocols without disrupting clinical workflows.

Biography:

Rachel Wong is a Year 3 medical student at the Yong Loo Lin School of Medicine, National University of Singapore. Her academic interests include internal medicine, infectious diseases, and obstetrics and gynaecology. She is actively engaged in clinical research on Group B Streptococcus screening as well as broader projects in gastroenterology and women's health. Beyond research, she contributes to public health initiatives and community outreach, with a strong interest in medical missions. She aims to pursue a career that integrates clinical medicine, academic research, and global health.



Sergey Suchkov[1-6*], Holland Cheng[12], Noel Rose[15,16]

[1]N.D. Zelinskii Institute for Organic Chemistry of the Russian Academy of Sciences, Moscow, Russia
[2]InMedStar, Russia
[3]China Hong Kong Innovation International Business Association, Hong Kong
[4]New York Academy of Sciences, USA
[5]EPMA (European Association for Predictive, Preventive and Personalized Medicine), Brussels, EU
[6]ISPM (International Society for Personalized Medicine), Japan
[7]PMC (Personalized Medicine Coalition), Washington, USA
[8]AMEE (Association for Medical Education in Europe), Centre for Medical Education, Dundee, Scotland
[9]ACS (American Chemical Society), Washington, DC, USA
[10]AHA (American Heart Association), Dallas, TX, USA
[11]ARVO (The Association in Research in Vision & Ophthalmology), Rockville, MD, USA
[12]ISER (International Society for Eye Research), Anchorage, AK USA
[13]The Russian Academy of Natural Sciences, Moscow, Russia
[14]T College of Biological Sciences, UC Davis, CA, USA
[15]Center for Autoimmune Disease Research, John Hopkins University, Baltimore, MD, USA
[16]Harvard Medical School, Boston, MA, USA

The promise of nanotechnology in personalized & precision medicine: Nano driven precision vaccinomics of the future

Biodesigners, biotechnologists and biomanufacturers are beginning to realize the promise of ***personalized and precision medicine (PPM)***, translating to direct benefit to patients or persons-at-risk.

Both PPM, personalized vaccinomics and nanobiotechnologies are being integrated into a panel of precision tools to manage an array of medical conditions. The next 'golden age' in vaccinomics will be ushered in by the new science of vaccinomics, which will inform and allow the development of ***personalized vaccines***, based on our increasing understanding of immune response phenotype: genotype information.

The ideal vaccine would induce a robust immune reaction without serious adverse effects. In this sense, personalized vaccines promise to fulfill those criteria, aided by in-depth genetic studies of variation in immune responses – ***vaccinomics,*** which jointly with nanotechnology have revolutionized global attempts to prevent, treat, and eradicate infectious diseases and cancer in the foreseen future. Nanotechnology is used in precision vaccinomics in conjunction with advanced tools such as OMICS technologies to achieve more personalized therapeutic strategies. For instance, nanoparticles and nanocarriers have been developed to overcome the limitations of design-driven engineered vaccines and navigate biological barriers - systemic, microenvironmental and cellular - that are heterogeneous across patient populations and diseases. Assuming such barriers can be overcome, the new systems and synthetic biology, in combination with increasing genotype, phenotype information and low cost, high output genetic screening will inevitably lead towards a more personalized approach to vaccines, just as it has with pharmaceuticals.

Meanwhile, nanovaccines are made up of nanoparticles that are associated with or prepared with components that can stimulate the host's immune system and have the potential to promote rapid as well as long-lasting humoral and cellular immunity. The nanovaccines have several possible benefits, including site-specific antigen delivery, increased antigen bioavailability, and a diminished adverse effect profile. For instance, peptide based vaccines (***proteomics-driven vaccines***) have shown significant promise in certain types of cancer treatment (***preventive and prophylactic pre-cancer vaccines***), but have had limited success in combating several viral infectious diseases. Vaccines based on peptides appear to hold the possibility of a quick response against sudden outbreaks of viral epidemics and pandemics, both for communities and individuals. Recent advances in treatment with multiple peptides, new knowledge of their interaction with the immune system and understanding of characteristics of peptides *in vivo* environment lead us to believe that the prospects of ***peptide vaccinomics*** are more promising clinical successes.

While vaccinomics concerns the effectiveness of vaccines, ***adversomics*** concerns their side effects. This area has great potential to address public concerns about vaccine safety and to promote increased public confidence, higher vaccination rates, and fewer serious adverse events in genetically predisposed individuals. Moreover, this knowledge gives us the opportunity in the event of viral epidemics to tailor making vaccines for different communities for maximum efficiency and for immunocompromised individuals. The latter means that advancements in nanobiomedicine have played a crucial role in driving the PPM-guided revolution and precision and personalized vaccinomics, in particular. With the ability to engineer and manipulate materials at the nanoscale, biodesigners have been able to develop innovative solutions for diagnostics, drug delivery, and imaging.
The Grand Change and Challenge to secure our Health and Wellness are rooted not in Medicine, and not even in Science! Just imagine WHERE?! In the upgraded Hi-Tech Culture!

Biography:

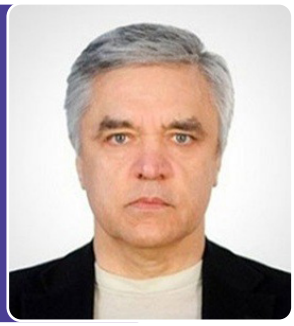
Sergey Suchkov was born in the City of Astrakhan, Russia, in a family of dynasty medical doctors. In 1980, graduated from Astrakhan State Medical University and was awarded with MD. In 1985, Suchkov maintained his PhD as a PhD student of the I.M. Sechenov Moscow Medical Academy and Institute of Medical Enzymology. In 2001, Suchkov maintained his Doctor Degree at the National Institute of Immunology, Russia. From 1989 through 1995, Dr Suchkov was being a Head of the Lab of Clinical Immunology, Helmholtz Eye Research Institute in Moscow. From 1995 through 2004 - a Chair of the Dept for Clinical Immunology, Moscow Clinical Research Institute (MONIKI). In 1993-1996, Dr Suchkov was a Secretary-in-Chief of the Editorial Board, Biomedical Science, an international journal published jointly by the USSR Academy of Sciences and the Royal Society of Chemistry, UK.

At present, Dr Sergey Suchkov, MD, PhD, is:

- Research and Development Director, National Center for Human Photosynthesis, Aguascalientes, México
- Senior Scientific Advisor, InMedStar, Russia-UAE
- Member, The Russian Academy of Natural Sciences, Moscow, Russia
- Member, New York Academy of Sciences, USA

Dr Suchkov is a member of the:

- American Chemical Society (ACS), USA;
- American Heart Association (AHA), USA;
- European Association for Medical Education (AMEE), Dundee, UK;
- EPMA (European Association for Predictive, Preventive and Personalized Medicine), Brussels, EU;
- ARVO (American Association for Research in Vision and Ophthalmology);
- ISER (International Society for Eye Research);
- Personalized Medicine Coalition (PMC), Washington, DC, USA



Sergey Suchkov[1-13*], Elena Antonova[14],Alan Wu[15,16], Carlos Malpica[17,18]

[1]N.D. Zelinskii Institute for Organic Chemistry of the Russian Academy of Sciences, Moscow, Russia
[2]InMedStar, Russia
[3]China Hong Kong Innovation International Business Association, Hong Kong
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[12]ISER (International Society for Eye Research), Anchorage, AK USA
[13]The Russian Academy of Natural Sciences, Moscow, Russia
[14]N.F. Filatov Moscow Municipal Clinical Pediatric Hospital, Moscow, Russia
[15]Clinical Chemistry Lab, SFGH and [16]Clinical Pharmacogenomics Lab, UCSF, San Francisco, CA, USA
[17]MLP Vision Biotech S.L. and [22]Valdia Health, Madrid-Spain and Doha-Qatar
[18]S-P National State Chemical & Pharmaceutical University, S-P, Russia

Precision genome-driven epidemiology and biostatistics forinfectious disease control

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.

Advances in genomics and computing are transforming the capacity for the characterization of biosystems, and practitioners are now poised for a precision-focused transformation in the way they prepare for, and respond to, infectious diseases. 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.

Meanwhile, despite being a forerunner PPM is not yet routinely applied in infectious patient care. Since, for instance, 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.

One thing is clear, as we embark into an era of increasing antimicrobial resistance coupled with the routine use of advanced immune modulating agents delivering deep, potent immune suppression, the role of PPM to better understand the clinical outcomes of infectious complications becomes more critical. Efforts to fund and support this nature of clinical and translational research is imperative. Finally, research into personalized medicine will serve as the foundation to develop cellular and immunotherapies specific for infectious pathogens.

For this scope, the next step PPM-oriented and driven education is a crucial step for the successful implementation of PPM

in the clinical applications in infectious diseases, and with this part, we would like to encourage learning about PPM in the communicable disease field.

Additionally, new biodesign-driven technologies are supporting the rapid identification of infective agents and targeted approaches based on the genetic resistance of pathogens to antibiotics. This information can lead to revising the data that can be used for personalized predicting diseases, improving the usage of precision biomarkers and personalized treatment, and also personalized prevention strategies specific to infectious pathogens.

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. In this sense, accurate diagnosis of malaria and the resilient capacity that the malaria parasite has in acquiring resistance to anti-malarial drugs (based on the phenotypic variations) form immediate barriers to the control and elimination of this disease. Those variations mentioned could be dependent on geo location or differential transmission setting or even the different ring developmental stage. So, PPM-based and driven OMICS- and IT-armamentarium would secure the advances in spectroscopic-based technologies which is able to reveal unique 'molecular fingerprint', and thus providing the much needed rapid phenotyping (rather than genotyping) platform in the field.

Moreover, PPM could help to improve precision diagnosis and individualized treatment of asthma, whilst determining some specific strategies for probing the situation in the tropics with special conditions to be considered for applying this strategy. The clinical impact of the advances in PPM for asthma in the tropics is mainly related to component resolved diagnosis,

and would need to be improved via identification of the biomarkers of the next step generation (including interactome- and network-related ones) that allow and accurate definition of phenotypes and endotypes of this heterogeneous disease to secure the proper choice pf personalized treatments.

These examples show how PPM-driven approach to wildlife health has in turn the potential to provide deeper insights into human health and the possibility of stemming and alleviating the impacts of parasite-induced diseases. The integration of the currently emerging PPM-related Initiative with the concepts of EcoHealth and One Health has great potential to deliver a deeper and broader interdisciplinary-based understanding of both wildlife and human parazyte-provoked and infectious diseases.

So, 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 and was awarded with MD. In 1985, Suchkov maintained his PhD as a PhD student of the I.M. Sechenov Moscow Medical Academy and Institute of Medical Enzymology. In 2001, Suchkov maintained his Doctor Degree at the National Institute of Immunology, Russia. From 1989 through 1995, Dr Suchkov was being a Head of the Lab of Clinical Immunology, Helmholtz Eye Research Institute in Moscow. From 1995 through 2004 - a Chair of the Dept for Clinical Immunology, Moscow Clinical Research Institute (MONIKI). In 1993-1996, Dr Suchkov was a Secretary-in-Chief of the Editorial Board, Biomedical Science, an international journal published jointly by the USSR Academy of Sciences and the Royal Society of Chemistry, UK.

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- Personalized Medicine Coalition (PMC), Washington, DC, USA



***Shem Otoi Sam1**
Daystar University, Nairobi, Kenya

Multipronged approach to panedmic surge surveillance: a case of lake region economic bloc, kenya

Introduction

Pandemic preparedness, response, mitigation, and recovery require accurate prediction, early detection, and surge monitoring for enhanced planning, and preparedness associated with allocation of resources. Surges are characterized by commodity stockout, fewer skilled health workers, little coordination, no referral mechanisms, and management protocols -health infrastructure can be overrun.

Objective: To predict surges early before infections begin; early detection of pathogens before they manifest in humans; and monitor infections.

Methods

1. Formulated predictive model which used local data to forecast infection surges.

2. Once the forecast period is established, waste water testing begins two weeks before the expected date.

3. For imported infections, samples of waste water at the points of entry are tested: airport, seaport, border points, and bus terminus.

4. Endemic infection sample of waste water in local markets, and residential sewer lines are collected and tested for pathogens (SARS-COV-2).

5. Positive samples and preserved for genome sequencing.

6. Real-time digital platform linked to dashboards are used to monitor the hospitalization and variants.

Results

Kenya's COVID-19 Surges were accurately predicted months in advance; wastewater testing detected SARS-CoV-2 pathogens two weeks before infections appeared. Real-time monitoring of infections and hospitalizations enabled timely responses, and genomic sequencing successfully identified and characterized variants driving each surge. Policy briefs on predictions, variants, and patient outcomes were widely disseminated to stakeholders and the media, enhancing informed decision-making. Over seven peer-reviewed publications emerged from these efforts, contributing to global knowledge. Importantly, despite seven waves, regional health infrastructure was not overwhelmed, reflecting effective planning and system resilience.

Conclusion

The region was kept safe by three steps of pandemic monitoring: mathematical prediction; waste water sample testing, and real-time dashboard infections/surge monitoring. Public safety was enhanced because the sequential policy briefs and advisories shared with authorities were implemented. The local media tracked implementation of policy briefs and advisories because they received copies.

Biography

Prof. Shem Otoi Odhiambo Sam is an Associate Professor of Statistics and Research Methods at Daystar University, Kenya. He is also an author. Prof. Otoi is a research statistician with PhD and Masters in Statistics from the University of Nairobi. He is a renowned infectious disease modelling expert whose solutions have improved disease governance locally and internationally. He is a former professor of Statistics at Great Lakes University of Kisumu (GLUK). Prof. Sam is also former lecturer at USIU-Africa. He was appointed the Kenya Country Representative for US-Based CORVUS HEALTH Organization supporting health pedagogy in Low- and Medium-Income Countries (LMICs). Shem is the Director of Grace Onyango Foundation for Digital Health in Africa (GOFDHA). He is also the Lake Region Economic Bock COVID-19 Advisory Committee Programs Coordinator. Prof. Otoi is in the review panel of: East African Medical Journal (EAMJ); invited author and reviewer panelist of London Journal Press; Journal of Advances in Medicine and Medical Research; and editorial board of African Journal of Monitoring and Evaluation (AFRIJME). He is committed to finding solutions to human challenges. Previously, he created and published three highly cited statistical models for solving youth unemployment in low and medium income countries. He conducted early research on the spread of COVID-19 and published seven internationally refereed papers. Outstanding among his works is the innovation of COVID-19 predictive model: OTOI-NARIMA model which helped Kenya to predict all surges months before they occurred. Because of his work on COVID-19 research he was awarded honorary professorship by Sri Sri University in India. The model was adopted in Kenya and \ Lake Region Economic Bloc and accurately predicted seven COVID-19 surges months before they occurred. He instantly became a member in the Kenya National COVID-19 Modelling Committee. He is constant invitee speaker at International Workshop on COVID19 Vaccines, Conference on Public health in Africa (CPHIA), World Congress on Pharmaceutical Research and Toxicology, International Conference on Infectious Diseases, among others. The Ministry of Health, the National Oxygen Committee, the National Emergency Response Committee, and the Council of Governors -Kenya used OTOI-NARIMA Model predictions to mobilize citizens to be vaccinated and enhance public health protocols.He has made presentation to the African Union, Africa CDC, African Society of Laboratory Medicine, International COVID-19 Workshop on COVID-19 Vaccines, the inaugural conference on public health in Africa, CPHIA 2021 and CPHIA 2022, World Congress on Pharmaceutical Research and Toxicology, among others.



Vladimir Zajac
Cancer Research Institute, Slovakia

Elimination of viruses hidden in carriers located in the intestinal tract after overcoming the infection: New medicine

Viruses are parasites. that cannot exist on its own and is completely dependent on its carrier. This is the basic condition of its existence. The host of the parasite is a living cell. Based on our long-term work with BLV in stables, we have come to the conclusion that the host of BLV is bacterial cells. This idea was subsequently tested in an HIV model. It has been confirmed that its host can be bacteria and yeast. Subsequently, rectal swabs were taken from people who had overcome infection with the new coronavirus. The RT PCR test found that 83% of infected people carry the virus in the intestinal tract, and if immunity weakens, it can penetrate the body and infect the infected person and others. In many cases, carriers containing the virus can penetrate the intestinal tract, settle for months or years and multiply and mutate. However, if the virus in the carrier reaches the intestinal tract, the vaccines are not effective there. Based on these results, it was concluded that many, if not all, viruses can be carried and transmitted by bacteria, yeasts, or other unicellular organisms. The detection of BLV, HIV and the new coronavirus hidden in carriers opened the door. It is the first direct evidence of viral pathogens localized in our intestinal tract. The high infectivity found in wastewater worldwide points to the presence of the novel coronavirus in the intestinal tract after overcoming the infection. This is also evidenced by the creation of new and new variants of the new coronavirus. If we want to stop viral infections, we have to identify viral carriers, eliminate them along with the virus, and that's how we stop viral infections. Very little is known about the contents of the intestinal tract. It is believed that after the immune system is weakened, pathogens from the tract enter the body, attack its organs and cause many degenerative diseases, including tumors. The mechanism of action of intestinal pathogens is similar to when a drop falls on a stone, after a long time a hole forms there. Their elimination will radically improve the health status of the entire human population. Future progress in medicine will focus on analyzing the context of the intestinal tract - that will be New Medicina.

Biography

Vladimir Zajac has completed his PhD. in 1982 at the Cancer Research Institute of Slovak Academy of Sciences in Bratislava (Slovakia), where he worked as the Head of Department of Cancer Genetics from 1996 to 2010. He joined the Medical Faculty of the Comenius University as Associate Professor of Genetics in 2007. He was the supervisor of eight PhD students. He has published 78 works, mostly in renowned journals, and is the author of chapters in four professional books. He is the editor of the book "Bacteria, Viruses and Parasites in the AIDS Process" (In Tech, 2011).



INFECTIOUS DISEASES CONGRESS 2026

23 April, 2026 | Online Event

POSTER SESSIONS





Gentian Stroni[1]*, Esmeralda Meta[2], Ilirian Laci[2], Arben Rroji[2]
[1]Faculty of Medical Technical Sciences, University of Medicine, Tirana
[2]University Hospital Center "Mother Theresa" Tirana

Invasive therapeutic procedures in infectious diseases

Background: Infectious diseases remain a persistent challenge for healthcare systems, particularly when specialized interventions are required for treatment. Invasive therapeutic procedures are indispensable in advanced infections where pharmacological therapy alone proves insufficient.

Objective: Through a comprehensive review of the literature and clinical practices, this study aims to provide a clear overview of the indications, protocols, and outcomes of invasive therapeutic interventions in infectious diseases.

Methods: The study is based on an analysis of scientific literature published between 2015 and 2025, complemented by clinical protocols from university hospitals in Albania and Kosovo. A total of 42 clinical cases were examined, involving invasive procedures for the management of bacterial, viral, and fungal infections.

Results:

- Abscess drainage was effective in 87% of cases involving soft tissue infections.
- Biopsy of infected tissues facilitated pathogen identification in 72% of cases.
- Intubation and mechanical ventilation were applied in 15% of patients with severe respiratory infections.
- Localized surgery (e.g., for osteomyelitis) achieved therapeutic success in 68% of cases.

Discussion: Invasive procedures are often essential for saving the lives of patients with advanced infections. However, they carry inherent risks such as secondary infections, hemorrhage, and postoperative complications. Therefore, strict adherence to hospital infection control protocols is crucial to minimize these risks.

Conclusion: Invasive therapeutic procedures represent a powerful tool in the management of severe infections. Their application must be guided by clear clinical indications and implemented in accordance with safety protocols. Continuous training of medical staff and rigorous monitoring are key factors for ensuring successful outcomes.

Keywords: Infections, invasive procedures, therapy, drainage, surgery, clinical management

Biography

Dr. Gentian Stroni is a distinguished medical professional and academic specializing in infectious diseases. He graduated from the Faculty of Medicine at the University of Tirana in 1993 and pursued advanced postgraduate training in Infectious Diseases. He holds both an MSc and a PhD in Medicine, reflecting his strong commitment to academic excellence and research.

Dr. Stroni's research focuses on HIV/AIDS in specific populations and food-borne illnesses (toxi-infections alimentaires), contributing significantly to the understanding and management of these public health concerns. His work bridges clinical practice and research, offering valuable insights into disease prevention and control.

He currently serves as a Teaching Professor and has held several important leadership roles, including Deputy Dean from 2016 to 2020 and Department Chief of Preclinical Subjects since 2020. Alongside his academic career, he has been working as a Medical Doctor and Specialist in Infectious Diseases since 2002.

Dr. Stroni is also a prolific author, having published several books, research articles, and scientific presentations in both national and international forums, demonstrating his ongoing dedication to advancing medical science and education.



Gentian Stroni; Msc.Erisa Grabocka
University of Medicine, Tirana; Faculty of Technical and Medical Sciences

Helicobacter pylori: From nobel discovery to gastric cancer prevention

Helicobacter pylori represents one of the most consequential infectious disease discoveries of the twentieth century, fundamentally transforming our understanding of gastric pathology and establishing an unprecedented paradigm linking chronic bacterial infection to human malignancy. This presentation traces the remarkable 40-year scientific journey from Barry Marshall and Robin Warren's revolutionary 1982 discovery—validated through Marshall's legendary self-experimentation—to contemporary population-based screen-and-treat strategies now being implemented for gastric cancer prevention worldwide.

H. pylori infects approximately half of the global population, with prevalence exceeding 70% in developing regions including Southeast Europe. The bacterium's sophisticated virulence mechanisms—including CagA pathogenicity island, VacA cytotoxin, and urease-mediated acid neutralization—enable lifelong colonization and drive a well-characterized pathogenic cascade from chronic active gastritis through atrophic gastritis, intestinal metaplasia, dysplasia, and ultimately gastric adenocarcinoma. This infection-to-cancer sequence, spanning decades, provides a unique window for secondary prevention through timely detection and eradication.

Recent evidence has substantially strengthened the gastric cancer prevention rationale. Meta-analyses demonstrate 45-50% reduction in gastric cancer incidence following successful eradication, with landmark trials from high-incidence regions—including GISTAR-China and Taiwan's population-based programs—providing compelling real-world effectiveness data. Concurrently, escalating antimicrobial resistance, particularly to clarithromycin and levofloxacin, threatens eradication success rates and necessitates susceptibility-guided therapeutic approaches and novel treatment combinations incorporating potassium-competitive acid blockers and bismuth quadruple regimens.

This presentation synthesizes current evidence across three interconnected dimensions: the microbiological and pathogenic mechanisms underlying H. pylori carcinogenesis; the evolving diagnostic landscape from invasive histopathology to noninvasive stool antigen and urea breath testing; and the therapeutic and preventive strategies spanning individual patient management to population-level screen-and-treat implementation. Special consideration is given to implications for Albania and the broader Balkan region, where H. pylori prevalence remains high yet organized screening programs are absent.

The presentation concludes by examining emerging frontiers, including therapeutic vaccine development, microbiome-based interventions, and precision medicine approaches targeting high-risk populations for intensified surveillance and prevention.

Keywords: Helicobacter pylori; gastric cancer prevention; antimicrobial resistance; carcinogenesis

Biography

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Pragati Yadav[1], Maryam[2], Jeysal Choudhary[3], Supriya Singh[4]
[1,2,3]B.Sc. (Hons.) Zoology, Gargi College, University of Delhi, New Delhi, India
[4]Ph.D., Assistant Professor, Department of Zoology, Gargi College, University of Delhi, New Delhi, India

Host–virus arms race: HLA-mediated evolution of HIV rev exon 1 — who prevails in the battle for immune escape?

HIV-1 is dependent on the protein Rev in order to leave the host nucleus and begin the process of replication. Rev is not much focused on, compared to structural genes. This study looked at Rev exon-1, in the understudied Indian HIV-1 Subtype C, with a view to identifying HLA footprints.

This research focused on the most frequent HLA allele in India, "HLA-B*35" allele. It is often referred to as a 'fast-track' allele as it recognizes the virus, but does not provide strong immune response to clear the infection. As a result, the HLA molecule allows certain mutations to persist in the viral genome, leaving behind certain 'footprints'. For this study, a large dataset was created consisting of 1,187Rev exon 1 HIV-1 Subtype C sequences; 506 Indian sequences and 681 African sequences from Kenya, Rwanda, Zambia and South Africa. These sequences were downloaded from the Los Alamos National HIV Database.

Nucleotide sequences were aligned and translated using MEGA 11 and other bioinformatics tools. Two-way entropy analysis was performed to identify positions at which the Indian sequences differed from the African sequences. These positions were then cross referenced with the known targets of HLA-B*35 to specifically highlight the mutations which could help HIV-1 virus to escape from host immune response in the Indian setting. The identified mutations may also provide potential vulnerable sites on the virus for future vaccine development.

From the entropy analysis, thirteen sites were found to be statistically significant with six of them (Positions 14, 16, 18, 20, 21 and 23) under HLA-B*35 epitope. These sites fall into three distinct biological categories:

Divergence (Position 14): Dominant amino acid at African position is Glutamine. But in India, Glutamine is replaced by Arginine and Lysine, helping virus to avoid immune detection while still maintaining its nuclear transport function.

The positions at which conservative changes occur are Positions 18, 20 and 21, which lie within or near the critical RNA-binding region of the protein. At Position 18, an Indian-specific change to Threonine is seen in 10.1% of sequences, which helps the virus escape HLA-B*35 recognition while still maintaining its function. Position 20 shows a K→R substitution, where positive charge is maintained. Position 21 involves conservative substitutions where one non-polar (hydrophobic) amino acid is replaced by another. These changes do not affect RNA binding but help the virus partially escape the CTL recognition.

Three sites are highly constrained and remain in their original form despite intense immune pressure. Position 23 remains 99% Tyrosine despite significant immune pressure because this position is an anchor for Rev multimerization and virus replication.

The polymorphisms observed within the RNA binding motif of Rev Exon 1 affect Rev–RRE function and viral fitness. These six sites therefore demonstrate that this region is under strong selection pressure, leaving non-random marks on the Indian HIV-1 population.

The Audience Take Away:

- Identifying sites in Rev Exon 1 that are under HLA-B*35 driven immune pressure in the Indian population.
- Evidence of population specific divergence.

- Recognised Functionally constrained sites, which remain highly conserved despite immune pressure.
- How Rev acts as a regulatory protein in the evolution of HIV.
- Balance between immune escape (diversifying selection) and functional constraint (purifying selection)

Biography :

Pragati Yadav is a final year student of B.Sc.(Hons.) Zoology at Gargi College, University of Delhi, India. She is working under the supervision of Dr.Supriya Singh. Her research interest lies in the field of infectious disease biology and bioinformatics, particularly HIV-1 evolution using large scale data from LANL Database. She is interested in learning about new bioinformatics tools and how they can simplify HIV evolutionary studies. The major aim of her research is to understand how HLA genetic variation, particularly in India, affects the evolution of HIV-1 Subtype C. She is working to identify the markers of immune pressure that exist on the viral genomes and how these markers vary in different geographic populations. Through this research, She aims to develop a regional specific understanding of HIV evolution, moving beyond general models.



Ayra Ali, Siham Mahgoub**
Howard University, United States

HIV in-familial hypercholesterolemia

This paper highlights the link between HIV and the increased risk of cardiovascular disease, using a case study on a patient with familial hypercholesterolemia (FH). Previous research has demonstrated the mechanisms through which HIV leads to higher incidents of cardiovascular disease. Even when virologically suppressed, patients living with HIV will experience increased baseline levels of inflammation. There is evidence that this may be related to HIV particle reservoirs within the body, causing plaque instability.

The case presented in this paper is of a 29-year-old male living with HIV, who was recently diagnosed with the genetic condition familial hypercholesterolemia (FH). The paper discusses the physiology of FH, as well as the interplay between HIV-associated inflammatory mechanisms and cardiovascular health. The chronic inflammation associated with HIV can increase the uptake of oxidized LDL-C by macrophages and lead to foam cell formation and plaque development. This may exacerbate the already elevated LDL-C due to FH. The release of pro-inflammatory cytokines, such as tumor necrosis factor-alpha and inter-leukin-6, may be increased due to HIV-related immune activation. Additionally, some antiretroviral therapies may aggravate lipid metabolism, especially in patients with FH.

Mutations which lead to FH are also reported in the paper, as there are several genetic factors through which LDL cholesterol levels may become elevated. The genetic mutations that result in FH are heterozygous FH (HeFH) and homozygous FH (HoFH). Patients with HeFH may have LDL cholesterol levels that range from two to three times higher than normal, causing advanced risk for premature cardiovascular diseases. Patients with HoFH, which is the rarer and more severe form of FH, can have cholesterol levels that exceed 500mg/dL. This form of FH requires aggressive treatment, or they will be at risk for severe cardiovascular events, starting as early as childhood.

As FH is typically diagnosed through clinical symptoms, the paper describes the clinical manifestations of FH and how it may progress into cardiovascular complications. Patients with FH may develop xanthomas or arcus senilis, caused by deposits of cholesterol. If left untreated, patients may experience cardiovascular complications, such as coronary artery disease or aortic stenosis. If left untreated, these events can prove fatal for patients. The paper concludes with treatment options, including lifestyle modifications and pharmacologic therapies, available to clinicians who treat patients with FH. Diet and exercise are the most common changes advised by clinicians, along with statins to inhibit cholesterol synthesis in the liver.

Biography

Dr. Siham Mahgoub completed her training at Beth Israel Medical Center and New York Medical College, New York. She is the Medical Director of the Center for Infectious Disease Management and Research. She was the Principal Investigator for the Novavax Vaccine trial, the COVID-19 Variant Immunologic Landscape Trial (COVAIL Trial), Howard University Principal Investigator for the convalescent plasma to treat COVID 19. She was also the co-Investigator for the Howard University Genetic Study. Dr Mahgoub is currently an Associate Professor at Howard University College of Medicine and the Acting Chief for the Infectious Diseases Division in the department of Medicine.

BOOK OF ABSTRACTS

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Ph: +1 214 731 7766 | Whatsapp: +1 214-831-3945

Or

infectiousdiseases@irisscientificgroup.org