

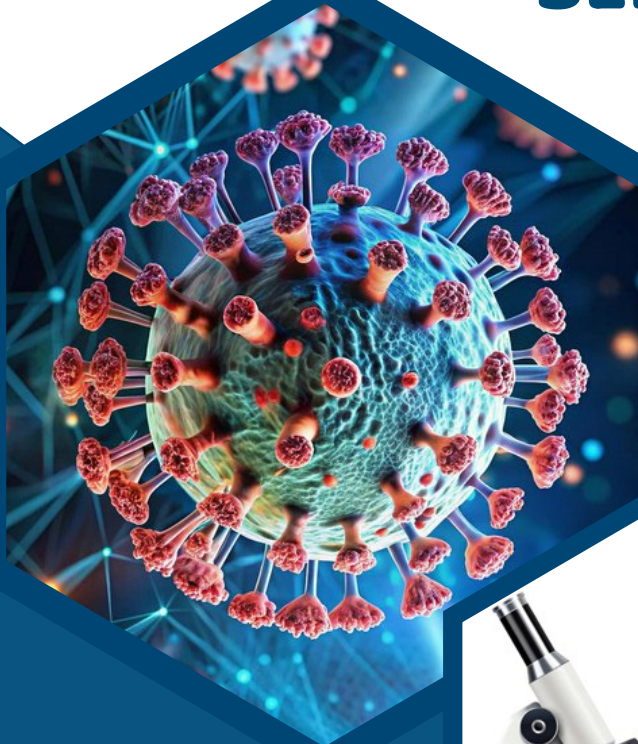
Joint Event

International Conference on
INFECTIOUS DISEASES

&

**APPLIED MICROBIOLOGY AND
BENEFICIAL MICROBES**

Dubai, UAE
November 20-21, 2024



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International Conference on
Infectious Diseases
&
Applied Microbiology and Beneficial Microbes
Dubai, UAE | November 20-21, 2024

CONFERENCE PROGRAMME

DAY 1- NOVEMBER 20, 2024

Meeting Hall - 5	
09:00-09:40	Registrations
09:40-10:00	Introduction
Keynote Presentations	
10:00-10:40	
Title: Antiviral Drugs and Virus Threats: 2024 Status Jocelyn Yelle, Antiviral InteliStrat, Canada	
10:40-11:20	
Title: Management of Post-Acute Infection Syndromes Gilbert Gladly, European Bio Immune(G)ene Medecine Association, France	
Networking & Refreshments: 11:20-11:50 @ Meeting Room 5 Assembly Area	
11:50-12:30	
Title: Thermophilic Bacteriophages and Their Potential Applications Mohammed Nabih Baeshen, University of Jeddah, Saudi Arabia	
Oral Presentations	
Session Chair	Jocelyn Yelle , Antiviral InteliStrat, Canada
Session Chair	Gilbert Gladly , European Bio Immune(G)ene Medecine Association, France
Sessions	Emerging and Re-Emerging Infectious Diseases Infectious Diseases and Post-Viral Syndromes Gastrointestinal Infections Viral Infectious Diseases Diagnosis of Infectious Diseases Public Health Infection Control Microbial Biotechnology Bacteriology Pulmonary and Chest Infections Microbiology Agricultural and Environmental Microbiology Food Microbiology Malaria
12:30- 12.55	
Title: The Differences in Routine CBC, Biochemical and Coagulation Test Results Between High and Low Hepatitis C Viremia Subjects Ieva Janulaityte, Lithuanian University of Health Sciences, Lithuania	
Group Photo: 12:55-13:05	
Lunch: 13:05-14:00 @ The Great Room Restaurant	

Keynote Presentation

14.00- 14.40

Title: Biocontainment Research Labs Management and Biosafety/Biosecurity Best Practices: An Overview

Moustafa Fadeel Awaden, City of Milwaukee Health Department Laboratory, USA

Oral Presentations

14.40- 15.05

Title: Epidemiological Monitoring and Spread of Avian Influenza Virus Among Wild Birds in Kazakhstan

Yerbol Burashev, Research Institute for Biological Safety Problems, Kazakhstan

15.05- 15.30

Title: Multicenter Evaluation Guiding Risk and Prognostic Factors for COVID-19 Omicron Variant on Patients in Home Medical Care (MEGURO Home Care Study)

Katsutoshi Ando, Meguro K Home Clinic, Japan

15.30- 15.55

Title: Bacteriological and Antibiotic Resistance Profile of Germs Isolated from Pyocultures at the Biomedical Laboratory of the China-Guinea Friendship Hospital of Kipe in Conakry (Guinea)

Abdoulaye Makanera, China-Guinea Friendship Hospital, Guinea

Networking & Refreshments: 15:55-16:30 @ Meeting Room 5 Assembly Area

16.30 - 16.55

Title: New Lanthipeptide with Broad Spectrum Activity, Revealed by Analytical Study and Genome Mining of Proteolytic *Bacillus cereus* Strain

Awatef Ouertani, Biotechpole Sidi Thabet, Tunisia

Poster Presentations: 16.55 - 18.00

Poster 01

Title: Intravenous Tobramycin Inhalation for Patients with Advanced Bronchiectasis with *Pseudomonas aeruginosa* Infection in Home Medical Care: A Report of Two Cases

Suzuki Ayumi, Meguro K Home Clinic, Japan

Poster 02

Title: Identification and Characterization of Infections with Antibiotic-Resistant Bacteria in Immunocompromised Patients

Krzysztof Lubocki & Monika Klepuszewska, Siec Badawcza Lukasiewicz PORT, Poland

Poster 03

Title: New Strain of *Bacillus thuringiensis* BtHp-01 and Prospects of its Use Against *Alfalfa weevil* *Phytonomus Variabilis*

Shemshura Olga, Scientific Production Center of Microbiology and Virology, Kazakhstan

Poster 04

Title: Microbial Cenosis of the Surface of Apple Fruits Before Storage

Elvira Ismailova, Scientific Production Center of Microbiology and Virology, Kazakhstan

Poster 05

Title: Assessment of the Performance of Lactate Dehydrogenase-Based Rapid Diagnostic Test for Malaria in Djibouti in 2022-2023

Rahma Abdi Moussa, Caisse Nationale de Sécurité Sociale, Djibouti

Day 1 Concludes by Certification Distribution

DAY 2- NOVEMBER 21, 2024

Meeting Hall - 5

Keynote Presentations

10:00-10:40

Title: Prevention of Harmful Microbes in Indoor Environments: Think as a Human *versus* as a Microbe

Haoxiang Wu, Hong Kong Baptist University, China

10:40-11:20

Title: 2 Years Results of a Case Series of Lipogems Microfragmented Fat for Joints Arthritis

Vasiliki Kalodimou, European University Cyprus-School of Medicine-Frankfurt Branch, Germany

Networking & Refreshments: 11.20- 11.45 @ Meeting Room 5 Assembly Area

Oral Presentations

Session Chair

Vasiliki Kalodimou, European University Cyprus-School of Medicine-Frankfurt Branch, Germany

Session Chair

Mohammed Nabih Baeshen, University of Jeddah, Saudi Arabia

Sessions

Disinfection Technologies| Orthopedic Infections|Viral Infectious Diseases |Microbiology and Virology | Critical Care and its Applications | Infectious Diseases | Microbial Biotechnology

11:45-12:10

Title: The Prevalence of Different HPV Genotypes and Different Level of Cytological Changes in Lithuanian Population

Ieva Janulaityte, Lithuanian University of Health Sciences, Lithuania

12:10-12:35

Title: Human Papillomavirus Types by Cervical Dysplasia, HIV-Status and the Diagnostic Value of Cervical Screening Methods in Eastern Kenya

James Kinoti Njue, Moi University, Kenya

12:35-13:00

Title: Impact of Antimicrobial Stewardship Program Activation in an Intensive Care Unit in King Khaled Hospital in Najran

Ali Dhafer Al-Swedan, King Khalid Hospital, Saudi Arabia

Lunch: 13:00 -14:00 @ The Great Room Restaurant

14:00-14:25

Title: Bacteriological Profile and Antibiotic Sensitivity of Germs Isolated from Blood Cultures at the China-Guinea Friendship Hospital of Kipe in Conakry

Abdoulaye Makanera, China-Guinea Friendship Hospital, Guinea

E- Poster

EP - 01

Title: Biosoap with Efficient Microorganisms to Reduce the Impact on Water Bodies

Danniela Scott, Universidade Federal Fluminense, Brazil

Video Presentation

VP - 01

Title: Inequality in the Distribution of Covid-19 Vaccine

Rayehe Noroozi, Shiraz University of Medical Sciences, Iran

VP - 02

Title: Host-Pathogen Interactions in Tuberculosis Co-infections: An Implication for Antimicrobial Resistance

Malami Aishatu Muhammad, Abubakar Tafawa Balewa University, Nigeria

Day 2 Concludes by Certification Distribution

Day 1

Keynote Presentations



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ANTIVIRAL DRUGS AND VIRUS THREATS: 2024 STATUS

Jocelyn Yelle

Antiviral InteliStrat, Canada

Abstract

Our societies are facing several major challenges globally. Among them, climate change provokes radical modifications in our environment, allowing expansion of insects carrying viruses able to infect humans and cause grave diseases, such as Dengue, Yellow Fever, and Equine Encephalitis viruses, and many more. In parallel, we have also seen the emergence of new viruses with pandemic potential, such as Avian Influenza viruses and the SARS-CoV-2 Coronavirus responsible for the worst pandemic the humanity has experienced since the Spanish Flu in the previous century. Unfortunately, even today, we are ill-prepared to face new viral entities and pandemics. While vaccines have been very useful to control the COVID-19 pandemic, the SARS-CoV-2 virus is still around with thousands of people dying around the world and emerging viral variants forcing the endless development of new adapted vaccines.

To control viral infections, small molecules acting as inhibitors of viral enzymes are an essential element of our arsenal. Sadly, this important aspect of our defense strategy against emergent viruses has been and still is in short supply. While about 64 new drugs and drug combinations have been approved to treat HIV-1 infections and 38 others for chronic Hepatitis C infections, as of today only 5 compounds represent novel treatments developed specifically for the SARS-CoV-2 Coronavirus infection and just a few more have reached advanced clinical development for other RNA viruses that may affect us in the near future. This presentation will summarize the current (2024) status of our quest for new antiviral drugs in development with details on compounds targeting specific viral enzymes. The review will cover the work done on most RNA virus families affecting humans, and show the urgency of revitalizing our efforts in this important arena of research.

Biography

Jocelyn Yelle is a virologist specializing in Retroviruses and Herpesviruses, with solid experience in antiviral drug discovery. He holds both an MSc degree and a PhD in Virology from Armand-Frappier Institute, a Canadian research center. After his studies, he launched his career by investigating HIV's ability to establish persistent infections in human cell cultures. He then started a collaboration with a chemist colleague, mounting a multidisciplinary research program focusing on small molecules as potential drugs for HIV/AIDS treatment. With his colleague, he later founded Pharmacor Inc., a small biopharmaceutical company to pursue the same goals. Some of these molecules were eventually acquired by a major pharma. Dr. Yelle is the Founder and President of Antiviral InteliStrat, a small firm that provides scientific advice to companies and other research organizations. Antiviral InteliStrat also owns a proprietary database that contains up-to-date information on thousands of antiviral drugs and vaccines against human viruses.



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MANAGEMENT OF POST-ACUTE INFECTION SYNDROMES

Gilbert Glady

EBMA - European Bio Immune(G)ene Medecine Association, France

Abstract

As the COVID-19 pandemic wears on, increasing attention has been given to post-acute sequelae of COVID-19 infection (PASC), which is commonly referred to as long-COVID. As tail-ends of infections, chronic sequelae caused by the inability to recover from acute infectious diseases are collectively called Post-Acute Infection Syndromes (PAIS). A long list of infectious agents, covering various bacterial, viral, and parasite species, is known to trigger the development of PAIS in a proportion of exposed individuals. The majority of these other PAIS show symptoms within 2–6 months after initial infection. Besides PASC, myalgic encephalomyelitis/chronic fatigue syndrome (ME/CFS) is another major syndrome that overlaps with the concept of PAIS. ME/CFS is a complex disease characterized by unexplained severe fatigue, with approximately 75% of cases reporting symptoms following an earlier infection. Throughout history, ME/CFS has also been named as post-polio syndrome and post-viral syndrome since patients develop chronic symptoms typically following infections with Polio virus, Epstein Barr virus, Influenza virus, or an array of other pathogens like Borrelia as part of so-called Post-treatment Lyme disease (PTLD).

The challenge is not only to diagnose these conditions, whose origins are far from being obvious, but also to treat them, for which there is little consensus. In this PAIS context, we use a relatively systematic diagnostic approach and a therapeutic strategy based on the use of biomimetic ultra-low doses. This method, called BI(G)MED for Bio Immune (G)en Medicine, is part of molecular medicine, and as such preferentially uses non-coding RNAs, which are real masterpieces of epigenetic regulatory networks.

Biography

Born in Strasbourg, France, Dr. Gilbert Glady graduated from Med School in 1977 and was then a resident in onco-hematology in the university clinic for several years. After a specialization in natural medicines in Paris, he returned to the Alsace region to work as a private practitioner. Through his work and encounters, he developed interest and expertise in immunology and immunogenetics, that led him to nanomedicine and nanobiotechnology. He thus became in 2010 the creator of the BI(G)MED method (Bio Immune (G)ene Medicine) and director of EBMA, the European association responsible for the communication and trainings in the field of BI(G)MED. He has participated in numerous international congresses in immuno-allergology, infectiology and oncology with posters and oral presentations, and is the author of several publications on nanobiotherapy in different journals.



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THERMOPHILIC BACTERIOPHAGES AND THEIR POTENTIAL APPLICATIONS

Mohammed Nabih Baeshen

University of Jeddah, Saudi Arabia

Abstract

Bacteria and their bacteriophages, also known as phages, have a dynamic and complex relationship that is constantly changing. Laboratory and field studies have demonstrated that phages may significantly affect bacterial populations. By lytic infection, phages can change the density of various bacteria, which will help to control the number of bacteria in the environment, and by lysogeny or transduction, they can change the genetic makeup of bacteria and may give the bacteria hosts good qualities. Phages are promiscuous mediators of genetic exchange and often carry genes capable of altering the phenotypes of their bacterial hosts. The genetic traits acquired from phages can influence the adaptation of bacteria to an environment by providing enhanced or novel metabolic properties. This may have an effect on the role of beneficial bacteria, which can be used in many biotechnological, agricultural, industrial, medicinal, and other settings. Recently, phage therapy drew the attention of scientific and medical communities as it will solve a lot of health issues and problems, especially the antimicrobial resistance phenomena. In our studies, we are investigating thermophilic bacteriophages isolated from Al- Lith hot springs, as we expect many applicable findings due to the properties of those stress-resistant phages, as they are capable of tolerating heat, salinity, and other harsh environmental conditions. Also, our metagenomic analysis of the Lith hot spring was encouraging to investigate the phageome communities of this environment, as we pinpointed pathogen bacterial phages, cyanobacterial phages, and other thermophilic bacteriophages.

Biography

Mohammed Nabih Baeshen is a Professor of Microbial Biotechnology in the Department of Environmental Sciences at the College of Science, University of Jeddah. He earned his Ph.D. in Microbiology in 2009, M.Sc. in Parasitology in 2000, and B.Sc. in Zoology in 1992, all from King Abdulaziz University.

Baeshen's academic journey includes serving as an Assistant Professor in various faculties at King Abdulaziz University from 2009 to 2013 and the University of Jeddah from 2013 to 2017. He later became an Associate Professor at the University of Jeddah in 2017 and was promoted to Professor in 2022.

His administrative roles include Vice Dean of the College of Health Sciences (2012-2014), Vice Dean of the Faculty of Science (2017-2018), Chairman of the Biochemistry Department (2018-2020), and Chairman of the Physics Department (2019-2020) at the University of Jeddah.

Baeshen's research interests focus on environmental sciences, environmental genomics (OMICS), and drug discovery from natural resources.



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BIOCONTAINMENT RESEARCH LABS MANAGEMENT AND BIOSAFETY/ BIOSECURITY BEST PRACTICES: AN OVERVIEW

Moustafa Fadeel Awaden

Fadeel Biotech, USA

Abstract

By the end of 2019/early 2020, the world was hit by a new pandemic that was caused by one of the coronaviruses, later called the SARS-cov-2 virus, and the disease was called COVID-19.

The pandemic took the lives of six million humans and caused trillions of dollars in economic loss. However, the pandemic represented a new challenge for infectious disease researchers all over the world, and efforts to know more about the virus and stop the pandemic started very early with the emergence of the pandemic. All these efforts and research activities took place in biocontainment or biosafety level three (BSL3) labs.

Biosafety level-3 (BSL-3) or BSL-4 laboratories are designed to contain pathogens to prevent their release into the environment and provide a safe setting to protect those working with these pathogens. Several motivations for building biocontainment labs exist including diagnostic needs, enhancing infectious disease surveillance capability and sustainability, promoting growth for life science and biotechnology, and improvements in scientific research capabilities. Despite operational and sustainment costs, this investment in biocontainment labs has helped many countries characterize emerging pathogens and control epidemics.

This presentation aims to provide an overview of the BSL3 biocontainment labs. Details related to design, systems, and operational overview will be covered. The presentation will provide more details on BSL3 regulations, policies, practices, main components of biosafety, biosecurity, and incident response plans, physical security and access controls, handling of experimental animals and decontamination, establishing and management of Select Agents (SAs) programs and getting ready for announced/unannounced inspections and how to respond to emergencies inside containment such as chemical spills, fire and/or HVAC system and power failures. An overview of the emerging research technologies that can be used inside containment will be mentioned as well during this presentation.

Biography

Moustafa Fadeel Awaden holds a PhD in biological sciences and established infectious disease researcher with more than 25 years of experience in academia, the US Navy, and other governmental agencies. In addition, he worked as an academic mentor for graduate students and a scientific advisor to reputable organizations and biotechnology vendors. He published 15 peer-reviewed original manuscripts and presented data at 20 international scientific conferences, developed, and evaluated innovative assays for diagnosis of infectious diseases of public health interests, managed the overall lab work of 250,000 biological samples, and increased the knowledge and awareness of 1000 infectious disease professionals. In addition, Dr Awaden designed and implemented several biosafety/biosecurity training workshops for infectious diseases researchers and other laboratory professionals on matters related to working safely inside medical facilities, blood-borne pathogens (BBPs), infectious waste management, biological select agents, and dual-use research of concern (DURC).

Day 1

Oral Presentations



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THE DIFFERENCES IN ROUTINE CBC, BIOCHEMICAL AND COAGULATION TEST RESULTS BETWEEN HIGH AND LOW HEPATITIS C VIREMIA SUBJECTS

Ieva Janulaityte and Lukas Vitkauskas

Lithuanian University of Health Sciences, Lithuania

Abstract

Introduction: The World Health Organization (WHO) has outlined a set of targets to eliminate hepatitis C by 2030, thus in 2022, Lithuanian authorities initiated an HCV screening program to eliminate HCV.

The aim was to evaluate CBC, biochemical, and coagulation tests in high and low HCV viremia.

Methods: The 300 random subjects who participated in a screening program for HCV infection were included in the study-230 subjects (144M/86F) with high viremia (>800000 cop/mL) as hiVG, and 70 subjects (32M/38F) with low viremia (<800000 cop/mL) as loVG. All subjects were anti-HCV positive. Viremia was evaluated using qRT-PCR, and the genotype was assessed using VERSANT HCV Genotype 2.0 Assay Kit, CBC-BC UNICel DxH800 analyzer, biochemical tests-BC AU680 Clinical Chemistry Analyzer, and coagulation tests-Stago STAR Max analyzer.

Results: The results showed significant differences between hiVG and loVG in biochemical, CBC, and coagulation tests results had significant differences between groups: RBC, HGB, HCT, WBC, PLT, PCT, AFP, ALP, DBIL, TBIL, ALB, SPA by sec., %, and INR, $p < 0.05$.

The hiVG and loVG were separated by gender into four groups. Results showed that the differences in males hiVG and loVG groups were the same as in the general subjects' pool; however, in females, differences were found only in RBC, HGB, and ALB, $p < 0.05$.

When comparing results to the normal range, we found that:

- males-hiVG had lower PLT, RBC, and PCT results but higher ALT, GGT, and AST;
- males-loVG had lower SPA(%), PCT, PLT results, but higher SPA(sec.), ALT, AST;
- females-hiVG had lower PLT, PCT, and SPA INR results but higher AST, ALT, and GGT;
- females-loVG had lower PLT, PCT, and ALB results but higher SPA (sec.), SPA(%), and GGT.

Conclusion: Active infection with the hepatitis C virus, depending on the gender and viremia level, changes the results of CBC, biochemical, and coagulation tests. Therefore, we recommend a complete workup of patients when HCV viremia is detected.

Biography

Ieva Janulaityte received her PhD in Biology in 2022, master's in laboratory medicine biology in 2017 in Lithuanian University of Health Sciences. She is a lecturer in the same University from 2022 teaching medicine, laboratory medicine biology, medicine and genetics and biochemistry students. Ieva Janulaityte is focused mainly on infectious and non-infectious inflammation, tissue remodeling, immune and structure cell biology. She is a member of the European Federation of Clinical Chemistry and Laboratory Medicine, European Respiratory Society, and several national societies and Member of the Lithuanian management methodological group of the program for early diagnosis of malignant tumors of the cervix.



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EPIDEMIOLOGICAL MONITORING AND SPREAD OF AVIAN INFLUENZA VIRUS AMONG WILD BIRDS IN KAZAKHSTAN

Yerbol Burashev, Nurdos Aubakir, Zamira Omarova, Ali Tulendibayev, Tanat Yermekbay, Takhmina Argimbayeva, Nurlan Kozhabergenov and Mukhit Orynbayev

Research Institute for Biological Safety Problems, Kazakhstan

Abstract

Avian influenza is an infectious disease caused by influenza viruses of type A, which poses a serious threat to poultry farming, wildlife and human health. The most dangerous subtypes, such as H5N1, have a high mortality rate among birds. Wild birds are the main reservoir of the virus. Seasonal migrations of birds contribute to the spread of the virus over significant distances.

The territory of Kazakhstan is a key region for the migration of wild birds, as important transcontinental routes connecting Europe, Asia and Africa pass through here. The main migration routes through Kazakhstan are the Central Asian migration route, which passes through the northern and central regions of Kazakhstan, linking Siberia and Central Asia with South Asia and Africa, and the West Asian-Indian migration route, which crosses the southern and southwestern regions of Kazakhstan, linking Eastern Europe and Western Asia with the Indian subcontinent.

Kazakhstan regularly monitors the condition of wild and domestic birds for epidemiological surveillance purposes. Monitoring includes collecting and analyzing samples from birds in large bodies of water and in areas where migration routes intersect with farms.

As a result of the analysis of the data from the autumn field expedition of 2023, three positive cases (Kostanay region No. 3 cloacal swab, No. 5 tracheal swab. Akmola region cloacal swab) for the avian influenza virus were identified out of 68 samples collected from wild birds, which is about 4.4% of the total number of samples examined. This case confirms the circulation of the virus among wild birds in Kazakhstan, as well as the need to continue monitoring influenza among wild and migratory birds.

Based on the above, avian influenza remains one of the main biological threats to public health, agriculture and the environment. Its impact is manifested both in direct consequences for human and animal health, and in broader economic and social threats.

These studies were carried out within the framework of the IRN grant funding project AP19676553 "Epidemiological monitoring and development of modern diagnostic tools for particularly dangerous viral diseases of birds".

Biography

BURASHEV YERBOL, in 2008 graduated from the Kazakh National Agrarian University with a bachelor degree in livestock technology. In 2011 graduated with a master's degree in biology. In March 2020, defended dissertation at the al-Farabi Kazakh National University, where he was awarded a PhD degree in the specialty "6D060700-Biology". Burashev E.D., head of the «Monitoring of Infectious Diseases» RIBSP, is a highly qualified specialist in the field of molecular biology, virology and genetic engineering.



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MULTICENTER EVALUATION GUIDING RISK AND PROGNOSTIC FACTORS FOR COVID-19 OMICRON VARIANT ON PATIENTS IN HOME MEDICAL CARE (MEGURO HOME CARE STUDY)

Katsutoshi Ando¹, Naoyuki Umezato^{2,3,9}, Taizo Murabayashi⁴, Katsuhiko Hanawa⁵, Fusaro Shibui⁶, Yoshiharu Shiroki⁷, Yukitaka Tanaka⁸, Hiroya Seta¹⁰, Hiroki Yoshida¹¹

¹Department of Respiratory Internal Medicine, Meguro K Home Clinic, Japan

²Home Ally Clinic Jonan, Setol Midorigaoka, Japan

³Home Ally Clinic Jonan, Japan

⁴Murabayashi Clinic, Japan

⁵Machino-Home Clinic, Japan

⁶Hozan Clinic, Japan

⁷Shiroki Zaitaku Clinic, Japan

⁸Marugoto Zaitaku Care Clinic, Japan

⁹Home Ally Clinic Fidoumae, Japan

¹⁰Loco Clinic Nakameguro, Japan

¹¹Data Seed Inc, Japan

Abstract

Old age, comorbidities, and vaccination status are established risk factors for hospitalization and mortality in patients with coronavirus disease 2019 (COVID-19). However, further investigation is required to elucidate the clinical course, hospitalization, and mortality risks among patients receiving home health care for COVID-19. In this multicenter retrospective cohort study, we reviewed 2,598 patients who received doctor-visiting care from 10 home medical care clinics in and around Meguro City, Tokyo, Japan, between January 2022 and September 2023. We enrolled 194 patients diagnosed with COVID-19 after initiating home medical care and classified them into hospitalization (n = 65) and non-hospitalization (n = 129); and non-survival (n = 22), and survival (n = 172) groups for background comparison, respectively. We assessed the patients' health status using the Charlson Comorbidity Index, and activity of daily living using the degrees of independent living for disabled elderly as previously reported. Among the 194 patients enrolled, COVID-19 severity emerged as a significant risk factor for hospitalization and mortality. Meanwhile, the level of daily life independence for disabled elderly patients was an independent risk factor for hospitalization but not for survival. A ROC analysis revealed that the "optimal" cutoff value for the daily life independence level of disabled associated with hospitalization was Rank "B1", which was a person who requires some assistance living indoors and spends most of the day in bed but can sit up. The 3- and 6-month survival rates for all enrolled patients were 89.1% and 83.9%, respectively. The non-survival group had a significantly higher proportion of patients with malignancies (50.0% vs. 9.3%, $p < 0.001$) and a higher Charlson Comorbidity Index (2.5 vs. 1.0, $p = 0.001$) than the survival group. Our data indicate that providing in-home caregiver support for individuals with high care dependency who contract coronavirus could reduce unnecessary hospital admissions.



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Biography

Katsutoshi Ando is a pulmonologist with board certification of Japanese Respiratory, Allergy and Infectious disease. He is a director of Meguro K Home Clinic, which was established in June 2018 and recently cared for 50-100 cases per year at their home with palliative care. He received his Ph.D. in Pulmonology from Juntendo University in 2016, and has continued a research of home medical care, respiratory medicine and infectious diseases. He previously received JRS Young Investigator Award to Attend ATS International Conference 2013 and 2015, Best Presentation Award of JSPCLD, 2014, Respiratory Research Award, Tokyo Respiratory Forum, 2014, IREF young investigator Award, 2015, Special Recognition Award, Tokyo Respiratory Research Forum, 2015, Best Poster Award, 1st Asia Oceania Workshop of Pulmonary Functional Imaging, 2016, Research Grant, Japan Intractable Diseases Research Foundation, 2016, and Chugai Clinical Science Strategy Dept Director Award, 2018.



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BACTERIOLOGICAL PROFILE AND ANTIBIOTIC SENSITIVITY OF GERMS ISOLATED FROM BLOOD CULTURES AT THE CHINA-GUINEA FRIENDSHIP HOSPITAL OF KIPE IN CONAKRY

Abdoulaye Makanéra, Taliby Dos Camara, Mariam Condé, Ariel Biagne, Mamadou Alpha Diallo, Alpha Oumar Barry and Oumar Souaré

Laboratoire biomédical de l'Hôpital de l'Amitié Sino-Guinéenne, République de Guinée
Université Gamal Abdel Nasser de Conakry, République de Guinée

Abstract

Bacteremia constitutes a major public health problem in developing countries, especially when associated with bacteria that are multi-resistant to antibiotics. Objective: To determine the bacteriological profile and antibiotic resistance of bacteria isolated from blood cultures at the China-Guinea Friendship Hospital (HASIGUI) in Kipe in Conakry.

Methods: This is a retrospective, descriptive study, carried out from January 12 to December 22, 2021. Blood cultures were taken using the Bact/Arlet machine (biomereux, France). Bacterial identification and antibiograms were carried out using the Vitek2 Compact automated system and the API system (bioMérieux, France).

Result: Out of a total of eighty (80) blood cultures, forty-five (45) were positive, with a rate of 56.25%. The most represented age group was 31-40 years old with an average age of 36.92 ± 10 years. Gram-positive bacteria were associated with 82.23% of bacteremias, 17.77% for Gram-negative bacteria. The most frequent species were: *Escherichia coli* (22.23%), *Staphylococcus xyloxy* (16.23%), *Staphylococcus haemolyticus* (13.51%), *Staphylococcus aureus* (13.51%), *Staphylococcus hominis* (10.81%). A high frequency of resistance of Enterobacteriaceae has been observed towards aztreonam, ceftazidime, gentamicin and tobramycin. On the other hand, the majority of strains were sensitive to imipenem, meropenem and amikacin. Gram-positive bacteria including *Staphylococcus xyloxy*, strains of *Staphylococcus haemolyticus* and those of *Staphylococcus aureus* were resistant to penicillin, Oxacillin, Oxacillin COAG and ceftoxin but sensitive to levofloxacin, nitrofurantoin and linezolid.

Conclusion: These results show that Gram-positive bacteria were more frequently associated with bacteremia, although *Escherichia coli* was in the majority. Finally, a high frequency of multi-antibiotic resistant strains was observed, thus requiring antibiotic therapy based on the results of antibiograms.

Biography

Abdoulaye Makanera is the Head of the Biomedical Laboratory Department at the China-Guinea Friendship Hospital of Kipé in Conakry and a University lecturer. Born on December 11, 1969, in Boké, Guinea, he has been a Teacher-Researcher (Bacteriology-Virology) at Gamal Abdel Nasser University of Conakry (UGANC) since 2005, leading the Microbiology-Parasitology-Myxology unit. With a career in medical biology spanning Tunisia and Guinea since 1999, he participated in key diagnostic courses in French-speaking Africa and has authored or co-authored 50 scientific articles.



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NEW LANTHIPEPTIDE WITH BROAD SPECTRUM ACTIVITY, REVEALED BY ANALYTICAL STUDY AND GENOME MINING OF PROTEOLYTIC BACILLUS CEREUS STRAIN

Awatef Ouertani¹, Amor Mosbah¹, Mohamed Brakat², Ines Chaabouni¹, Nedra rached¹, Ahmed Saleheddine Masmoudi¹, Pascal Mansuel³, Didier Gigmes⁴, Kamel Mabrouk⁴ and Ameer Cherif¹

¹University Manouba, ISBST, Biotechpole Sidi Thabet, Tunisia

²Aix-Marseille University, CEA, CNRS, LEMiRE, Saint-Paul-lez-Durance, France

³Aix Marseille University, Centre National de la Recherche Scientifique, France

⁴Aix Marseille University, CNRS, France

Abstract

The growing challenge of antibiotic resistance poses a serious threat to global health, highlighting the urgent need for new antimicrobial agents. In the present study, a proteolytic bacterial strain designated RC6 was isolated from Ricotta and identified as *Bacillus cereus*. It produces lanthipeptide during log growth phase, which is active against several species of *Bacillus* and the food borne pathogen *Listeria monocytogenes*. The antibacterial peptide present in the supernatant of the *B. cereus* strain was purified with ultrafiltration followed by RP-HPLC. The excellent correlation between LCMS, MALDI Tof analysis of the RP-HPLC purified fraction and genome analysis revealed a molecular mass of 7750.606 Da. Cross inhibition tests with bacteriocin producer strains indicated that RC6 lanthipeptide is a new bacteriocin. Genome mining shed light on the lanthipeptide biosynthetic gene cluster and reveals that it belongs to the class II lanthipeptide. Furthermore, structural analysis and molecular docking reveals van Der Waals interactions with Gluc Nac, Mur Nac and the pentapeptide groups of the Lipid II receptor. These interactions illustrate a pore forming mode of action. This finding could be valuable in the development of new antimicrobial drugs.

Biography

Awatef Ouertani earned her PhD in 2019 from the Faculty of Science at Tunis, Tunisia. Currently, she holds a postdoctoral position at the Laboratory of Biotechnology and Bio-Geo Resources Valorization, located at Biotechpole Sidi Thabet, Tunisia. As a distinguished biochemist and researcher, she has made significant contributions in the field of protein biochemistry. Her research efforts have yielded numerous notable publications that have not only reinforced her expertise but also enriched the scientific community's comprehension of protein structures, interactions, and enzymatic functions.

Day 1
Poster Presentations



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**INTRAVENOUS TOBRAMYCIN INHALATION FOR PATIENTS WITH
ADVANCED BRONCHIECTASIS WITH *PSEUDOMONAS AERUGINOSA*
INFECTION IN HOME MEDICAL CARE: A REPORT OF TWO CASES**

Ayumi Suzuki and Katsutoshi Ando

Meguro K Home Clinic, Japan

Abstract

Bronchiectasis is a chronic lung disease characterized by permanent damage to the smaller and medium sized airways, resulting in a progressive decline in pulmonary function. *Pseudomonas aeruginosa* infection is associated with an increased risk of death and exacerbation in patients with bronchiectasis. Anti-pseudomonal antibiotics such as tazobactam/piperacillin, cefepime, and imipenem are commonly used, but most require intravenous administration. Home medical care faces limitations in the number of doctor and nurse visits, availability of medical devices, and economic factors, making daily injections difficult for in-home patients. Tobramycin is an aminoglycoside antibiotic with potent antipseudomonal effects. Nebulized tobramycin inhalation solution (TIS; TOBI®, 300 mg twice daily) is indicated for the management of cystic fibrosis with *P. aeruginosa* infection. It provides a high dose of tobramycin to the lungs while maintaining low serum concentrations of the drug, thus reducing the risk of systemic toxicity and contributing to improved lung function and quality of life. However, in Japan, TIS is not covered by the national insurance system for patients with NCFBE, and it costs approximately 18,000 yen per day at the patient's own expense (9,045 yen/TOBI® 300 mg); therefore, it is generally not a realistic treatment option. In addition, case reports have indicated the effectiveness of intravenous tobramycin inhalation, which was prepared from intravenous tobramycin products, but the method of preparing aseptic inhalation solutions from injection ampoules was an issue in the in-home medical care environment.

We describe two cases of advanced bronchiectasis with *P. aeruginosa* infection treated with inhaled tobramycin in a home setting, demonstrating clinical effectiveness. Using commercially available empty eye drop containers to prepare an aseptic inhalation solution and nebulizers easily usable at home, our experience suggests that this could be a viable therapeutic alternative in home medical care.

Biography

Ayumi Suzuki is a visiting nurse at Meguro K Home Clinic, which was established in June 2018 and recently cared for 50-100 cases per year at their home with palliative care. She researches the field of home medical care, respiratory medicine and infectious diseases.



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IDENTIFICATION AND CHARACTERIZATION OF INFECTIONS WITH ANTIBIOTIC-RESISTANT BACTERIA IN IMMUNOCOMPROMISED PATIENTS

Krzysztof Lubocki¹, Monika Klepuszewska¹, Natalia Marczevska¹, Jowita Wesołowska-Waliszewska¹, Karolina Łapin², Katarzyna Fleischer-Stepniewska^{3,4} and Anna Paziewska-Harris¹

¹Lukasiewicz Research Network - PORT Polish Center for Technology Development, Poland

²Wroclaw Technology Park, Poland

³Wroclaw Medical University, Poland

⁴Gromkowski Regional Specialist Hospital in Wroclaw, Poland

Abstract

Antibiotic-resistant bacterial infections pose a serious threat to global health, impacting heavily immunocompromised patients. The aim of the project was to characterize infections caused by antibiotic-resistant bacteria in immunocompromised patients, and to build up a collection of alert pathogens and those with multiple drug resistance, for the future use in research.

Collected samples from immunocompromised patients were analysed to identify bacteria in the samples and determine the Minimum Inhibitory Concentration (MIC) values for antibiotics, using Micro Scan Auto scan 4 (Beckman Coulter). Obtained data were subjected to statistical analysis.

In the study 125 samples from immunocompromised patients were analysed. Patients from whom the samples were collected fell mainly into 3 groups: oncological (36%), diabetes (19,2%) and alcohol dependence syndrome patients (15,2%). The rest of patients (29,6%) were diagnosed with chronic respiratory, cardiovascular and nephrological diseases, obesity and rheumatoid arthritis, but due to non-representative numbers, they were excluded from the analysis. Of all isolated bacteria in the study, the most prevalent was *K. pneumoniae* (in 65,6% of collected samples) followed by *E. coli* (20%). The antibiotic resistance analysis was based on the MIC values of antibiotics, of which β -lactam antibiotics were selected. Resistance mechanisms, especially MBL coexisting with ESBL and ESBL alone, were observed across patient groups.

In the group of oncological patients, the most common resistance mechanisms were MBL coexisting with ESBL (59.46%) and ESBL (32.43%). Similar mechanisms predominated in diabetic patients MBL+ESBL and ESBL (38.9% each). In patients with alcohol dependence syndrome, ESBL (46.67%) predominated as in the other patient groups and CPE (26.67%).

The prevalence of resistance mechanisms, MBL and ESBL, across analysed patient groups highlights the need for personalized treatment approaches during antibiotic selection.

Biography

Krzysztof Lubocki graduated in microbiology from the University of Wroclaw in 2019. After completing my studies, I have been involved in microbiological and genetic diagnostics. Currently, I work as a microbiologist at the Population Diagnostics Center. Lukasiewicz – PORT Center for Population Diagnostics is the first center of its kind in Poland. It aims to research in the field of modern diagnostic methods for many infectious and civilization diseases. The Center for Population Diagnostics will significantly contribute



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to increasing the biomedical safety of society. Research on pathogens causing infectious diseases (e.g. SARS-CoV-2, AH1N1, SARS) will enable immediate action in the event of an epidemiological threat. The center will include the BSL-3 standard epidemiological rapid response laboratory – the first in western Poland and one of only a few in the whole country. It will be characterized by one of the highest classes of biosafety, giving the possibility to work with microorganisms from various risk groups.

Monika Klepuszewska graduated with a master's degree in medical biotechnology from the University of Opole, Poland. Already during my studies I started my professional work as a microbiologist. Currently, as a Specialist Process Engineer at the Centre for Population Diagnostics, I am, among other things, implementing a research project aimed at understanding the resistance mechanisms of multi-drug resistant bacteria in immunocompromised patients. I also carry out research for commercial clients in the broad field of classical and molecular microbiology and diagnostics using the latest methods.



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NEW STRAIN OF BACILLUS THURINGIENSIS BTHP-01 AND PROSPECTS OF ITS USE AGAINST ALFALFA WEEVIL PHYTONOMUS VARIABILIS

Shemshura Olga N and Sadanov Amankeldy K

Scientific Production Center of Microbiology and Virology, Republic of Kazakhstan

Abstract

The BtHp-01 isolate was allocated from the larvae *Phytonomus variabilis* and identified as *Bacillus thuringiensis* based on morphological, microscopic, physiological and molecular genetic characteristics. The insecticidal activity of the BtHp-01 strain against the second instar *P. variabilis* larvae was studied under laboratory conditions. It was found that soybean medium No. 2 was optimal for the insecticidal activity of the BtHp-01 strain. When using the culture broth of the strain obtained during growth on medium No. 2, the mortality of insects on the third day was $50.6 \pm 3.1\%$, on the fifth - $61.6 \pm 1.5\%$; on the seventh day - $90.0 \pm 2.0\%$, on the 10th day 100% mortality of *P. variabilis* larvae was observed. During field tests of the BtHp-01 strain on alfalfa plantings affected by the alfalfa weevil, it was shown that already on the first day after treating alfalfa plants with the BtHp-01 strain culture broth with a titer of 3.2×10^8 CFU/ml, the mortality of the 1-2 instar alfalfa weevil larvae was $68.0 \pm 3.1\%$, on the second day - 75.3 ± 3.8 , on the third - $75.3 \pm 3.8\%$. Based on the obtained results, a conclusion was made about the prospects of the new *B. thuringiensis* BtHp-01 strain as a biological agent for controlling phytonomus on alfalfa crops.

Biography

Shemshura Olga N. Leading Researcher. Author ID Scopus 57214899291 Researcher ID Web of Science AAM-8848-2020 Laboratory of ecological and agricultural microbiology, Scientific and Production Center of Microbiology and Virology LLP, Republic of Kazakhstan. Almaty, Bogenbay Batyr St. 105. scientific experience

Interests: agricultural microbiology; phytopathogens, development of microbial biopreparations for plant protection.



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MICROBIAL CENOSIS OF THE SURFACE OF APPLE FRUITS BEFORE STORAGE

Elvira Ismailova and Amankeldi Sadanov

Scientific Production Center of Microbiology and Virology, Republic of Kazakhstan

Abstract

The article presents the results of the study of the microbial cenosis of the apple fruits surface during the period of commercial maturity before storage. Fruits of the apple varieties “Aport”, “Starkrimson”, “Golden Delicious”, “Gala” were selected from farms in the Almaty region, which grew in different natural and climatic zones of growth (550 m, 750 m, 900 m above sea level). A total of 360 apple fruits were analyzed. In the course of the studies, 164 colonies of various microorganisms were isolated. It was found that fungal samples mainly prevailed. The maximum number in the fungal one is made up of representatives of the Ascomycetes department (*Monilia*, *Fusicladium*, *Cladosporium*, *Botrytis*). They dominated in all samples and accounted for 82% of the total number of detected microorganisms. Next were mold fungi of the Deuteromycetes department (*Fusarium*, *Alternaria*, *Aspergillus*, *Penicillium*) (15%) and unidentified fungi (2%), bacteria (0.7%) and yeast (0.3%). It was established that there is a variation in the species composition of microorganisms by the place of sampling (foothill, steppe zone) and by their association with the variety. The varieties “Aport” and “Gala”, selected in the lower mountain and foothill zones, are maximally populated by fungi that cause fruit rot.

Biography

Elvira Ismailova is leading researcher of the laboratory of “Ecological and agricultural microbiology” of the Research Production Center of Microbiology and Virology. Specialist in microbiology, phytopathology and plant protection. Main areas of work: applied research on the creation of biopreparations of microbial origin. Work experience: over 36 years. Over the past 5 years: was the head and co-head of 2 grant projects and a program. Author of over 100 scientific papers, 6 articles in foreign publications indexed by Web-of-Science/Scopus, 2 patents.



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ASSESSMENT OF THE PERFORMANCE OF LACTATE DEHYDROGENASE-BASED RAPID DIAGNOSTIC TEST FOR MALARIA IN DJIBOUTI IN 2022-2023

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⁹Unité Parasitologie et Entomologie, Institut de Recherche Biomédicale des Armées, France

Abstract

Until 2020, Djiboutian health authorities relied on histidine-rich protein-2 (HRP2)-based rapid diagnostic tests (RDTs) to establish the diagnosis of *Plasmodium falciparum*. The rapid spread of *P. falciparum* histidine-rich protein-2 and -3 (p_{fh}rp2/3) gene-deleted parasite strains in Djibouti has led the authorities to switch from HRP2-based RDTs to lactate dehydrogenase (LDH)-based RDTs targeting the plasmodial lactate dehydrogenase (pLDH) specific for *P. falciparum* and *P. vivax* (RapiGEN BIOCREDIT Malaria Ag Pf/Pv pLDH/pLDH) in 2021. This study was conducted with the primary objective of evaluating the diagnostic performance of this alternative RDT. Operational constraints related, in particular, to the implementation of this RDT during the COVID-19 pandemic were also considered. The performance of BIOCREDIT Malaria Ag Pf/Pv (pLDH/pLDH) RDT was also compared to our previously published data on the performance of two HRP2-based RDTs deployed in Djibouti in 2018-2020. The diagnosis of 350 febrile patients with suspected malaria in Djibouti city was established using two batches of RapiGEN BIOCREDIT Malaria Ag Pf/Pv (pLDH/pLDH) RDT over a two-year period (2022 and 2023) and confirmed by real-time quantitative polymerase chain reaction. The sensitivity and specificity for the detection of *P. falciparum* were 88.2% and 100%, respectively. For *P. vivax*, the sensitivity was 86.7% and the specificity was 100%. Re-training and closer supervision of the technicians between 2022 and 2023 have led to an increased sensitivity to detect *P. falciparum* (69.8% in 2022 versus 88.2% in 2023; $p < 0.01$). The receiver operating characteristic curve analysis highlighted a better performance in the diagnosis of *P. falciparum* with pLDH-based RDTs compared with previous HRP2-based RDTs. In Djibouti, where p_{fh}rp2-deleted strains are rapidly gaining ground, LDH-based RDTs seem to be more suitable for diagnosing *P. falciparum* than HRP2-based RDTs. Awareness-raising and training for technical staff have also been beneficial.



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Biography

Rahma Abdi Moussa have been a healthcare professional in Djibouti since 2015. In 2020, I had the chance to do a research thesis in the field of infectious disease particularly antimalarial resistance and the failure to diagnose human malaria. Finally, in 2023, I obtained my doctorate in biology and health, specializing in infectious diseases, from the University of Aix Marseille in French. This diploma enabled me to work as a biologist in the health center of the national social security fund in Djibouti.

Day 2

Keynote Presentations



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**PREVENTION OF HARMFUL MICROBES IN INDOOR ENVIRONMENTS:
THINK AS A HUMAN VERSUS AS A MICROBE**

Haoxiang Wu

Hong Kong Baptist University, China

Abstract

Microbes in the indoor environment, such as indoor moulds grown on surfaces of building materials and airborne microbes, can significantly impact occupant's health. Therefore, it is generally considered as a good practice to prevent mould growth and reduce the transmission of airborne microbes in the indoor environment. Current research studies on prevention of microbial contamination/infection are mainly focused on the examination of effectiveness of different prevention measures, which is a perspective of thinking from a human. There are very limited studies attempting to look into the underlying mechanism that regulate the effectiveness of preventive measures. With mechanistic understandings in what microbes do to withstand unfavorable conditions; i.e., think as a microbe, it would be more likely for people to locate the vulnerable target of microbes and thus further enhance the effectiveness of measures for preventing microbial contamination/infection. In this talk, I will share my research in indoor mycology and aerobiology studies, which is largely focused on understanding the mechanism of indoor mould growth under transient moisture conditions and that regulates the survival of airborne microbes under various environmental conditions. The philosophy of thinking as a microbe when doing microbiology research will also be discussed.

Biography

Haoxiang Wu received his PhD in Microbiology from Hong Kong Baptist University in 2020. He has been working as a Lecturer since 2020 in the Department of Biology, Hong Kong Baptist University. His research interests include indoor mycology and aerobiology. He is interested in studying how indoor moulds respond to changing water conditions and how airborne microbes respond to environmental conditions as well as disinfection technologies.



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2 YEARS RESULTS OF A CASE SERIES OF LIPOGEMS MICROFRAGMENTED FAT FOR JOINTS ARTHRITIS

**Vasiliki E. Kalodimou¹, Maria Toumazou⁴, Marios Kozakos³, Susanna Gotor⁴,
Dimitrios Tsoukas² and Christos Simos²**

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²Orthopaedic Clinic for Advanced Arthroscopic Sports and Regenerative Medicine MITERA Hospital Athens, Greece

³Sankt Katharinen Krankenhaus Hospital, Germany

⁴European University Cyprus (EUC)-School of Medicine, Germany

Abstract

Osteoarthritis (OA) is a kind of joint degenerative disease caused by many factors and leads to irreversible cartilage damage, subchondral osteosclerosis and synovitis. It is caused by degeneration of articular cartilage and subchondral bone. Currently, many treatment modalities for knee OA, such as lifestyle modification and pharmaceuticals, are advocated. However, advanced knee OA eventually requires joint surgery as the disease progresses.

Orthobiologics and cell therapies are a new frontier. Micro-fragmented adipose tissue (MFAT) is composed of three-dimensional biological scaffolds and colonies of cells in which the three-dimensional biological scaffolds are composed of collagen and connective tissue and microvascular networks, and the clustered cells consist of pericytes, adipocytes, MSCs and exosomes.

The study hypothesis is that MFAT would improve the clinical and radiological outcomes in patients with osteoarthritis Kellgren- Lawrence 3-4.

Biography

Vasiliki E. Kalodimou is the Assist. Professor as well as the Chair, School of Medicine at the European University-Cyprus Ltd. Frankfurt Branch, the collaborative Partner for the Greek Research Infrastructure for the visualization and monitoring of fundamental Processes in Biology and Medicine (BIOIMAGING-GR) at NCSR "DEMOKRITOS", Athens-Greece, the collaborative partner for training and research for Regenerative Medicine Program at the Institute of Personalized Molecular Medicine at the Medical City Hospital, Philippines, the Board/Committee on Research Ethics at the National Hellenic Research Foundation (E.I.E), she elected to serve as the Vice-Chair of the UEL Alumni Advisory Board, previously was the Director at the Flow Cytometry-Research and Regenerative Medicine Department of IASO Maternity-Pediatric and Research Hospital in Athens, Greece, as well as the CBB Director & Processing Facility Director at MedStem-Cryobanks of IASO.

Day 2

Oral Presentations



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THE PREVALENCE OF DIFFERENT HPV GENOTYPES AND DIFFERENT LEVEL OF CYTOLOGICAL CHANGES IN LITHUANIAN POPULATION

Ieva Janulaityte , Gabriele Vitkauskiene and Erika Skrodeniene

Lithuanian University of Health Sciences, Lithuania

Abstract

Introduction: Lithuania has a population of 1.26 million women ages 15 years and older who are at risk of developing cervical cancer. Current estimates indicate that every year 412 women are diagnosed with cervical cancer and 193 die from the disease. Cervical cancer ranks as the 4th most frequent cancer among women in Lithuania and the 2nd most frequent cancer among women between 15 and 44 years of age.

The aim was to evaluate cytological changes and HPV prevalence in Lithuanian population.

Methods: Between 2010 and 2024 LUHS Hospital Kaunas Clinics tested 13519 women for both: cytology and HPV. 2010-2018 HPV pooled results were given as the found/not found, in 2018 the genotyping was started.

Results: In 2010-2024 the 13159 women were tested and 23.45% were HPV positive. In HPV positive group of 3170 women the cytology changes were as following:

- Normal cytology/NILM – 592 (18.67 %);
- Atypical Squamous Cells of Undetermined Significance/ASC-US 485 (15.30 %);
- Low-grade cervical lesions/LSIL 1147 (36.18 %);
- High-grade cervical lesions/HSIL 880 (27.76 %);
- Cervical cancer 66 (2.08 %).

HPV-pos women who had LSIL and LSIL were significantly younger than those who had ASC-US, NILM or cervical cancer, accordingly.

HPV 16 was found to be most frequent genotype in population, and it was found together with cytology changes: ASC-US 21.50%, LSIL 21.05%, HSIL 46.15 %, and cervical cancer 27.78 %. HPV 18 was found to be the second most frequent genotype in population: ASC-US 6.54%, LSIL 5.92%, HSIL 9.05%, and cervical cancer 16.67 %. Interestingly, the HPV 31 and HPV 33 were found to be in high prevalence in Lithuanian population with high incidence rate, accordingly: ASC-US 9.35 and 4.67%, LSIL 12.17 and 4.28%, HSIL 6.79 and 8.14 %, and cervical cancer 16.67 and 11.11 %. Also, the age of women with cytology changes including LSIL and HSIL were found to be significantly younger than those who had ASC-US and cervical cancer.

Conclusion: The prevalence of HPV at a young age with intracellular changes suggests that HPV can be applied to younger women to detect potential changes as early as possible.

Biography

Ieva Janulaityte received her PhD in Biology in 2022, master's in laboratory medicine biology in 2017 in Lithuanian University of health Sciences. She is a lecturer in the same University from 2022 teaching medicine, laboratory medicine biology, medicine and



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genetics and biochemistry students. Ieva Janulaityte is focused on infectious and non-infectious inflammation, tissue remodeling, immune and structure cell biology. She is a member of the European Federation of Clinical Chemistry and Laboratory Medicine, European Respiratory Society, and several national societies and Member of the Lithuanian management methodological group of the program for early diagnosis of malignant tumors of the cervix.



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HUMAN PAPILLOMAVIRUS TYPES BY CERVICAL DYSPLASIA, HIV-STATUS AND THE DIAGNOSTIC VALUE OF CERVICAL SCREENING METHODS IN EASTERN KENYA

James Kinoti Njue¹, Margaret Muturi², Lucy Kamau² and Raphael Lwembe³

¹Moi University, Kenya

²Kenyatta University, Kenya

³Kenya Medical Research Institute (KEMRI), Kenya

Abstract

Background: Human papillomavirus (HPV) causes over 99% of all cervical cancer globally. In 2022, it was responsible for over 3200 deaths in Kenya. Data on the epidemiological distribution of HPV genotypes by cervical dysplasia and HIV status which is important in designing prevention strategies and monitoring treatment of cervical cancer is lacking in Eastern Kenya.

Objective: The study aims to determine HPV type's prevalence, diagnostic value of primary and sequential triage tests, and awareness of cervical cancer among HIV-infected and non-infected women aged 18-48 years in Eastern Kenya.

Methods: HPV genotyping, Pap smear, and VIA tests were conducted on the cervical transformation zone, squamocolumnar junction, and endocervical canal exudates, with social-demographic and awareness data collected using a questionnaire. Statistical relationships between laboratory outcomes and questionnaire data were computed using SPSS software.

Results: 317 women (161 (50.8%) HIV-positive and 156 (49.2%) HIV-negative, mean age: 34.3, range 18-46 years) were recruited. Of these, 27.4% (21.5% HIV-positive and 5.9% HIV-negative) had abnormal VIA (81/317 (25.6%)), HPV-genotyping (84/317 (26.5%)), Pap smear (96/317 (30.2%)), and histology (78/122 (63.9%)) test. A wide spectrum of HPV types was detected by CIN2+ (HIV-positive: HPV81 (18/317 (5.6%)) and HPV11 (3/317 (0.9%)); and Invasive cervical cancer: (HIV-positive: HPV16 (1/317 (0.3%)); HIV-negative: HPV16 (1/317 (0.3%)). HPV genotyping and Pap smear tests showed high diagnostic accuracy and specificity in HIV-infected women, with increased specificity in both primary and triage testing approaches. High awareness of cervical cancer disease was established, but it lacks understanding of its causes, signs, symptoms, and risk factors.

Conclusion: The study reveals higher HPV type frequency in HIV-infected women, with non-vaccine HPV types linked to cervical dysplasia, highlighting the need for accurate cervical screening methods. High cervical dysplasia is likely due to inadequate and inaccurate understanding of cervical cancer disease and risk factors.

Biography

James Kinoti Njue a lecturer in the Department of Microbiology and Parasitology, at Moi University, Kenya received his PhD in Medical Virology from Kenyatta University in 2022. He holds a Master of Science in Infectious diseases degree (Kenyatta University, Kenya), a bachelor's degree in Medical Microbiology from the Jomo Kenyatta University of Agriculture and Technology, Kenya and a fellowship in Monitoring & Evaluation, Bioinformatics and Epidemiology from the University of Nairobi, Kenya.

His research interests include molecular biology, diagnosis and epidemiology of viral infections especially Human papillomavirus-associated diseases such as cervical cancer, and expanding scientific knowledge to benefit the entire research community.



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IMPACT OF ANTIMICROBIAL STEWARDSHIP PROGRAM ACTIVATION IN AN INTENSIVE CARE UNIT IN KING KHALED HOSPITAL IN NAJRAN

Ali Dhafer Al-Swedan

King Khalid Hospital- Najran, Saudi Arabia

Abstract

Antimicrobial resistance poses a significant global threat, driven by the misuse of antibiotics and the rise of multidrug-resistant organisms in intensive care units (ICUs). To address this issue, the implementation of an Antimicrobial Stewardship Program (ASP) at King Khaled Hospital in Najran focuses on improving patient care through strategic interventions. The ASP monitors and tracks various aspects of antimicrobial therapy, including drug selection, dosing (loading and maintenance), frequency, route of administration, therapy duration, de-escalation techniques, and adherence to ASP recommendations.

Furthermore, periodic antibiograms provide a comprehensive overview of bacterial resistance patterns by analyzing cumulative susceptibilities to antibiotics. By comparing antibiogram data from 2022 to the year of 2023, researchers seek to identify trends in antimicrobial resistance and multidrug-resistant (MDR) surveillance. Utilizing Excel for data analysis, the study aims to uncover shifts in resistance profiles and inform future antimicrobial management strategies.

This prospective study spans 12 months and focuses on a single-center acute care hospital with approximately 80 ICU beds within a 360-bed facility. The evaluation period runs from January to December 2023, capturing the impact of the newly implemented ASP on patient outcomes and resistance patterns. The primary outcome measures will assess the differences in antimicrobial resistance and bacterial susceptibilities between the baseline data from 2022 and the data collected by the end of December 2023. Secondary outcomes will delve into changes in MDR surveillance between the years 2022 and 2023, providing a comprehensive understanding of the ASP's effectiveness in combating antimicrobial resistance in the ICU setting.

In our study, we observed a notable statistically significant decrease in the number of cultured organisms in the ICU that were multidrug-resistant, particularly a decrease of over 15% in Gram-negative MDR organisms. There was also an increase in the number of MDR *Klebsiella pneumoniae* and a decrease in the number of *Acinetobacter baumannii*.

Based on our findings, we recommend the implementation of Antimicrobial Stewardship Programs in all hospitals and advocate for the support and expansion of such programs in both in-patient and out-patient settings.



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BACTERIOLOGICAL AND ANTIBIOTIC RESISTANCE PROFILE OF GERMS ISOLATED FROM PYOCULTURES AT THE BIOMEDICAL LABORATORY OF THE CHINA-GUINEA FRIENDSHIP HOSPITAL OF KIPE IN CONAKRY (GUINEA)

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Laboratoire biomédical de l'Hôpital de l'Amitié Sino-Guinéenne, République de Guinée
Université Gamal Abdel Nasser de Conakry, République de Guinée

Abstract

The rapid evolution of bacterial multi-resistance to antibiotics is a worrying phenomenon in the world and particularly in Africa.

Objective: The aim of this study was to describe the bacteriological and antibiotic resistance profile of germs isolated from pyocultures at the China-Guinea Friendship Hospital in Conakry (HASIGUI).

Methods: This is a retrospective study carried out at the HASIGUI Biomedical Laboratory from June 15th, 2017 to December 22th, 2021). Thus, 432 pus samples were analyzed. Bacterial identification and antibiograms were carried out using the Vitek2 Compact machine, and by the API and microdilution system (bioMérieux, France).

Results: Male were predominant with a sex ratio (Male/Female) = 2.04, and the age group from 0 to 20 years was in the majority. The distribution according to professions showed that students were predominant. Of 432 pyocultures performed, 291 (67%) were positive. Bacterial identification showed that the species identified were *Staphylococcus aureus* (15.81%), *Staphylococcus xylosus* (6.53%), *Staphylococcus lentus* (4.81%) and *Escherichia coli* (4.47%). The majority of strains were susceptible to linezolid (82.47%), imipenem (71.51%), clindamycin (67.27%), fosfomycin (62.99%), levofloxacin (59.62%), ciprofloxacin (52.66%). On the other hand, the majority of strains were resistant to benzylpenicillin (94.11%), cephalin (90.47%), cefixime (86.29%), cefuroxime (83.67%), ampicillin (77.17%), cefotaxime (73.94%), nalidixic acid (72.8%), cotrimoxazole (60.81%).

Conclusion: All of these results show multi-resistance to antibiotics in bacteria isolated from pyocultures requiring treatment based on the results of antibiograms.

Biography

Abdoulaye Makanera is the Head of the Biomedical Laboratory Department at the China-Guinea Friendship Hospital of Kipé in Conakry and a University lecturer. Born on December 11, 1969, in Boké, Guinea, he has been a Teacher-Researcher (Bacteriology-Virology) at Gamal Abdel Nasser University of Conakry (UGANC) since 2005, leading the Microbiology-Parasitology-Myecology unit. With a career in medical biology spanning Tunisia and Guinea since 1999, he participated in key diagnostic courses in French-speaking Africa and has authored or co-authored 50 scientific articles.

Day 2

Video Presentations



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INEQUALITY IN THE DISTRIBUTION OF COVID-19 VACCINE

Rayehe Noroozi and Mohsen Bayati

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Abstract

Background: The equality in the distribution of vaccines between and within countries along with follow sanitation tips and observe social distance, are effective strategies to rid the world of COVID-19 pandemic. Inequality in the distribution of COVID-19 vaccine, in addition to causing inequity to the population health, has a significant impact on the process of economic recovery.

Methods: All published original papers on the inequality of Covid-19 vaccine distribution and the factors affecting it were searched in PubMed, Web of Science, Scopus and ProQuest databases between December 2020 to 30 May 2022. Selection of articles, extraction of their data and qualitative assessment (by STROBE) were performed by two researchers separately. Data graphing form was used to extract detailed data from each study and then, the collected data were classified.

Results: A total of 4623 articles were evaluated. After removing duplicates and screening the title, abstract and full text of articles, 22 articles were selected and entered into the study. Fifteen (68.17%) studies were conducted in the United States, three (13.64%) in Europe, three (13.64%) in Asia and one (6.66%) in Oceania. Factors affecting the inequality in the distribution of COVID-19 vaccine were classified into macro and micro levels determinants.

Conclusion: Macro determinants of inequality in the Covid-19 vaccine distribution were consisted of economic (stability and country's economic status, Gross Domestic Product (GDP) per capita, financial support and human development index), infrastructure and health system (appropriate information system, functional cold chains in vaccine transport, transport infrastructure, medical and non-medical facilities per capita, healthcare access and quality), legal and politics (vaccination allocation rules, health policies, political ideology and racial bias), and epidemiologic and demographic factors (Covid-19 incidence and deaths rate, life expectancy, vulnerability to Covid-19, working in medical setting, comorbidities, social vulnerability, incarceration and education index). Moreover, micro/ individual level

Biography

Rayehe Noroozi (April 1999, Iran, Shiraz) is already a health Economics PhD Candidate in Shiraz University of Medical Sciences, Shiraz, Iran. Have gotten Diploma of science from Shiraz Governmental Genius school, started to study Bachelor and master of Health Administration at September 2017 and then at October 2021

She finished her bachelor thesis on Inequality in COVID vaccine distribution which is published as an article: "Inequality in the distribution of Covid-19 vaccine: a systematic review". She has further research on mental and maternal health disparity later during higher education.

"Most important thing in my life is to achieve my goals and help people with humanity, peace and health. I like communication with people and helping them out." Says Rayehe as her mission statement.



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HOST-PATHOGEN INTERACTIONS IN TUBERCULOSIS CO-INFECTIONS: AN IMPLICATION FOR ANTIMICROBIAL RESISTANCE

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Sa'adu Zungur University, Gadau, Bauchi, Nigeria

Abstract

Infectious diseases remain a significant global health challenge, particularly in the context of tuberculosis (TB) co-infections with other microbial pathogens. The relationship between tuberculosis (TB) and co-occurring infections poses significant challenges in infectious disease diagnosis and management, particularly in immunosuppressed populations. Those populations are up to 30 times more likely to develop TB according to the World Health Organization. This abstract presents the complex host-pathogen interactions that characterize TB co-infections, focusing on how these dynamics contribute to antimicrobial resistance (AMR). Utilizing molecular characterization techniques, can investigate the prevalence of co-pathogens in TB patients correctly, employing next-generation sequencing and bioinformatics tools to analyze genetic markers of resistance. Many findings reveal a correlation between TB and various co-infections, highlighting the adaptive mechanisms pathogens uses in immunocompromised host. This underscores the necessity for comprehensive diagnostic approaches that consider the full spectrum of infectious agents in TB patients with tailored therapeutic strategies.

Emerging precision-based and evidence highlights the prevalence of microbial co-infections in TB patients, often complicating clinical outcomes and treatment strategies. The mechanisms by which co-pathogens exploit host immunity and the resulting impact on the efficacy of standard TB therapies are critical areas and a research path to be explored enough. Furthermore, the current research trends and their implications for future therapeutic strategies at combating AMR is crucial and timely. As the global health platform evolves, understanding these important interactions will be necessary for developing integrated management protocols that address both TB and its associated co-infections. Bauchi state of Nigeria is a case study to this regards.

By synthesizing recent findings and expert opinions, The purpose of this information is to stimulate dialogue among researchers and clinicians at this International Conference on Infectious Diseases, fostering discussions on innovative methodologies for studying microbial resistance mechanisms and collaboration to enhance our fight against microbial challenges in an increasingly interconnected world and, to the development of effective interventions against multifaceted infectious disease challenges.

Biography

Aishatu received her MSc in Medical Microbiology from Sa'adu Zungur University in 2024 and a bachelor's degree in Microbiology from the same institution, She received her Post graduate Diploma in Public Health Education and Promotion from the University of Maiduguri (Affiliate) in 2021. She has been an early career researcher with professional attachment to the Abubakar Tafawa Balewa



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University and Teaching Hospital's joint Molecular Genetics and Infectious Diseases (MOGID) Research Laboratory in Bauchi, Nigeria since 2021. She's currently leading African region within the International Union of Biochemistry and Molecular Biology (IUBMB) Trainee Initiative, where science is promoted to young scientists and researchers and global career development opportunities are shared. Her research interests include the microbial genetics and metagenomics for antimicrobial resistance in bacterial and infectious diseases, One Health Approach, public health education on diseases and prevention. Microbial co-infections research has granted her travel to Central Europe, Germany in 2023

Day 2

E-Poster Presentations



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BIOSOAP WITH EFFICIENT MICROORGANISMS TO REDUCE THE IMPACT ON WATER BODIES

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Abstract

The development of more sustainable sanitizers is crucial to reducing the environmental impact of domestic effluents. Biosoap enriched with Effective Microorganisms (ME) presents itself as an ecological alternative to synthetic detergents. Comparatively, natural ingredients such as vegetable oils and fats demonstrate greater biodegradability. In this study, it was observed that the initial Biosoap formulations achieved significant effectiveness in the parameters of conditioning, cleaning, bubble formation, persistence, hardness, solubility and drying. However, the viability of microorganisms in the initial formulations proved to be low, which led to the development of a microencapsulation technique to protect microorganisms during the saponification process. This technique, validated by previous studies, proved to be effective in preserving viable cells, facilitating the incorporation and action of ME, which resulted in improvements in the degradation processes of organic matter in simulated conditions of sanitary effluents. This study highlights the potential of microencapsulated Biosoap as a viable and efficient solution, encouraging more sustainable practices in waste management and effluent treatment.

The research demonstrated that it is highly viable for the manufacture of a sanitizing product using the cold process, where inoculation with micro-encapsulated microorganisms not only provided a favorable cost-benefit due to process efficiency and reduced energy consumption, but also resulted in a product with superior visual appearance and improved security and usability features. Furthermore, the use of microencapsulated effective microorganisms contributed significantly to the stability and prolonged effectiveness of the product, making it a sustainable and efficient alternative to conventional detergents. Considering the proven capabilities of *Bacillus* species as effective bioremediation agents in reducing heavy metals and reducing BOD_{5,20} and COD levels, as well as in the transformation of nitrogenous compounds and phosphorus, the Biosoap formulation was optimized to include a blend of specially selected microorganisms. The proposed composition includes *Bacillus subtilis*, *Bacillus licheniformis*, *Bacillus amyloliquefaciens* and *Bacillus megaterium*, each contributing 1.5×10^8 UFC/g, complemented by *Saccharomyces cerevisiae* with the same concentration, to maximize bioremediation efficacy. This strategic approach not only improves the product's functionality as a cleaning agent, but also amplifies its role in mitigating adverse environmental impacts associated with the treatment and disposal of domestic wastewater.

Biography

Graduated in Environmental Engineering from UniFTC University in 2010, Specialized in Basic Sanitation Engineering from INBEC in 2015 and PhD student in Ocean and Earth Dynamics at Federal Fluminense University. Professional experience in Coordination of Environmental and Socio-Environmental Projects, Execution of Degraded Area Recovery Projects, Monitoring Services, Operation and Training of Water and Effluent Treatment Plant Employees; - Experience in Environmental Licensing; - Experience in Calculation and Descriptive Memory, Equipment Specification in Domestic and Industrial Effluent Treatment Plants, Water Reuse, Basic Sanitation; - Environmental Impacts.

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