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ABSTRACT BOOK

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Infectious Diseases

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Adrien Lokangaka
Kinshasa School of Public Health, Kinshasa, Democratic Republic of the Congo

Incidence of possible serious bacterial infection in young infants in the three high-burden countries of the Democratic Republic of the Congo, Kenya and Nigeria

Abstract

Neonatal infections are a major public health concern worldwide, particularly in low- and middle-income countries where most of the worldwide infection-related deaths in children under five years old occur. Sub-Saharan Africa has the highest mortality rates, but there is a lack of data on the incidence of sepsis from this region, which hinders efforts to improve child survival. The objective of this study was to determine the incidence of possible serious bacterial infection (PSBI) in young infants in three high-burden countries in Africa. This is a secondary analysis of data from the AFRINEST trial, which was conducted in the Democratic Republic of the Congo (DRC), Kenya, and Nigeria between March 15, 2012 and July 15, 2013. We recorded baseline characteristics, the incidence of PSBI (as defined by the World Health Organization), and the incidence of local infections among infants from 0-59 days after birth. We report descriptive statistics. The incidence of PSBI among 0–59-day-old infants across all three countries was 11.2% (95%CI= 11.0-11.4). The DRC had the highest incidence of PSBI: 19.0% (95%CI= 18.2-19.8). Low birth weight infants and infants born to mothers aged less than 20 years had a higher rate of PSBI (24.5%, 95%CI= 23.1-26.0) and 14.1%, 95%CI= 13.4-14.8), respectively. The incidence of PSBI was higher among infants delivered at home (11.7%, 95%CI= 11.4-12.0). The high burden of PSBI among young infants in DRC, Kenya, and Nigeria demonstrates the importance of addressing PSBI in improving child survival in Sub-Saharan Africa to reach the Sustainable Development Goals (SDGs). These data can support government authorities, policymakers, program

implementers, non-governmental organisations, and international partners in reducing preventable under-five deaths.

Biography

Dr. Adrien Lokangaka Longombe, MD, MPH, is a physician and public health researcher with extensive experience in maternal, newborn, and child health research in low- and middle-income countries, particularly the Democratic Republic of the Congo. He currently serves as Country Coordinator for the Global Network for Women's and Children's Health Research in the DRC and as a Research Assistant at the Kinshasa School of Public Health. Dr. Lokangaka holds a medical degree from the University of Kinshasa and a Master of Public Health in Maternal and Child Health from the University of North Carolina at Chapel Hill, and he is currently pursuing a PhD in Public Health at the Université Libre de Bruxelles. His work focuses on neonatal infections, simplified antibiotic regimens, and implementation research in resource-constrained settings. He has coordinated multiple NIH-funded clinical trials and is the author of several peer-reviewed publications in leading global health journals.

Dr. Nadya kagansky
Tel Aviv University, Israel

Comparison of Clostridioides difficile Infection Incidence in a General and a Geriatric Hospital Prior to and During the COVID-19

Abstract

Background: Clostridioides difficile (CD) is the main cause of nosocomial diarrhea, resulting in increased morbidity and mortality, and is thought to be greatly affected by strict hygiene. In this study, we assessed changes in CD infection prevalence and outcomes pre- and during the COVID-19 pandemic (CP).

Methods: This was an observational cohort performed at a tertiary medical center (MC) and a geriatric hospital (GH). Patients from both hospitals diagnosed with CD were included, and the period of one year prior to the pandemic to one year after was compared. Data was extracted from electronic medical records (EMR).

Results: A total of 145 CD-associated diarrhea (CDAD) cases were diagnosed in the MC and 54 in the GH. There was no change in CDAD prevalence or mortality between the study periods in either hospital. Disease duration, measured as days with diarrhea (DWD), was shorter during the CP in the GH (10.6 days vs. 8.1 days, $p < 0.01$). CDAD was more prevalent in the GH during both periods; however, the disease was milder, with only three mortality cases and a significantly shorter disease duration (3.19 DWD vs. 10.67 in the MC before CP; 3.11 vs. 8.1 during CP, $p < 0.01$). In a survival analysis for MC patients, no significant differences were found between periods before and after adjustment for age, gender and period.

Conclusions: The CP affected the duration but not the prevalence of CDAD. The milder course of CDAD in the GH may have been due to the quality of treatment provided in an academic GH and the subsequent faster diagnosis and treatment.

Dave SB Hoon
Saint Johns Cancer Institute, USA

Multiomics cfDNA Fragmentomics Monitoring Methylation Variants and SNPs Of Melanoma Patients Receiving Checkpoint Inhibitor Immunotherapy

Abstract

Checkpoint inhibitor immunotherapy (CII) has significantly prolonged AJCC stage III/IV melanoma patients' survival in the past several years through multiple human monoclonal antibodies targeting checkpoint proteins on both melanoma and immune cells. However, there are no efficient blood biomarkers to determine the efficiency of CII in realtime and determining when to switch therapy to improve patient overall survival. We have developed various forms of cfDNA blood melanoma biomarkers in the past. Traditional approaches assessing specific cfDNA genes for mutations and metthylation changes which we pioneered used realtime PCR assays then developed into multiple gene-based probe assays. More recent we developed a novel multiomic whole genome sequence (WGS) cfDNA fragmentomic platform based on 6 base sequences that covered methylation associated variants (MAV) of both 5-methyl cystine(5-mC) and 5-hydroxy mC(5-hmC) of gene promoters, bodies and non-coding regions of the genome. The MAVs fragmentomics analysis using machine learning were performed on the same WGS platform involving NGS 30x paired end reads. Through this platform we carried out analysis on longitudinal clinically well annotated CII patients blood categorized with progressive disease. death, partial response, stable disease on specific patients's bleeds during treatments between 3- 24 mos. Results of patients demonstrated both significant 5-mC and 5-hmC were detected whereby, levels of quantitative changes were related to patient responses during treatment. In addition, we detected WGS SNVs changes during CII treatment which demonstrated significant

changes parallel to clinical changes. Specific melanoma-related gene SNVs such as in BRAF, EGFR, ARIDIA, JAK, and TERT genes, etc were monitored for changes during treatment. These studies demonstrated through WGS genomics/epigenomic multiomics analysis of CII patients cfDNA have clinical utility .

Biography

Is Professor and Director Depts Translational Molecular Medicine and NGS Center, Saint Johns Cancer Institute, Providence Health System. His Google Scholar H-score is 123 with > 450 peer-reviewed publicatiion mostly in molecular oncology as related to solid human tumor clinical studies of which many in high impact journals. He is a pioneer of cfDNA and has published and patented assays in mutation, methylation, amplification, and more recently methylation associated variants and SNP fragmentomics in clinical studies since the 90s. He has been involved in multiple clinical phase CDx clinical studies that include immunotherapies and sentinel lymph node multicenter clinical trials. His focus is in melanoma but also as well in other solid tumors. He also researchs on ubiquitin proteomic cancer regulatory events in tumor progression and resistance. He is a senior reviewer on multiple NCI/DOD grant study sections for >25 yrs; also founding member of NCI Cancer Biomarker study section.

Qingjie Li
The University of Texas Medical Branch at Galveston, USA

Erlotinib Suppresses Tumorigenesis in a Mouse Model of Colitis-Associated

Abstract

Colorectal cancer is the third most diagnosed cancer and second most common cause of cancer mortality worldwide. Colitis-associated cancer (CAC) in inflammatory bowel diseases exhibits more aggressive behavior than sporadic colorectal cancer; however, the molecular mechanisms remain unclear. No definitive preventative agent against CAC is currently established in the clinical setting. We investigated the molecular mechanisms of CAC in the azoxymethane/dextran sulfate sodium (AOM/DSS) mouse model and assessed the antitumor efficacy of erlotinib, a small molecule inhibitor of the epidermal growth factor receptor (EGFR). Erlotinib premixed with AIN-93G diet at 70 or 140 parts per million (ppm) inhibited tumor multiplicity significantly by 96%, with ~60% of the treated mice exhibiting zero polyps at 12 weeks. Bulk RNA-sequencing revealed more than a thousand significant gene alterations in the colons of AOM/DSS-treated mice, with KEGG enrichment analysis highlighting 46 signaling pathways in CAC development. Erlotinib altered several signaling pathways and rescued 40 key genes dysregulated in CAC, including those involved in the Hippo and Wnt signaling. These findings suggest that the clinically-used antitumor agent erlotinib might be repurposed for suppression of CAC, and that further studies are warranted on the crosstalk between dysregulated Wnt and EGFR signaling in the corresponding patient population..

Biography

Dr. Qingjie Li is a Professor in the Division of Gastroenterology and Hepatology, Department of Internal Medicine at the University of Texas Medical Branch (UTMB) at Galveston and the President/Founder of ClearLi Biomedicines LLC. He received his PhD from Central South University in China and completed postdoctoral training at Oregon State University. Dr. Li's research centers on colorectal cancer, the gut microbiome, inflammatory bowel disease (IBD), and its extraintestinal manifestations, as well as the development of novel therapeutics for digestive diseases and aging-related conditions. He serves as a reviewer for several NIH study sections, Digestive Disease Week, and multiple scientific journals. Dr. Li has published more than 50 peer-reviewed articles in leading journals, including Gastroenterology.

Ronit Ilouz
Bar-Ilan University, Israel

Spatial Profiling of Protein Kinase A Subunits Identifies Aggressive Prostate Cancer in MRI-Targeted Biopsies

Abstract

Prostate cancer is a multifocal disease with substantial spatial and biological heterogeneity that challenges accurate risk assessment. Most molecular biomarker studies rely on bulk or cross-sectional analyses that average signals across patients and lesions, often obscuring spatially localized molecular alterations relevant to tumor aggressiveness.

To address this limitation, we performed lesion-matched molecular profiling of MRI-targeted prostate biopsies obtained from both suspicious and non-suspicious regions within the same prostate. Protein Kinase A (PKA) subunit expression and pathway activity were analyzed using quantitative immunofluorescence with a custom image-analysis pipeline, Western blotting of paired biopsy samples, and re-analysis of publicly available proteomics datasets from diagnostic (n=116) and recurrence (n=306) prostate cancer cohorts.

We identified a grade-dependent shift in PKA signaling characterized by progressive loss of the regulatory subunit RIβ, redistribution of the catalytic subunit PKAC into proliferating tumor cells, and increased global phosphorylation of PKA substrates in suspicious lesions. These spatial alterations were consistently observed within individual patients and correlated with tumor Grade Group. Analysis of bulk proteomics datasets revealed high inter-patient variability of RIβ and enrichment of catalytic subunits in recurrence-associated tumors, highlighting the limitations of non-spatial analyses. Notably, nearly half of recurrence-associated proteins contained predicted PKA phosphorylation motifs, supporting increased pathway activity in aggressive disease.

In conclusion, spatial profiling of PKA subunits in MRI-targeted biopsies reveals a reproducible molecular signature associated with prostate cancer aggressiveness. These findings establish the PKAC:RIβ imbalance as a potential biomarker and demonstrate the value of intra-patient, spatially resolved molecular analysis for improving prostate cancer diagnostics and risk stratification.

Biography

Dr. Ronit Ilouz is an Assistent Professor at the Azrieli Faculty of Medicine, Bar-Ilan University. Her research focuses on spatial signaling mechanisms in cancer and neurodegeneration, combining quantitative imaging, proteomics, and structural biology to identify clinically relevant biomarkers. She has contributed to defining Protein Kinase A (PKA) dysregulation in human disease, including lesion-specific biomarkers in prostate cancer. Dr. Ilouz is supported by the Israel Science Foundation, Israel Cancer Research Fund, and the U.S.–Israel Binational Science Foundation.

Meital Gal-Tanamy
Bar-Ilan University, Israel

Epigenetic mechanisms of hepatocellular carcinoma post HCV cure

Abstract

Hepatitis C virus (HCV) is a major cause of death and morbidity globally and the leading cause of hepatocellular carcinoma (HCC). Although now, with new direct-acting antivirals (DAAs) therapy available, HCV is a curable cancer-associated infectious agent, HCC prevalence is expected to continue to rise because HCC risk still persists after HCV cure. Understanding the factors that lead from HCV infection to HCC pre- and post-cure may open-up opportunities to novel strategies for HCC prevention. We recently reported the induction of alterations in the transcriptome of host cells via epigenetic dysregulation by HCV that persist after cure by DAAs as an epigenetic signature. This epigenetic signature is associated with hepatocarcinogenesis. Different treatment regimes show range of persistence of the epigenetic signature that correlate with treatment efficiency. Moreover, HCV induce the epigenetic and oncogenic signatures by perturbation of host signaling pathway, such as EGFR. We also identified correlation between HCV-induced changes in epigenetic marks associated with chromatin decompaction and mutation loads in HCV-related HCC. Inhibitors for epigenetic modifiers showed promising results as means for reversion of HCV-related epigenetic signature and oncogenic phenotypes. These studies have important contribution for understanding of the mechanisms of HCV-induced cancer pre and post cure.

Biography

Associate Professor at the Azrieli Faculty of Medicine, Bar-Ilan University, I lead the Molecular Virology Lab and serve as President of the Israel Society of Microbiology (ISM). With 22 years of experience in virology, my work centers on Hepatitis C virus (HCV) pathogenesis and virus–host interactions that contribute to liver disease and hepatocellular carcinoma (HCC). My research dissects the interplay between HCV-driven inflammation, chromatin and epigenetic remodeling, tumor-associated mutations, viral evolution, and immune responses to explain mechanisms linking infection to HCC risk. Our lab generated the first comprehensive map of HCV-induced epigenetic alterations and was first to show persistence of an HCV-induced "epigenetic signature" after viral clearance with direct-acting antivirals (DAAs). I have been invited to speak at national and international conferences, including keynote presentations at the HCV 2021 international meeting and the 2024 APASL meeting in Taiwan on post-cure epigenetic signatures.

Dr. P. Atchuthan
Sathyabama Insitute of Science and Technology, India

First Report of Ocular Pathology in Litopenaeus vannamei Attributed to a Novel Aeromonas Species from the Kovalam Coast, India

Abstract

Litopenaeus vannamei (whiteleg shrimp) is a cornerstone of global aquaculture, especially in India, due to its rapid growth and salinity tolerance. However, sustainability is increasingly challenged by multifactorial disease outbreaks linked to climate variability, antimicrobial misuse, and environmental degradation. While several pathogens of L. vannamei have been characterized, non- traumatic ocular infections remain undocumented.

During a routine epidemiological survey on March 17, 2025, in Kovalam, India, 6 out of 21 market specimens (28.6%) of L. vannamei exhibited conspicuous, milky-white ocular opacities. Histopathological examination of affected tissues revealed epithelial desquamation, focal necrosis, and leukocytic infiltration. Aerobic culturing yielded a consistent Gram-negative bacillus, which was identified by 16S rRNA gene sequencing (1,431 bp) as a putative novel Aeromonas species with 96.44% similarity to known taxa. The strain has been provisionally designated Aeromonas kovalamii sp. nov.

To trace its environmental origin and ecological relevance, gut content 18S rRNA-based DNA barcoding was performed. Identified prey included Paracalanus parvus, Microsetella norvegica, and Prionospio cirrifera organisms typical of eutrophic, polluted habitats. The gut metagenomics and microbiota were dominated by Proteobacteria, Bacteroidetes, Firmicutes, and other typical phyla, with opportunistic genera such as Vibrio, Shewanella, and Photobacterium detected. However, A. kovalamii was consistently isolated only from ocular lesions, not from gut or other tissues, suggesting

its extrinsic role under stress-induced dysbiosis.
Phylogenetic analysis placed A. kovalamii in a distinct clade adjacent to A. dhakensis. Metabolite profiling via GC-MS identified bioactive compounds, including Pyrrolo[1,2-a] pyrazine-1,4-dione and Nitro-L-arginine. FTIR spectroscopy confirmed characteristic functional groups, while SDS- PAGE demonstrated distinct protein bands (70, 55, and 35 kDa), suggesting unique biosynthetic capabilities.
Diagnostic PCR assays ruled out major shrimp pathogens (WSSV, EHP, VpAHPND, IHHNV, and NHPB) in samples from hemolymph, hepatopancreas, gills, and muscle. This represents the first confirmed case of ocular pathology in L. vannamei caused by a novel Aeromonas species. These findings underscore the need for integrative diagnostics, environmental biomonitoring, and One Health–based management strategies to mitigate emerging threats in shrimp aquaculture.

Biography

Dr. Atchuthan holds a Ph.D. in Marine Science from Goa University, with research conducted at CSIR-NIO on macrobenthic communities in Indian ports. He has nine years of experience in benthic ecology, molecular taxonomy, and polychaete culture. He previously worked as a Junior Research Fellow at ICAR–CIBA, focusing on grow-out technologies for marine worms used in hatcheries. He has published 7 research papers, contributed 2 book chapters, identified key polychaete species, and submitted gene sequences to NCBI. Currently, he is an Assistant Professor (Research) at Sathyabama Institute of Science and Technology, working on live-feed culture and disease control in commercially important fish species.

Carmen Pavelescu
University of Medicine and Pharmacy Carol Davila, Bucharest, Romania

National Survey of Pediatric Respiratory Infections in Romania Before and After the COVID-19 Pandemic: Impact of Low Vaccination Coverage on Epidemiologic Trends

Abstract

Background: The COVID-19 pandemic profoundly disrupted the landscape of pediatric respiratory infections worldwide. Romania represents a unique epidemiological setting due to persistently low vaccination coverage for seasonal influenza (<20%), COVID-19 (≈5% in 5–11 years during peak waves), and absence of universal RSV prophylaxis before 2023. This study presents the first national comparative analysis of respiratory infections in children before and after the COVID-19 pandemic, emphasizing the role of vaccination uptake.

Methods: We conducted a national multicenter descriptive survey using aggregated pediatric data from hospitals and outpatient clinics across Romania. Data were collected for two defined periods: Pre-pandemic: January 2018 – February 2020, and Post-pandemic: January 2022 – December 2024 The survey included >15,000 pediatric cases diagnosed with acute respiratory infections and >5,000 multiplex respiratory PCR panels. Vaccination records (influenza and COVID-19) were analyzed when available. Primary outcomes: pathogen distribution, seasonality, age group severity, co-infection patterns, and associations with vaccination status.

Results: Across all regions, the post-pandemic years demonstrated marked shifts in respiratory pathogen circulation: RSV showed early, intense, and atypical seasonal peaks (autumn rather than winter) in 2022–2023, with a 60–80% increase in

hospitalization rates among infants <1 year.

Influenza A/B circulation collapsed during 2020–2021, followed by a strong rebound in 2022–2024, displaying higher positivity rates than pre-pandemic seasons. Rhinovirus/enterovirus became the dominant year-round pathogen, particularly in school-aged children. Co-infection rates doubled, from 7–10% pre-pandemic to 15–22% post-pandemic. Children without influenza vaccination (>80% nationally) demonstrated significantly higher influenza positivity ($p<0.001$) and increased risk of febrile complications. COVID-19 vaccine uptake remained critically low, limiting population-level protection and contributing to recurrent SARS-CoV-2 waves in 2022–2023. The absence of a national RSV immunization strategy before 2023 was associated with the highest burden of severe lower respiratory tract infections in infants.

Conclusions: This national survey highlights profound epidemiological changes in pediatric respiratory infections following the COVID-19 pandemic in Romania. Low vaccination coverage—for influenza, COVID-19, and RSV—was a key amplifying factor for the resurgence and severity of major viral pathogens. Strengthening pediatric immunization strategies, improving parental awareness, and integrating broader multiplex diagnostic use are crucial priorities to optimize respiratory infection control in Romania.

Keywords: pediatric respiratory infections; RSV; influenza; COVID-19; vaccination coverage; epidemiology; Romania; post-pandemic trends.

Biography

Dr. Carmen Pavelescu is a General Pediatrician with Ultrasound Competency,

and General Practitioner licensed since 2005, and Infectious Disease resident doctor who joins National Institute of Infectious Diseases, "Prof.Dr.Matei Bals", Bucharest, Romania- PediatricDepartment. As the organization providing specialized pediatric care, she is responsible for sharing the wealth of expertise of the Pediatrics staff with patients and families everywhere. She is specialized in Pediatric Infectious Diseases and care for hospitalized children. For her doctoral project, she focused on cytokines storm and variations of cytokines in HIV-AIDS in pediatrics. She comes prepared for all types of learning situations, having researched the relevant topics so that she can provide quality care as well as participate actively in class and clinical supervision. Dr. Pavelescu is articulate, well-read, and able to utilize her knowledge effectively in the clinical setting. She has extensive media experience including TV, radio, and online and has been a regular medical contributor on Primetime shows and has had multiple appearances as a medical expert on a variety of channels. Medical reviewers are responsible for reviewing medical records and other documents related to healthcare

services. They're tasked with ensuring that all information is accurate, complete, and in compliance with relevant standards and regulations. She participated in a number of competitive projects, conferences as Congresses. As a medical reviewer for MDPI, Dr. CP is also responsible for providing feedback or recommendations on the quality of care provided by a physician or other healthcare provider. This could include anything from minor suggestions to more serious concerns about the quality of care being delivered. She has competence in General Ultrasound for adults and Pediatric patients; she perform abdominal ultrasound to follow identification of normal abdominal structures (i.e., liver, spleen, kidney) and typical abnormal images (i.e.,intussusception, acute appendicitis, hydronephrosis), performance of FAST (focused assessment with sonography for trauma).Dr. Carmen lives in Romania, Bucharest with her family where she loves reading and programming, tennis, and traveling. She has two school-age children who remind her why every day is precious and full of energy and laughs. Her professional goals will be in accordance with the standards of good practice and will always be updated and put into practice with all her skill, based on experience and performance.Her research interests include Vaccine, Immunology,Cytokine, Pediatrics, Ultrasound Specialist, Infectious Disease, and pediatric Dermatology.

Adama Ahmad Abubakar
Nigeria Center for Disease Control and Prevention – National Reference Laboratory, Nigeria

Evaluation of the COVID-19 Laboratory-Based Surveillance System in Nigeria from 2019-May 2021

Abstract

Periodic evaluations of surveillance systems to identify areas for improvement and evidence of data reliability is essential. We evaluated the National Reference Laboratory (NRL) surveillance system for COVID-19 to identify its strengths, weaknesses, attributes, and other process characteristics that require improvement. Observational study design comprising a survey using a structured questionnaire, secondary data analysis, and review of processes was employed. United States Centers for Disease Control and Prevention guidelines (2001) for evaluating public health surveillance systems were used. Key stakeholders were identified, and a retrospective record review and data analysis were conducted. From February 2020 to February 2021, a total number of 204238 samples were received from suspected cases in 32 (89%) states in the country. Out of which 22935 (11%) were positive. Up to 194,068 (95%) were initial tests, 6,407 (3%) were repeat tests and 3,763 (2%) were follow-up tests. And 106,744 (52%) were males, 83,714 (41%) were females, total test with missing gender 13,780 (7%), total test with age variable only 170,112 (83%), total test with missing age only 34,126 (17%). Of the total received, 106744 (52.3%) were males and 83714(41%) were female and the missing gender was 13780 (6.7). The usefulness of the system was found to be 96%, the Simplicity of case definition was (87%), while generally, 67% gave a positive response. Flexibility was 83% and completeness of data was found to be 68%. Timeliness of reporting and sending data were found to be 48% and 45% respectively. Even though 81% of respondents reported having policies on reporting data,

PHL surveillance system was found to be useful, flexible, simple, and acceptable, but the challenges of timeliness of data were not representative of all the health facilities. The timeliness of reporting was suboptimal. We recommended reporting from private health facilities, strengthening human resource capacity for supportive supervision, and ensuring adequate government funding to enhance

the system's representativeness and improve data quality. And strengthen public-private partnerships on other infectious diseases.

Biography

Adama Ahmad Abubakar is a Medical Laboratory Scientist/Epidemiologist with over 15 years of progressive experience in public health. Her career started with the Ministry of Health before joining the Nigeria Centre for Disease Control and Prevention, where she held pivotal roles in strengthening laboratory systems.

Her expertise covers biosafety and biosecurity, quality management systems (QMS), auditing, molecular biology, and strategic program development. She has progressed from Safety Officer to Quality Officer, later Virology Lead, and now serves as Laboratory Manager at the National Reference Laboratory, Abuja, Nigeria.

Recognized for her leadership, mentorship, and management skills, Adama is committed to building resilient laboratory networks, advancing outbreak preparedness, and driving innovations in global health security. She has authored and co-authored peer-reviewed publications on infectious diseases, underscoring her dedication to evidence-based practice and collaborative research. She welcomes opportunities to partner with colleagues, institutions, and networks working to strengthen public health systems worldwide.

Adama Ahmad Abubakar
Nigeria Center for Disease Control and Prevention – National Reference Laboratory, Nigeria

Temporal and Demographic Patterns of Mpox in Nigeria from 2021 to 2025: A Nationwide Analysis of Epidemiological Factors

Abstract

Mpox remains a significant public health concern in Nigeria, with patterns of transmission evolving in recent years. This study analysed nationwide surveillance data from January 2021 to November 2025 to describe the demographic, geographic, and temporal characteristics of Mpox cases. A total of 3,675 suspected samples were tested, and descriptive and comparative statistical analyses were conducted using Welch's t-test for age and Chi-square tests for gender differences.

Overall, 13.8% of samples were confirmed positive. Confirmed cases were significantly older than negatives (mean age 26.5 vs. 19.8 years; $p < 0.001$), with young adults aged 20–40 years representing the most affected group. Males had a slightly higher positivity rate (15%) compared with females (12%) ($p = 0.014$). Spatially, the South-South region particularly Rivers, Delta, and Cross River showed the highest concentration of confirmed infections, with positivity ranging from 22–38%. Temporally, surveillance data showed a transition from low and sporadic case occurrence between 2021 and 2024 to a distinct escalation in early 2025, suggesting a shift toward a more sustained epidemic phase.

These findings highlight the need for targeted interventions focusing on high-burden regions and the young adult population, refined case definitions, and strengthened surveillance strategies to improve outbreak control.

Biography

Adama Ahmad Abubakar is a Medical Laboratory Scientist/Epidemiologist with over 15 years of progressive experience in public health. Her career started with the Ministry of Health before joining the Nigeria Centre for Disease Control and Prevention, where she held pivotal roles in strengthening laboratory systems.

Her expertise covers biosafety and biosecurity, quality management systems (QMS), auditing, molecular biology, and strategic program development. She has progressed from Safety Officer to Quality Officer, later Virology Lead, and now serves as Laboratory Manager at the National Reference Laboratory, Abuja, Nigeria.

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Elad Eliahoo
Kimron Veterinary Institute, Israel

Serological and molecular evidences of Crimean-Congo Hemorrhagic Fever virus (CCHFV) among animals and ticks in Israel

Abstract

Background
CCHFV, an RNA virus (family Nairoviridae), is the etiological agent of CCHF, a tick-borne disease, endemic in many parts of Asia, Europe and Africa. Ticks, mainly of the genus Hyalomma, are considered the main vector as well as reservoir of the virus. Generally, animals are asymptomatic to the disease with transient short viremia. In contrary, CCHFV infections in humans may develop into a severe hemorrhagic fever that could be lethal. Most human infections result from tick bites, although direct contact with infected blood or tissues of animals or humans is considered as an alternate way of infection.

Methods
Twenty beef cattle herds sampled during 2024-2025 and thirty-three camel herds sampled during 2013-2025 for sera and ticks. Presence of antibodies in the sera samples was studied using ELISA test. Additionally, the presence of CCHFV in the ticks was tested using RT-qPCR.

Results
In seventeen of the beef cattle herds, located in the north and central Israel, we have found seropositivity ranging from 3-100%. Moreover, we have identified prior exposure of camels in thirty of the herds collected during 2013 to 2025 in ranging prevalence of

5-30%. Lastly, we detected the presence of CCHFV in several species of ticks collected from the cattle herds and from wild animals. Phylogenetic analysis of a partial sequence of the S segment, have clustered to the Asia-1 genotype, suggesting the origin of the virus relates to the Middle-east linage.

Conclusions

These results demonstrate the presence of CCHFV in Israel. The high prevalence of prior exposure to CCHFV in cattle herds in the north and center part of Israel and in camels in the south part of the country, back traced as early as 2013. In addition, we have identified the presence of the virus in ticks, demonstrating the spread of CCHFV to new locations across the Mediterranean basin. Although no human cases were reported, so far, the prevalence, distribution and history of the animals' exposure suggest the virus is circulating in the country for at least 12 years. This One Health approach emphasizes the risk for populations such as animal breeders, veterinarians and healthcare workers.

Julie Black
Dominican University of New York, USA

Development of breast cancer survivorship program within a community-based hospital in New York

Abstract

As breast cancer survivorship continues to rise due to advances in early detection and treatment, there is a growing need for comprehensive, community-based survivorship care. This Doctor of Nursing Practice (DNP) capstone project proposes the establishment of a formalized breast cancer survivorship program within a community hospital in the Greater New York area. Guided by the Corbin-Strauss Chronic Illness Trajectory Model, as its theoretical framework, the project developed a protocol to establish a structured breast cancer survivorship program tailored to the needs of post-treatment patients.

The initiative included a detailed literature review,and stakeholder engagement to assess feasibility and support. The proposed program features individualized survivorship care plans (SCPs), multidisciplinary collaboration with ancillary services, coordination with primary care providers, and integration of community resources. Key components include symptom management, lifestyle counseling, family support services, and education on recurrence surveillance.

A patient survey conducted to assess interest and feasibility revealed strong support for the program, validating the demand for structured survivorship care. The implementation protocol outlines team roles, care workflows, educational materials, and metrics for evaluation. The program aims to improve clinical outcomes, reduce recurrence risk, and enhance patient quality of life.

By enhancing care continuity and addressing physical, emotional, and socioeconomic challenges, this program aims to improve patient outcomes and quality of life. The model aligns with national guidelines and DNP competencies, offering an accessible solution for other community-based cancer centers.

Biography

Julie Black, FNP-C, is a dedicated Family Nurse Practitioner with extensive experience in both hospitalist and emergency/urgent care settings. Fluent in English and Creole, she brings over a decade of clinical expertise from respected institutions including, CrystalRun Healthcare, Montefiore St. Luke's, The Valley Hospital, and Good Samaritan Hospital. Julie is recognized for her calm, organized approach to high-acuity situations, strong collaboration skills, and compassionate patient care. She holds a Master of Science in Nursing from Dominican College, where she also completed her BSN, and currently working on her Doctorate. Julie is certified by the AANP and licensed in both New York and New Jersey. Beyond the bedside, she served over a decade as an EMT with Spring Hill Ambulance Corps, where she held several leadership roles. Julie remains committed to advancing healthcare access and safety for diverse populations across the Hudson Valley and beyond.

Mahtab Azhdar
University of Alberta, Canada

Exploring the Impact of Taxane-Based Chemotherapy on the Physical Function of Breast Cancer Patients Using Markerless Motion Capture

Abstract

Breast cancer survivors often experience declines in physical function during and after chemotherapy, particularly with taxane-based regimens known to cause neuropathy, fatigue, and reduced endurance. Monitoring these changes is critical for timely rehabilitation planning, yet conventional clinical measures may lack sensitivity to subtle impairments. Markerless motion capture (MMC) technology offers an innovative, non-invasive approach to quantify body functions such as balance, and sit-to-stand performance.

This study will longitudinally evaluate the effects of taxane-based chemotherapy on the physical function of women with breast cancer stage I–III using clinic-based 3D MMC and home-based 2D MMC systems. A single-group longitudinal cohort (n=32) will be assessed at baseline, mid- treatment, end-of-treatment, and at 1.5 and 3 months post-treatment. Objective measures will include the Short Physical Performance Battery and 1-Minute Sit-to-Stand Test, and motion capture-derived metrics of sway, gait, and sit-to-stand performance. Patient-reported outcomes will be collected using the Functional Assessment of Cancer Therapy/Gynecologic Oncology Group- Neurotoxicity and the Edmonton Symptom Assessment System. Data will be analyzed using linear mixed-effects models to evaluate longitudinal changes in body functions over time. In addition, correlations and regression analyses will be conducted to examine associations between objective MMC-derived metrics and patient-reported outcomes.

This protocol is designed to highlight the potential of MMC to capture treatment-related functional decline and recovery in breast cancer patients, while also serving as a bridge between lab-based technologies and practical clinical assessment tools. Findings from this work are expected to inform survivorship care planning and support the integration of advanced technologies into oncology rehabilitation.

Biography

Mahtab Azhdar is a PhD candidate in Rehabilitation Science at the University of Alberta whose work integrates markerless motion capture (MMC) into oncology and rehabilitation practice. An internationally trained occupational therapist with four years of clinical experience, she completed an eight-month internship in Canada successfully implementing MMC workflows in a physical therapy clinic, translating lab-based methods into practical assessment pathways. Her research focuses on bridging engineering innovations with clinician-friendly tools to quantify functional performance and, ultimately, to improve quality of life for clients. She has authored three publications on balance and physical function, secured competitive grants and scholarships, and has been recognized as the top-ranked graduate with the highest GPA in both her bachelor's and master's programs. Through her doctoral studies, Mahtab collaborates to advance the bench-to- bedside translation of advanced technologies.

Mitchell Boshkos
Baylor College of Medicine, USA

Adult Lymphoma-Associated Hemophagocytic Lymphohistiocytosis: A 24-Year Single-Center Retrospective Analysis of Clinical Features, Diagnostic Hurdles, and Treatment Outcomes

Abstract

Lymphomas can often trigger immune dysregulation, leading to hemophagocytic lymphohistiocytosis (HLH), a systemic disorder characterized by excessive inflammatory cytokine production and widespread tissue damage. The co-occurrence of lymphoma, various infections (especially EBV), and HLH presents significant challenges due to overlapping clinical features and complex treatment decisions. Currently, no established treatment guidelines exist for lymphoma-associated HLH (LA-HLH).

This study aimed to investigate the clinical characteristics, diagnostic associations/difficulties, and treatment outcomes in adult lymphoma patients with concurrent HLH. We conducted a retrospective study identifying adult patients diagnosed with both lymphoma and HLH between January 2000 and January 2024. Of 78 total HLH cases identified over the 24-year period, 39.7% were malignancy-associated, 25.6% linked to infections, and 20.5% associated with autoimmune diseases. Among malignancy-associated cases, 20 patients (16 males, 4 females; median age 45.5 years) had LA-HLH, with the majority being Hispanic (75%). The most common lymphoma subtype was Hodgkin lymphoma (60%), followed by T-cell lymphoma (20%) (including cutaneous, peripheral, NK-/T-cell), diffuse large B-cell lymphoma (10%), marginal zone lymphoma (10%), and EBV-positive CNS lymphoma (5%). Additionally, 30% of patients were HIV-positive, with 66.7% receiving antiretroviral therapy.

Regarding patients with HLH linked to infection (26% of total HLH cases), we sought to determine if active EBV infection or the malignancy itself drove the hyperinflammatory response. While EBV-HLH is well-described, only 5 of 19 patients with infectious processes and concomitant HLH had detectable EBV viral loads at HLH diagnosis. Five additional patients lacked EBV viral load measurements, and 9 had undetectable viral loads. Notably, all 19 patients had positive IgG against EBV, consistent with widespread prior infection.

Median IL2R level was 26,915.5 pg/mL (IQR: 9,734.5–39,871). Hemophagocytosis was observed in 47.4% of bone marrow samples (median HLH score 253). Elevated EBV levels were seen in 72.2% of patients. Clinical features included hepatomegaly (94.4%) and splenomegaly (60%). Median laboratory values were: max temperature 101.4°F, hemoglobin 6.25 g/dL, platelet count 18.5 × 10^3/µL, ANC 0.45 × 10^3/µL. Ferritin was elevated (median 7,500 ng/mL), LDH 743 U/L. Other notable findings: median triglycerides 307 mg/dL, fibrinogen 257 mg/dL, AST 439.5 U/L, median INR 1.7. Furthermore, 55% of patients experienced acute liver failure.
For treatment, 40% received AVD/ABVD chemotherapy, 20% ICE, 26.7% R-CEOP/R-CHOP/DA-CHOP, and 6.7% SMILE. The median number of chemotherapy cycles was 3. HLH-directed therapies included steroids (90%) and etoposide (70%), with 50% of etoposide recipients requiring dose reductions. Concurrent HLH and lymphoma therapies were administered to 72.2% of patients.

Regarding outcomes, 45% of patients died, 45% achieved clinical response (CR), and 10% had refractory LA-HLH entering hospice. Notably, 71.4% of CR patients received concurrent etoposide/steroids and lymphoma treatment. Among HIV-positive patients, 33.3% achieved CR, and 25% of those with EBV infections also achieved CR. For patients with liver failure, 18.2% achieved CR; both had Stage 4 Hodgkin lymphoma and received etoposide with ICE and AVD. This study provides a comprehensive 24-year analysis of LA-HLH. Our findings suggest that the lymphomatous malignancy itself, rather than active EBV infection, was the primary driver of HLH, based on temporal symptom onset and undetectable viral loads in most patients. The study further highlights the complexity of managing g HLH in lymphoma, especially involving T-cell lymphomas, viral infections, and liver failure.

Mufakir Qamar Ansari
The University of Toledo, Toledo, USA

High-Sensitivity Detection of Invasive Ductal Carcinoma via Domain-Specific SimCLR Pre-Training

Abstract

Automated detection of Invasive Ductal Carcinoma (IDC) in digital histopathology images remains challenging due to the domain gap between natural image pre-training and tissue-specific features, as well as significant class imbalance in patch-level datasets. We investigate domain-specific self-supervised learning (SSL) using the SimCLR contrastive framework to pre-train a ResNet50 encoder on 277,524 unlabeled 50 × 50-pixel IDC patches from 162 patients, employing a rigorous patient-stratified split (90% train, 5% validation, 5% test) to prevent data leakage. Following pre-training, we fine-tuned the encoder for binary classification with weighted cross-entropy loss to address the 71.6%/28.4% class imbalance. The SimCLR-pretrained model achieved an AUC-ROC of 0.950 and AUC-PR of 0.886 on the held-out test set, improvements of +0.032 and +0.044 over ImageNet transfer learning, while maintaining high sensitivity (Recall 0.932) and a low false-negative rate (47/13,876 patches). t-SNE and UMAP visualizations demonstrate superior class separation in SSL-derived embeddings, and Grad-CAM heatmaps confirm focus on histologically relevant features. These findings underscore the methodological rigor of large-scale, stratified evaluation and highlight the efficacy of domain-specific SSL for robust, interpretable computational pathology.

Biography

Mufakir Qamar Ansari finished his MS at The University of Toledo in computer science and engineering.

Omar TOURE
Hospital Principal de Dakar, Senegal

Biliary Tract Cancer at the Principal Hospital of Dakar: Epidemiological, Clinical, Morphological, and Histological Aspects

Abstract

Introduction:
Cholangiocarcinomas represent the second primary malignant liver tumor after Hepatocellular carcinoma. Epidemiological studies have shown an increase in its incidence. Histological confirmation is sometimes difficult because of their location. It is a tumor whose diagnosis is often delayed and whose prognosis is poor. The aim of our study was to analyze the epidemiological, clinical, morphological, and histological characteristics of patients with cholangiocarcinoma and to determine the associated risk factors.

Patients and Methods:
This is a retrospective study including all patients treated in the gastroenterology department for cholangiocarcinoma between January 2023 and December 2024.

Results:
Twenty-seven patients were included with an average age of 60.25 years (range 27–93 years) and a male-to-female ratio of 2:1. The average duration of symptoms was 3 months (0.5–8 months). Jaundice was the most common presenting symptom (70.37%), followed by pruritus and general health deterioration (62.9% and 62.96% respectively), and abdominal pain in 55.6% of cases. One patient consumed alcohol (3.7%), and four were smokers (14.8%).

Hypertension was found in six patients (22.27%), Hepatitis B in six patients (22.2%), and diabetes in 11.7%. Five patients were overweight, and one patient had Crohn's disease. Three patients had a family history of chronic viral hepatitis B (11.1%), and one patient reported a maternal history of Stomach cancer. Physical examination showed hepatomegaly in six patients (22.2%). Abdominal ultrasound was performed in 37% of patients, Computed Tomography (CT) in 100%, Magnetic Resonance Imaging (MRI) in 33.3%, and Endoscopic Retrograde Cholangiopancreatography in 22.2% of patients. Imaging classified these cholangiocarcinomas as intrahepatic (33.33%), hilar (37.03%), distal (11.1%), Ampulla of Vater adenocarcinoma (7.4%), and Gallbladder cancer (11.11%). Dilation of the intrahepatic bile ducts was observed in 62.96% of patients. Vascular invasion was present in 14.5% of patients and metastases in 63%, including lymph node metastases (57%), liver metastases (22.22%), and lung metastases (7.4%). Peritoneal carcinomatosis was observed in 11.11% of patients. Histology was obtained in fourteen patients, and the type identified was adenocarcinoma. None of the patients underwent genetic analysis of their tumor. Treatment was mainly symptomatic for most patients. Only five patients were referred for surgery, six received palliative chemotherapy, and six underwent endoscopic biliary drainage. Eleven patients died with an average survival of 4.4 months, and the remaining sixteen patients were lost to follow-up.

Conclusion:

Cholangiocarcinomas have a poor prognosis. Only early diagnosis allowing detection of the tumor at a localized stage can improve prognosis and survival. It is necessary to develop molecular biology approaches to detect mutations, especially in cases of cholangiocarcinoma in young patients.

Patrycja Nowak-Sliwinska
University of Geneva, Switzerland

Reprogramming the Tumor Microenvironment: Novel Combination Strategies to Overcome Immune Exclusion

Abstract

The immunosuppressive and immune-excluded tumor microenvironment (TME) of microsatellite-stable (MSS) colorectal cancer (CRC) is a fundamental barrier to immunotherapy efficacy. Here, we directly targeted this niche using optimized drug combinations (ODCs) rationally designed via the Therapeutically Guided Multidrug Optimization platform. We systematically evaluated four low-dose ODCs in murine AKP organoids, complex 3D co-cultures with endothelial and immune components, and immunocompetent syngeneic models.

The lead ODC containing regorafenib, vemurafenib, erlotinib, and selumetinib profoundly remodeled the TME. In co-cultures, it induced a pro-inflammatory endothelial state, marked by significant upregulation of ICAM-1, VCAM-1, and E-selectin. In vivo, ODC suppressed tumor growth comparably to oxaliplatin but with a superior safety profile. Critically, while both agents reduced cancer cell proliferation, immunofluorescence revealed a distinct mechanism: ODC uniquely promoted vascular normalization and fostered an immune-permissive TME, facilitating the recruitment and perivascular positioning of cytotoxic CD8+ T cells. In contrast, oxaliplatin exhibited broader immunosuppressive effects. This TME reprogramming was underpinned by synergistic inhibition of overlapping oncogenic and survival pathways within stromal and tumor compartments, as predicted by computational modeling.

Our findings demonstrate that a rational, low-dose multidrug strategy can directly dismantle the immune-excluded architecture of the MSS CRC TME, offering a

compelling combinatorial approach to unlock immunotherapy responses.

Biography

Patrycja completed her PhD from Jagiellonian University and the Swiss Federal Institute of Technology. She conducted her postdoctoral investigations at the UMC Amsterdam (The Netherlands) and at the University Hospital in Lausanne (Switzerland). She was awarded aprestigious Marie Curie Intra-European Fellowship for Career Development and the ERC Starting grant. She is associete professor and vice-president of the School of Pharmaceutical Sciences at the University of Geneva, Switzerland. She published over 100 scientific publications in high-impact journals and co-authored 4 international patents.

Rihab MELLITI KHALIL
General Hospital of Aix en Provence, France

Immune checkpoint inhibitor–induced sarcoidosis is a rare but increasingly reported adverse event, particularly with anti-PD-1 therapies. We report a case of systemic sarcoidosis in a patient treated with pembrolizumab

Abstract

Case report

A 52-year-old woman with a past medical history of myocardial infarction, type II diabetes, hypertension, hypercholesterolemia and L5–S1 vertebral compression fracture was diagnosed in January 2024 with bilateral invasive ductal carcinomas (NST): Right breast: triple-negative tumor, grade II, Ki-67 40% and Left breast: hormone receptor-positive tumor (ER 40%, PR 100%), HER2-negative, Ki-67 30%. After discussion at the multidisciplinary tumor board, a neoadjuvant chemotherapy regimen combined with pembrolizumab was initiated and completed on June 26, 2024, achieving a complete metabolic response on PET–CT and marked tumor regression on breast MRI. At the time of the last neoadjuvant cycle, the patient developed painless, non-inflammatory subcutaneous nodules on the limbs. PET–CT revealed intense hypermetabolism of bilateral mediastinal and hilar lymph nodes, along with pulmonary lesions suspicious for sarcoidosis. Skin biopsy confirmed non-caseating epithelioid and giant cell granulomas, consistent with pembrolizumab-induced sarcoidosis. Pulmonary, cardiac and ophthalmologic evaluations were normal. The patient underwent bilateral mastectomy, and histopathology showed an RCB-I response. Pembrolizumab was continued in the adjuvant setting (9 doses) without respiratory symptoms. Cutaneous lesions improved with low-dose corticosteroid therapy, discontinued one month after the last dose of immunotherapy. Outcome: One year after discontinuing pembrolizumab, the patient

remains asymptomatic, with complete resolution of mediastino-hilar lymphadenopathy and pulmonary abnormalities, and no recurrence of cutaneous lesions.

Conclusion: PD-1 inhibitor-induced sarcoidosis, although rare, should be recognized by clinicians to avoid misdiagnosis as tumor progression. This case highlights the importance of histological confirmation and multidisciplinary management, allowing continuation of immunotherapy in paucisymptomatic forms.

Biography

I am MELLITI Rihab, a medical oncologist trained in Tunisia and currently practicing in France. I completed my medical degree at the Faculty of medicine of Monastir and specilized in medical oncology through national residency training across leading tunisian oncology centers. I subsequently pursued multiple postgraduate diplomas in

breast cancer, thoracic oncology, oncogenetics, cervicofacial an gynecologic oncology. I am currently a medical oncologist associate practitioner at Aix en Provence general Hospital. I have presented scientific work at the NCCN, ESMO and MASCC congresses and am a member of several international oncology societies.

Tamina, ELIAS-RIZK
Lebanese American University, Lebanon

Breast cancer screening in Lebanon: Understanding knowledge, attitudes barriers. Practices during economic crisis/Covid 19 Pandemics

Abstract

Breast cancer (BC) has been increasing in both prevalence and incidence in Lebanon. Knowing the positive impact mammographic screening has on reducing mortality rates, we sought to investigate the knowledge, attitudes and barriers towards BC screening amongst Lebanese women across all districts. In addition, public health efforts towards breast cancer (BC) prevention have been largely absent from healthcare planning in modern-day Lebanon. Mammography screening campaigns have been present since 2002, but their implementation has been inconsistent in terms of pricing, locations, and the centers involved. In 2020, Lebanon was caught in the whirlwind of the Covid pandemic while facing a brewing economic crisis and a direct hit to the capital's center of commerce. We wanted to evaluate the impact of the complex situation created by these crises on BC screening. We conducted a cross-sectional study with 400 Lebanese women aged 35–75, with no prior or current diagnosis of BC, employing an online questionnaire filled face-to-face with participants to gather sociodemographic data and assess BC history and screening practices. We utilized the Breast Cancer Screening Beliefs Questionnaire (BCSBQ) and Champion Health Belief Model Scale (CHBMS) to evaluate knowledge, attitudes, and barriers. Andwe assessed the BC screening practices of these 400 women.

Findings revealed inadequate attitudes towards general health check-ups (77.5 %) and insufficient BC screening knowledge (56.4 %). Furthermore, 38.5 % encountered obstacles to mammography screening. Education significantly affected BC knowledge.

Interestingly, increased knowledge of BC reduced barriers to mammographic screening. Participants with healthcare connections or background exhibited better attitudes towards health check-ups and encountered fewer screening obstacles. One tenth of participants halted mammography screening during the multifaceted crisis, while more than half of participants had continued or improved their BC screening practices after 2020. Women with an unfavorable attitude towards general health check-ups and single participants were more vulnerable to experience change in their BC screenings. Contrarily, women with relatives affected by BC and those financially stable to cover basic needs and more had higher proclivities to undergo BC screening. Our data highlight the crucial role of education in advocating for early BC screening and the necessity to reevaluate national campaigns, particularly in communication methods, to ensure equitable access to screening across the country. Future campaigns should nurture a culture that promotes general health check-ups, clearly advertised and communicated to the general public, especially in terms of cost and centers involved, while still offering financial support.

Biography

Chief of Breast diagnosis and interventional at LAU Medical Centers, Lebanon since 2011. Earned medical Degree (MD) at the Faculty of Medicine from Saint-Joseph University, Beirut, Lebanon. After residency training in Medical radiology at Hotel Dieu de France Beirut, pursued a specialized training in Radiology in breast and body MR imaging at Henri Mondor CHU- Creteil- Paris12, France, Pierre et Marie Curie University Paris 6 and Descartes Medical Faculty, Paris 5.

Obtained a Master in Biological and Medical Sciences Saint-Joseph University Beirut with certificates of Genetics and molecular bases with M2 in breast cancer diagnosis at Cancer and Metabolism Laboratory Saint-Joseph University.

hold many diplomas and certificates in Clinical Simulation, Healthcare Leadership and Medical Education.

Member of Lebanese and international societies of Radiology/ Breast Imaging. Have given many lectures/co-Organized symposiums in breast cancer.

Involved in many research projects related to Breast Cancer.

Dr. Dilkhush Jahan
National Institute of Preventive and Social Medicine (NIPSOM), Dhaka, Bangladesh

Phase-wise comparison of depression and stigma among tuberculosis patients undergoing treatment in Dhaka, Bangladesh

Abstract

Tuberculosis (TB) remains a significant global health concern with established links to depression and stigma. Both outcomes have been found to vary between treatment phases of TB. This study compared depression and stigma among patients with TB in the intensive and continuation treatment phases in Dhaka, Bangladesh. A cross-sectional comparative study was conducted during August and September 2023 among 111 patients in the intensive phase and 113 in the continuation phase of TB treatment (a total of 224) at directly observed treatment short-course centers. Depression was assessed using the Patient Health Questionnaire-9, and stigma was measured using Van Rie's TB/HIV Stigma Scale. Multivariable logistic regression identified associated factors. The prevalence of depression was 56.2% overall, with no significant difference between the intensive (59.5%) and continuation phases (53.1%). Anticipated stigma was more prevalent (74.6%) than social stigma (37.5%), with neither showing significant phase variation. Pulmonary TB was associated with both social stigma (odds ratio [OR] = 3.27, 95% confidence interval [CI]: 1.69-6.52) and anticipated stigma (OR = 3.29, 95% CI: 1.70-6.59). Living with family increased the odds of experiencing anticipated stigma, while patient counseling demonstrated protective effects. Depression was associated with treatment adherence difficulties (OR = 3.55, 95% CI: 1.75-7.51), persistent TB symptoms (OR = 2.23, 95% CI: 1.04-4.91), and social stigma (OR = 2.06, 95% CI: 1.02-4.22). The high prevalence of depression and persistent stigma throughout treatment highlight the need for continuous mental health support across all

phases. TB care should integrate depression screening, stigma reduction strategies, and enhanced counseling to improve outcomes.

Biography

Dr. Dilkhush Jahan finished her MPH (Epidemiology) from National Institute of Preventive and Social Medicine (NIPSOM), Dhaka, Bangladesh. She is working as Lecturer, Department of Entomology, National Institute of Preventive and Social Medicine (NIPSOM), Dhaka, Bangladesh. She has Published one paper as principal author and two papers as co-author.

Tshepang Motlhaping
School of Biological Sciences, Potchefstroom, South Africa

Genomic insights into Shigella species isolated from small ruminants and manure in the North West Province, South Africa

Abstract

This study investigated Shigella species' antibiotic resistance patterns and genomic characteristics from small ruminants and manure collected in Potchefstroom, North West, South Africa. Whole genome sequencing was used to determine resistome profiles of Shigella flexneri isolates from small ruminants' manure and Shigella boydii from sheep faeces. Comparative genomics was employed on the South African 261 S. flexneri strains available from GenBank, including the sequenced strains in this study, by investigating the serovars, antibiotic resistance genes (ARGs), and plasmid replicon types. The S. flexneri strains could not be assigned to known sequence types, suggesting novel or uncharacterized lineages. S. boydii R7-1A was assigned to sequence type 202 (ST202). Serovar 2A was the most common among South African S. flexneri strains, found in 96% of the 250 compared human-derived isolates. The shared mdf(A) was the most prevalent gene, identified in 99% of 261 S. flexneri genomes, including plasmid replicon types ColRNAI_1 (99%) and IncFII_1 (98%). Both species share a core set of resistance determinants mainly involving β- lactams (ampC 1, ampC, ampH), macrolides (mphB), polymyxins (eptA, pmrF), multidrug efflux pumps (AcrAB-TolC, Mdt, Emr, Kpn families), and regulatory systems (marA, hns, crp, baeRS, evgAS, cpxA, gadX). However, S. boydii possesses additional resistance genes conferring resistance to tetracyclines (tet(A)), phenicols (floR), sulfonamides (sul2), and aminoglycosides (APH(3")-Ib, APH(6)-Id), along with the acrEF efflux pump components (acrE, acrF). In contrast, S. flexneri harboured unique genes linked to

polymyxin resistance (ugd) and regulatory functions (sdiA, gadW) that were absent in S. boydii. These findings highlight Shigella strains' genomic diversity and antimicrobial resistance potential in livestock-associated environments. Moreover, S. boydii highlights the potential risk of multidrug-resistant bacteria in farming and environmental routes.

Biography

Tshepang is a dedicated doctoral (PhD) student in Environmental Sciences at North-West University, specializing in antimicrobial resistance (AMR) and genomic surveillance of Enterobacteriaceae. With advanced expertise in molecular diagnostics, whole-genome sequencing, and bioinformatics, Tshepang contributes to cutting-edge research that bridges science, public health, and policy. Beyond the laboratory, Tshepang serves as a laboratory demonstrator, supporting academic access and fostering knowledge-sharing within the university community. Passionate about zoonotic risk, environmental health, and resistome surveillance, Tshepang aims to lead regional initiatives that inform evidence-based policy and contribute to vaccine development strategies targeting resistant pathogens. Their long-term vision is to produce impactful, ethically grounded research that strengthens AMR control in African livestock systems and beyond.

Kathryn Briggs
University of Southampton, United Kingdom

Local attitudes to scabies mass drug administration programmes in the Northern Region of Ghana: a household survey

Abstract

Scabies is a parasitic disease which results in pruritus and the appearance of a rash on the skin. Scabies is classified as a neglected tropical disease (NTD) but was left out of Ghana's five-year master plan for NTDs for 2021 to 2025. Mass drug administration (MDA) is the World Health Organisation (WHO) recommended control method for regions with a prevalence of scabies that is greater than 10% or it can be used for outbreaks of scabies.

The aims of this study were to: understand the population knowledge and attitudes towards the symptoms and causes of scabies. Describe populations health-seeking behaviour for treating possible scabies. To understand the population's experience of previous, and attitudes towards future, mass drug administrations. This study is a cross-sectional primary household survey done between 5th September 2025 and 9th October 2025. 180 surveys were collected using the 'random-walk' method (as mentioned by UNICEF in field documents) from 4 communities in Karaga district of the Northern region of Ghana, 175 of these 180 responses were later analysed on StataSE and Excel. Of the 175 participants, 96.6% of participants had heard of scabies with 91.4% correctly identifying the transmission of scabies occurring through person-to-person contact. Of those that reported a probable previous infection from scabies, 66.67% sought formal medical care. Almost all (99.4%) participants said they would take part in a mass drug administration for scabies. Study findings show a good population knowledge of scabies and positive attitudes towards previous mass drug administration for diseases such as malaria. People would be willing to take part in an

MDA for scabies as long as they trust those giving out the drug. Hence, the Ghanaian government could utilise pre-existing methods of MDA which have been successful to encourage future uptake of MDA for scabies.

Biography

Kathryn Briggs is a current 3rd year medical student studying at the University of Southampton. Her research interests are in global health, particularly in rural Ghana, West Africa. Specifically, this includes interests in scabies, a skin-related neglected tropical disease. In 2025, she undertook a research project as part of her course, in which she spent 2 months in Ghana (primarily the rural area) collecting data and networking with local health and policy makers.

NDONG MENGOME CHRISTINE
Independent Researcher, Cancer Biology, Gabon

In vitro and in silico evaluation of talinum fruticosum tumor cell co-culture derived molecules as predicted precision biotherapy for inflammatory breast cancer

Abstract

Current cancer therapies face major limitations, including lack of specificity, drug resistance, and systemic side effects. These challenges are particularly pronounced in inflammatory breast cancer (IBC), an aggressive and highly prevalent subtype worldwide. Understanding the metabolic and molecular pathways through which therapeutic agents act is essential for developing more targeted and effective interventions. Aim: This proposed study aims to investigate the autologous molecular modulation of Talinum fruticosum (waterleaf) when co-cultured with patient- derived breast tumor cells, as part of a precision biotherapy development framework. The objective is to validate predicted drug candidates in vitro by integrating plant-based molecular modification with computational drug-target prediction. Methodology: We plan to screen fifty breast cancer related genes from samples obtained from consented participants using proteomic profiling techniques, followed by RT-qPCR to assess the diagnostic and prognostic relevance of candidate targets. T. fruticosum tissue cultures will be established in tumor-cell enriched media to enable plant tissues to acquire potential tumor-specific molecular characteristics. Subsequent analyses including genetic profiling, mass spectrometry, and in silico molecular docking will be performed to evaluate the potential interactions between plant derived compounds and key tumor-associated proteins such as HER2. Through computational modeling, we aim to identify strong mRNA-protein interaction signatures and predict binding affinities that may indicate therapeutic potential. Expected results: The anticipated outcome

is to determine whether tumor-modulated T. fruticosum extracts can yield bioactive derivatives with enhanced tumor-targeting capacity. Conclusion: To our knowledge, this will be the first study to explore T. fruticosum derived molecular conjugates in the context of human tumor biology. This work is expected to support the feasibility of combining plant-based molecular modulation with AI-guided drug design to develop novel, patient-specific therapeutic candidates for aggressive cancers such as IBC.

Biography

Christine Ndong Mengome is a biomedical scientist with a strong background in molecular biology, immunology, and bioinformatics. She studied Biotechnology and completed her Master's degree in Biology in 2024 at Catholic University of Central Africa, School of Health Sciences. Since 2019, she has been part of the Centre de Recherches Médicales de Lambaréné (CERMEL) in Gabon, where she also manages laboratory operations and archives. Christine has contributed to several research projects focused on infection biology, vaccine development, and aim to specialize in precision therapies. Significantly, she played a key role in establishing the production of Necator americanus for Africa's first controlled human hookworm infection study. Passionate about innovation and personalized medicine, Christine is committed to advancing biomedical research and improving health outcomes in sub-Saharan Africa.

Seo Lyn Choi
Sungkyunkwan University, Korea

alcone derivative induces reactive oxygen species- mediated Bax activation and apoptosis in CD133+ lung cancer organoids

Abstract

Backgrounds ung cancer remains a leading cause of cancer-related mortality worldwide primarily due to therapeutic resistance and tumor recurrence. Accumulating evidence indicates that CD133⁺ cancer stem–like cells (CSCs) play a critical role in tumor initiation, maintenance and resistance to chemotherapy. These cells exhibit enhanced survival signaling reduced apoptotic sensitivity and increased tumorigenic potential. Reactive oxygen species (ROS)–dependent redox homeostasis is essential for CSC survival. Disruption of intracellular redox balance can sensitize CSCs to mitochondrial apoptotic signaling particularly through Bax activation. However, effective therapeutic strategies to selectively eliminate CD133⁺ lung cancer stem–like cells remain limited. UR-2, a hydroxylated chalcone derivative, has demonstrated anticancer potential but its molecular mechanism in lung CSCs has not been fully elucidated.

Methods: CD133⁺ and CD133⁻ lung cancer organoids were established and characterized. Proteomic profiling was performed to identify signaling pathways affected by UR-2 treatment. Cell viability and clonogenic assays were conducted to assess growth suppression. Intracellular ROS levels and mitochondrial membrane potential were analyzed to evaluate redox and mitochondrial responses. Western blot analysis was performed to examine death receptor signaling, Bax activation, cytochrome c release and caspase-3 cleavage. Chemoresistance was evaluated using 5-fluorouracil and cisplatin treatment models. In vivo validation was conducted using xenograft

models derived from CD133⁺ organoids..

Results: Proteomic analysis revealed that UR-2 significantly modulated apoptosis-related signaling networks involving FAS, Bax, and ROS-associated pathways. UR-2 selectively suppressed the growth and clonogenic capacity of CD133⁺ lung cancer organoids while exerting minimal effects on CD133⁻ counterparts. Mechanistically, UR-2 induced intracellular ROS accumulation leading to activation of death receptor signaling mitochondrial membrane depolarization, cytochrome c release, enhanced Bax activation and caspase-3–mediated apoptotic cell death. UR-2 effectively overcame chemoresistance to 5-fluorouracil and cisplatin in CD133⁺ organoid models. Consistently in CD133⁺ organoid-derived xenografts UR-2 treatment significantly reduced tumor growth decreased CD133 expression and shifted the BCL-2/Bax ratio toward a pro-apoptotic state.

Conclusion: Our findings demonstrate that UR-2 induces ROS-mediated Bax activation and mitochondrial apoptotic signaling in CD133⁺ lung cancer stem–like cells. By disrupting redox homeostasis and enhancing apoptotic susceptibility, UR-2 selectively targets chemoresistant CSC populations in both organoid and in vivo models. These findings suggest that modulation of ROS–Bax–dependent apoptotic vulnerability represents a promising therapeutic strategy for overcoming lung cancer chemoresistance.

Biography

SeoLyn Choi is an integrated Master's program student in the Department of Meta-BioHealth at Sungkyunkwan University. She is interested in cancer stem-like cells (CSCs) and therapeutic resistance and is currently conducting research in this field. In particular, she explores how changes in gene expression are associated with tumor aggressiveness and metastasis, focusing on CD44⁺ and CD133⁺ CSC populations. She currently utilizes three-dimensional spheroid and organoid models, as well as organoid-derived xenograft models, to analyze CSC-related characteristics and tumor progression.

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The MORC2/CREB Axis Promotes Stemness and Aggressive Phenotypes in CD133+ Hepatocellular Carcinoma Cells

Abstract

Background: Hepatocellular carcinoma (HCC) is a highly heterogeneous malignancy driven in part by populations of cancer stem-like cells (CSCs), which are associated with poor prognosis, metastasis, and resistance to sorafenib. While chromatin remodeling proteins have emerged as key regulators of CSC plasticity, the role of microrchidia family CW-type zinc finger protein 2 (MORC2), a multifunctional epigenetic modulator, in $CD133^+$ HCC remains unclear.

Methods: We investigated the expression and function of MORC2 in HCC using $CD133^+$ spheroid and organoid cultures, CD133-based cell sorting, shRNA-mediated knockdown, and xenograft and metastasis mouse models. Molecular assays, immunohistochemistry, and drug sensitivity analyses were employed to evaluate stemness, EMT, and anti-cancer drug sorafenib response.

Results: MORC2 was overexpressed in HCC tissues and cell lines and positively correlated with CD133 and expression. It was enriched in spheroid cultures and $CD133^+$ cells, where it supported spheroid formation, stemness marker expression (Sox2), and epithelial–mesenchymal transition (EMT) features (Snail, Slug, Vimentin). MORC2 knockdown impaired these CSC-associated traits, significantly reduced invasiveness in vitro, and suppressed tumor growth and lung metastasis in vivo. In $CD133^+$ organoids, MORC2 knockdown reduced proliferation and sensitized cells to sorafenib, with combined treatment showing enhanced suppression of viability and increased apoptosis.

Conclusions: Our findings identify MORC2 as a key regulator of stemness, EMT, and drug resistance in CD133^{+} HCC. MORC2 may serve as both a prognostic biomarker and a therapeutic target to overcome CSC-driven tumor progression and sorafenib resistance in HCC.

Biography

Seohee Park is a Ph.D. student in the Department of MetaBioHealth at Sungkyunkwan University. She earned her Master's degree from the Samsung Advanced Institute for Health Sciences & Technology (SAIHST) at the same university. Her research focuses on the molecular mechanisms of tumor development, specifically investigating the role of the gene MORC2 in the DNA damage response. Her recent work examines how dysregulated MORC2 expression drives oncogenic processes using cancer stem-like cell (CSLC) models. By integrating molecular genetics with oncology, she aims to identify novel therapeutic targets and advance the understanding of cancer progression to improve patient care.


Thank You