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Abstract Book

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Influenza and SARS-CoV-2 co-circulation in Kenya, April 2020 – March 2022

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Biography:
Dr. Daniel Owusu is a Regional Epidemiologist for Africa in the Influenza Division of the Centers for Disease Control and Prevention (CDC). He was an Epidemic Intelligence Service (EIS) Officer, class of 2019, in the same division. Dr. Owusu holds a DrPH degree from East Tennessee State University, MPhil in Public Health from University of Cambridge, and BA in Nursing and Psychology from University of Ghana. He has authored or co-authored 46 peer-reviewed articles in international journals, presented at multiple national and international scientific conferences, and served as a peer reviewer for highly ranked public health journals and scientific conferences.

Background: We aimed to describe influenza and SARS-CoV-2 co-circulation, and assess factors associated with severity of illness. We also describe how the SARS-CoV-2 data from the influenza sentinel surveillance aligned with the universal national SARS-CoV-2 data.

Methods: Data were collected from 8 influenza sentinel surveillance sites in Kenya during April 2020 through Mar 2022. National SARS-CoV-2 surveillance data were obtained from the Ministry of Health. Logistic regression models were used to assess factors associated with severe clinical illness. Severe clinical illness was defined as any of oxygen saturation <90%, in-hospital death, admission to intensive care unit / high dependency unit, mechanical ventilation, or a report of any danger sign (i.e., inability to drink or eat, severe vomiting, grunting, stridor, or unconsciousness in children <5 years).

Results: Among 7,349 patients enrolled from sentinel sites, 76.3% were aged <5 years, and 12.2% had at least one underlying medical condition. We detected any influenza (A or B) in 8.7% (629/7,224), SARS-CoV-2 in 10.7% (768/7,199), and co-infection in 0.9% (63/7,165) of the samples tested. The odds of severe illness among participants with co-infection were similar to those of patients with influenza only and SARS-CoV-2 only. Malnourished patients with co-infection had increased odds of severe illness (aOR:19.6; 95% CI 1.32-290.19). Although the number of samples tested from the sentinel surveillance was only 0.2% of the number tested in the national surveillance data (60/week vs 36,000/week), peak positivity in the sentinel surveillance data aligned with that of the national data.

Conclusion: Influenza co-circulated with SARS-CoV-2 in Kenya, and peaks in SARS-CoV-2 positivity from the influenza sentinel surveillances data were comparable to those of the universal national surveillance. These findings demonstrate the need for all countries to implement or strengthen national influenza sentinel surveillance system as a sustainable platform to monitor respiratory pathogens of public health importance.

Intent and practice of influenza vaccination among health professionals in Côte d'Ivoire from 2018 to 2021.

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Biography:

Dr Daouda COULIBALY is an Epidemiologist and specialist in public health. He is also Research Officer in health sciences.

He is the Deputy Director in charge of epidemiological surveillance, general hygiene of studies and research at the National Institute of Public Hygiene (INHP). He is the coordinator of the influenza surveillance project.

He has extensive experience in managing epidemics and other public health emergencies. In particular, he coordinated the plan to fight the Ebola virus disease epidemic in 2014 and is currently contributing to the implementation of the health response plan to COVID-19 in Côte d'Ivoire.

BACKGROUND

The WHO prioritizes health workers (HW) for influenza vaccination due to the risk of healthcare associated transmission of influenza virus infection. Influenza virus circulates year-round in Côte d'Ivoire, with waves of varying intensity. Health worker vaccination was piloted in Cote d’Ivoire during 2019-2021 in collaboration with the Partnership for Influenza Vaccine Introduction. Before introducing vaccines, we conducted a survey of HWs to assess influenza vaccine acceptability.

METHODS

To determine vaccination intent among HWs, we conducted a cross-sectional survey of 472 HWs in the city of Abidjan in April 2018. HWs in selected public and private health facilities were interviewed about their knowledge and acceptance of influenza vaccines. Following our survey, vaccination campaigns offering free-of-charge vaccination for HWs were organized in Abidjan 2019 and 2020 and expanded nationwide in 2021. We compared the intent to receive vaccines observed in our survey with the vaccine coverage achieved during these campaigns.

RESULTS

HW intent to be vaccinated against influenza was 74% (351/472), or 84% (398/472) if the vaccine was free, despite only half (48% (226/472)) believing that influenza vaccine helps protect against influenza illness. Intent to be vaccinated was higher among midwives (89%) and nurses (87%) than among doctors (75%). We found that vaccine coverage during campaigns held in Abidjan in 2019 and 2020 was higher than intent observed in our survey (97% both years vs. 84%), while the national campaign in 2021 yielded coverage equal with intent (84%) from our survey.

CONCLUSION

The high intent (84%) to be vaccinated against influenza by HWs was reflected in high vaccine coverage during three consecutive pilot vaccination campaigns. These results indicate high

acceptance of influenza vaccines by HWs and could shape policies by Ivorian health authorities to support a national seasonal influenza vaccination program for HWs.

KEYWORDS: Influenza, vaccination, acceptability

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Pre-season antibody titers and protection against influenza infection in a South African community cohort (PHIRST), 2016-2017

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Biography:

Dr Nicole Wolter is a Principal Medical Scientist at the National Institute for Communicable Diseases (NICD), South Africa. She received her PhD in Molecular Microbiology in 2007 from the University of the Witwatersrand, and an MSc in Epidemiology from the London School of Hygiene and Tropical Medicine (LSHTM) in 2019. Dr Wolter is an NRF-rated scientist, and has more than 100 publications in peer-reviewed journals. As the director of the National Influenza Centre, she leads a team of scientists in surveillance and research focused on the epidemiology, advanced diagnostics and molecular characterisation of pathogens causing respiratory disease in South Africa.

Background

In a community cohort study, we determined whether higher pre-season influenza antibody titers were protective against subsequent infection.

Methods

Approximately 50 randomly-selected households were enrolled each in Klerksdorp and Agincourt in 2016 and 2017. Participants were followed for 6 (2016) and 10 (2017) months. Nasopharyngeal swabs were collected twice-weekly and tested for influenza by PCR. Serum specimens were collected at beginning and end of follow-up, with ≥4-fold increase in hemagglutination inhibition (HAI) titer considered indicative of infection. A multivariable mixed-effects hierarchical logistic regression model, controlling for clustering by site and household, was used to assess the association between pre-season titers (reference group <40) and subsequent influenza infection, adjusting for HIV and age.

Results

Of 1100 individuals enrolled, 850 (77%) had pre- and post-season serology results. Serology attack rate was 34% (143/420) in 2016 and 37% (161/430) in 2017, while PCR attack rate was 30% (125/420) in 2016 and 37% (157/430) in 2017. Among individuals with pre-season titers, 10% (96/937), 17% (163/937), 15% (141/937) and 10% (97/937) had A(H1N1)pdm09, A(H3N2), B/Victoria or B/Yamagata subsequent infection respectively. Individuals with pre-season A(H1N1)pdm09 titers of 40-59 (adjusted odds ratio (aOR) 0.37, 95% confidence interval (CI) 0.16-0.85) and ≥60 (aOR 0.09, 95%CI 0.04-0.21) were less likely to be infected with A(H1N1)pdm09. Individuals with pre-season A(H3N2) titers of 40-59 (aOR 0.29, 95%CI 0.14-0.62) and ≥60 (aOR 0.33, 95%CI 0.19-0.56) were less likely to be infected with A(H3N2). Similar results were observed for B/Victoria (40-59: aOR 0.33, 95%CI 0.17-0.64 and ≥60: aOR 0.35, 95%CI 0.19-0.65) and B/Yamagata (40-59: aOR 0.50, 95%CI 0.24-1.01 and ≥60: aOR 0.21, 95%CI 0.10-0.44).

Conclusion

Serology showed higher infection attack rates than PCR. High pre-season titers protected against infection with the matching influenza subtypes for influenza A and B. This highlights the potential of prior immunity to reduce the risk of infection.

“Respiratory Syncytial Virus and Vaccination in Kenya; What are the Healthcare Workers’ Preference?”

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Biography:

Victor Opere works with the Influenza program at KEMRI -CGHR in collaboration with US CDC. Victor works as a Research Scientist, trained in Project management (University of Washington) and Social Science from Kenyatta University.

Background

RSV is a major cause of childhood pneumonia, especially among infants aged below 6 months who bare the biggest burden of RSV disease. Little is known about healthcare workers’ (HCWs) knowledge and attitudes around RSV and vaccination. We investigated general and RSV-specific knowledge and attitudes of HCWs towards RSV and vaccination in two Kenyan counties.

Methods

Between September-October 2021, we conducted a cross-sectional survey among HCWs in eight health facilities (Siaya-5, Nairobi-3) and Ministry of Health (MoH) officials. We enrolled HCWs delivering services directly to mothers at the maternal and child health departments and MoH officials in-charge of vaccine distribution, policy and management.

Results

We interviewed 104 HCWs (from facilities-94 and officials-10; Siaya-60, Nairobi-44); 65 (62.5%) were nurses and 49 (47.1%) had 5-10 years of experience. In general, most participants would recommend maternal vaccination to protect the mother 91 (88.4%) and baby 76 (73.8), a single-dose vaccine schedule 62 (59.6%) for maximal compliance 38/62 (61.3%) and single-dose/device vaccines 50/86 (58.1%) to prevent wastage and contamination. Of the 104, only 41 (39.4%) knew about RSV and 38/41 (92.7%) reported that pregnant women should be vaccinated against RSV. Nearly all (39/41) respondents were not aware of RSV vaccination products in the market but would recommend the vaccine if available.

Conclusion

There is a huge gap in knowledge around RSV and RSV vaccination among Kenyan HCWs. Most HCWs would recommend maternal vaccination, preferring single-dose scheduling and single-dose vials/devices should the vaccines be available. We recommend creation of RSV awareness among the HCWs.

Estimates of the national burden of respiratory syncytial virus in Kenyan children aged under 5 years, 2010–2018

Mr Bryan Nyawanda[1], Mr. Nickson Murunga[2], Ms. Nancy A. Otieno[1], Dr. Godfrey Bigogo[1], Dr. Joyce U. Nyiro[2], Dr. Elisabeth Vodicka[3], Dr. Marc Bulterys[4], Prof. D. James Nokes[2], Dr. Patrick K. Munywoki[4], Dr. Gideon O. Emukule[4]
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Biography:
Bryan Nyawanda currently works with the Influenza program at KEMRI-CGHR in collaboration with the US CDC. Bryan is a biostatistician trained in Bayesian and frequentist methods with interests in statistics, disease modelling & epidemiology. Bryan does research on respiratory pathogens, malaria and climate change. He holds a bachelor's degree in statistics, Master's degree in epidemiology and biostatistics and currently a PhD student (epidemiology) at the Swiss TPH and the University of Basel (Switzerland).

Respiratory syncytial virus (RSV) is among the leading childhood causes of viral pneumonia worldwide. Establishing RSV-associated morbidity and mortality is important in informing the development, delivery strategies and evaluation of interventions. Using data collected during 2010-2018, we estimated age-specific rates of acute respiratory illness (ARI), severe acute respiratory illness (SARI - defined as hospitalization with cough or difficulty breathing with onset within the past 10 days) and SARI-associated deaths. We extrapolated the rates from base regions to other regions of Kenya while adjusting for risk factors of ARI and healthcare seeking behaviour, and finally applied the proportions of RSV positive cases identified from various study facilities to the rates to obtain regional age-specific rates of RSV associated outpatient and non-medically attended ARI, and hospitalized SARI and severe ARI that was not hospitalized (non-hospitalized SARI). We applied age-specific RSV case fatality ratios to SARI to obtain estimates of RSV-associated in- and out-of-hospital deaths. Among Kenyan children aged <5 years, the estimated annual incidence of outpatient and non-medically attended RSV-associated ARI was 206 (95% Credible Interval, CI; 186-229) and 226 (95% CI; 204-252) per 1,000 children, respectively. The estimated annual rates of hospitalized and non-hospitalized RSV-associated SARI were 349 (95% CI; 303-404) and 1,077 (95% CI; 934-1,247) per 100,000 children respectively. The estimated annual number of in- and out-of-hospital deaths associated with RSV infection in Kenya were 539 (95% CI; 420-779) and 1,921 (95% CI; 1,495-2,774), respectively. Children aged <6 months had the highest burden of RSV associated severe disease; 2,075 (95% CI; 1,818-2,394) and 44 (95% CI 25-71) cases per 100,000 children for hospitalized SARI and in-hospital deaths, respectively. Our findings suggest a substantial disease burden due to RSV infection, particularly among younger children. Prioritizing development and use of maternal vaccines and affordable long-lasting monoclonal antibodies could help reduce this burden.

MIRA: Interactive Dashboard for Influenza Genome Assembly and Curation

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Biography:
Dr. Rambo-Martin leads the Bioinformatics Activity in the Virology, Surveillance and Diagnosis Branch. He focuses on bioinformatic tool development to facilitate the generation, evaluation and sharing of respiratory virus' genome sequences. In these efforts he collaborates with the WHO to provide bioinformatics training to partner countries worldwide.

The US Centers for Disease Control and Prevention's Influenza Division relies on an internally developed product to generate high quality consensus genome sequences from Next Generation Sequencing data called the Iterative Refinement Meta Assembler (IRMA). IRMA distinguishes itself from other read-mapping assemblers by first selecting the seed reference from composite references representing the breadth of influenza subtypes and then by performing iterative mapping and reference editing.

IRMA is operated through a command line interface (CLI) which is a barrier to its use for laboratories without bioinformatics staff. MIRA has been developed to address this challenge by providing a graphical user interface (GUI) within a web browser to control running genome assembly, presenting automatically applied quality control criteria and aggregating IRMA's most relevant outputs into a small number of files including fastas ready for upload to public repositories.

MIRA's GUI is written in python with Plotly's Dash library. Through the GUI, users define their samplesheet, launch the assembly and QC automation and evaluate the results through interactive figures. The backend process relies on Snakemake orchestration of assembly, annotation and quality control for which parameters are defined in configuration files, managed by the developers. MIRA can be rapidly deployed on any operating system through a single Docker-compose command which installs and builds the multiple containers on which it relies. As more jurisdictions around the world adopt NGS pipelines to both contribute to and directly benefit from pathogen genetic surveillance, as does the need for targeted bioinformatics solutions. MIRA addresses the needs of the global influenza community in assuring that high quality consensus genomes from a pipeline validated on tens of thousands of viral genomes are generated.

Feasibility of assessing influenza vaccine efficacy and correlates of protection against infection and disease among children aged 6-23 months in South Africa

Mrs Jackie Kleynhans[1,2], Dr Mignon du Plessis[1,3], Prof Neil Martinson[4,5,6], Dr Jocelyn Moyes[1], Dr Sibongile Walaza[1,2], Dr Nicole Wolter[1,3], Mr Mvuyo Makhasi[1], Mrs Fahima Moosa[1,3], Dr Sarah Spenser[7], Dr Myrna Charles[7], Dr Aaron Samuels[7,8], Dr Stefano Tempia[8,10], Dr Tumelo Moloantoa[4], Sr Bekiwe Ncwana[4], Sr Louisa Phalatse[4], Mrs Amelia Buys[1], Dr Alica Fry[7], Dr Eduardo Azziz Baumgartner[7], Prof Anne von Gottberg[1,3], Prof Cheryl Cohen[1,2]
[1]Centre for Respiratory Disease and Meningitis, National Institute for Communicable Diseases, [2]School of Public Health, Faculty of Health Sciences, University of the Witwatersrand, [3]School of Pathology, Faculty of Health Sciences, University of the Witwatersrand, [4]Perinatal HIV Research Unit, MRC Soweto Matlosana Collaborating Centre for HIV/AIDS and TB, University of the Witwatersrand, [5]DST/NRF Centre of Excellence for Biomedical Tuberculosis Research, University of the Witwatersrand, [6]Johns Hopkins University Center for TB Research, [7]Influenza Program, Centers for Disease Control and Prevention, [8]Influenza Program, Centers for Disease Control and Prevention, [9]Coronavirus and Other Respiratory Viruses Division (proposed), Centers for Disease Control and Prevention, [10]MassGenics

Biography:

Jackie joined the Centre for Respiratory Diseases and Meningitis at the National Institute for Communicable Diseases (NICD) as an epidemiologist in 2018 where she supports the development and implementation of epidemiological studies. Her PhD focused on the burden and household transmission of SARS-CoV-2, and how social contact patterns influence the transmission of SARS-CoV-2. Her primary research interests include the epidemiology of respiratory diseases like influenza and COVID-19, vaccine impact studies, contact patterns in the context of disease transmission, and modelling of infectious disease transmission dynamics.

Background

Determining whether influenza vaccination prevents infection, attenuates illness, or both is important for modelling influenza vaccine effectiveness. We estimated influenza infection attack rate and assessed symptom ascertainment methodologies to inform future vaccine trials.

Methods

We conducted a prospective cohort study, enrolling children aged 6-23 months. From May through October 2022, we ascertained symptoms and temperature, measured by nurses twice weekly at home, and daily by caregivers using electronic symptom diaries. Mid-turbinate nasal swabs were collected thrice weekly (two by study nurse, one by caregiver) irrespective of symptoms and subjected to influenza rRT-PCR testing.

Results

Of 230 healthy screened children, 93 were enrolled and 87 (94%) completed six months follow-up. 95% (4245/4476) of scheduled nurse and 90% (2045/2276) of caregiver swabs were collected. PCR-confirmed influenza infection attack rate was 65% (60/93) for ≥1 infection. RNase P human DNA marker (quality proxy) was present in 99% (2032/2045) of caregiver-collected swabs, through which 5 additional episodes were identified. Median infection duration was 7 days (interquartile range 4-9). Of 73 infection episodes, 55 (75%) had ≥1 symptom, 37 (51%) had fever (measured and/or reported), and 29 (40%) had fever and cough. 67% (9245/13768) of daily symptom diaries were completed. Caregiver's recording of reported and measured fever were 19% (25/73, 34%) and 11% (15/73, 21%) higher than nurse-reported (11/73, 15%) and -measured fevers (7/73, 10%) by episode, respectively.

Conclusions

Despite an intensive follow-up schedule, we successfully retained 94% of enrolled children for 6-months and achieved >90% swab collection compliance. The influenza attack rate in these young children was high (65%) and most episodes (75%) were associated with ≥1 reported symptom. Caregivers collected high quality swabs similar to study nurses and diary completion added >10% of symptom data. This platform could be suitable for future vaccine efficacy trials against infection and illness in children.

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Implementation of integrated surveillance for influenza and other respiratory pathogens in Somalia; September 2021-March 2023

Dr Mutaawe Lubogo[1], Miss Sahra Mohamed
[1]Emergency Program of World Health Organization

Biography:
Dr. Mutaawe is a medical epidemiologist with 10 years' experience in working with the Emergency Program of the World Health Organization in complex emergency countries. His area of interest is prevention and control of emerging respiratory pathogens in complex humanitarian settings. He has experience in establishing Early Warning Alert and Response surveillance systems for complex emergencies.

Background
Following COVID-19 outbreak in Somalia in 2020, MOH adopted a strategy for integrated surveillance for influenza and other respiratory pathogens based at four sentinel sites. The sentinel sites are supported by two public health laboratories in two states. We describe the epidemiologic characteristics of confirmed cases of influenza and other respiratory pathogens from the four sentinel sites for the period September 2021 to March 2023.

Methodology
We extracted epidemiological and virologic data for Influenza-like illnesses (ILI) and severe acute respiratory illnesses (SARI) from the EMFLU online reporting system. Positivity rates, gender and age disaggregation were calculated for each type of influenza and other respiratory pathogens.

Results
A total of 3070 ILI samples were tested out of which 305 were positive representing a positivity rate of 9.9% (1.9% for COVID-19, 3.9% for Influenza A, 3.8% for Influenza B and 0.2% for RSV). A total of 259 SARI samples were tested out of which 22 were positive representing a positivity rate of 10.5% (0% for COVID-19, 8.1% for Influenza A, 0.4% for Influenza B and 0% for RSV). Overall, positivity rate was 2.8% for Influenza B (Victoria lineage), 1.8% for Influenza A H1N1(pdm009), 1.7% for COVID-19, 1.4% for Influenza A (H3N2), 1% for Influenza A (not sub-typed), 0.7% for Influenza B (not sub-typed) and 0.2% for RSV. There is no difference in positivity rate by gender. 30% of the positive cases were in the age range of 16-50 years. 27% of the positive cases were in the age range of less than or equal to 2 years. 75% of the positive case were from Banadir.

Conclusion
The current epidemiologic and virologic data shows circulation of COVID-19, RSV and multiple sub-types of Influenza A and Influenza B. There is need to scale up influenza surveillance to additional sentinel sites in new states.

Circulation of influenza virus before and during the COVID-19 pandemics in Cameroon: 2019-2022

Dr Chavely Gwladys Monamele[1,2], Dr Serge Alain Sadeuh-Mba[1], Mrs Pauliana Vanessa Ilouga[1], M Moïse Henri Moumbeket Yifomnjou[1], M Loique Landry Messanga Essengue[1], M Aristide Njifon Mounchili[1], Dr Estelle Longla Madaha[1], M Ripa Njankouo Mohamadou[1], Dr Paul Alain Ngoupo Tagnouokam[1], Dr Jules Brice Mbougua Tchatchueng[1], Dr Mathurin Cyrille Tejiokem[1], Dr Ronald Perraut[3], Dr Sara Eyangoh[1], Dr Richard Njouom[1]
[1]Centre Pasteur Cameroon, [2]University of Buea, [3]Garoua Annex, Centre Pasteur of Cameroon

Biography:

As an infectious diseases' specialist, I am interested in understanding the interaction between pathogens and hosts as well as host, pathogen or external factors that may explain this relationship. It is to achieve this ultimate goal that my prior research experience has focused. In my past research experience, I have worked on respiratory pathogens including influenza virus and their geome characterization. This conference is an opportunity to share ideas and network with other scientists in the field.

Introduction: The advent of the COVID-19 pandemics has resulted in influenza sentinel surveillance systems being leveraged to integrate severe acute respiratory syndrome–corona virus 2 (SARS-CoV-2) testing. This study gives a report of one year of influenza surveillance before the COVID-19 pandemic (2019) and three years (2020-2022) of integrated influenza and SARS-CoV-2 surveillance in Cameroon.

Methods: As the National Influenza Centre, the Centre Pasteur Cameroon received specimens from sentinel sites located in all regions of the country for influenza and SARS-CoV-2 virus testing. Respiratory specimen consisted of nasopharyngeal swabs collected from persons with influenza-like illness or severe acute respiratory illness. Molecular assays were used to detect the presence of both viruses based on standard procedures.

Results: The overall virus detection rate during the study period was 21.6%. Influenza viruses alone accounted for about 92% of all cases dominated by A(H3N2) at 33.7%, and A(H1N1)pdm09 at 31.3%. One case of influenza and SARS-CoV-2 co-infection was detected (0.1%). Highest detection rates of influenza viruses and SARS-CoV-2 were observed in the years 2019 (30.3%) and 2022 (25.4%), respectively. Significantly higher influenza positivity rates were observed in the 2-4- and 5-14-years age groups (OR: 1.7; P-value <0.001). Meanwhile, for SARS-CoV-2, all age groups above 15 years were associated with increased frequency of infection (OR: 2.1-4.3; P-value <0.05). We observed no distinct seasonal pattern of influenza virus during the pandemics period.

Conclusion: The COVID-19 pandemic has significantly affected the influenza surveillance system by altering the seasonality of the latter and reducing its detection rates.

Partial Spike gene sequencing for the identification of SARS-CoV-2 variants circulating in Cameroon in 2021

Dr Chavely Gwladys Monamele[1], Dr Serge Alain Sadeuh-Mba[1], Mrs Pauliana Vanessa Ilouga[1], M Moïse Henri Moumbeket Yifomnjou[1], M Loique Landry Messanga Essengue[1], M Aristide Njifon Mounchili[1], Dr Estelle Longla Madaha[1], M Ripa Njankouo Mohamadou[1], Dr Paul Alain Ngoupo Tagnouokam[1], Dr Jules Brice Mbougua Tchatchueng[1], Dr Mathurin Cyrille Tejiokem[1], Dr Ronald Perraut[3], Dr Sara Eyangoh[1], Dr Richard Njouom[1]

[1]Centre Pasteur Cameroon, [2]University of Buea, [3]Garoua Annex, Centre Pasteur of Cameroon

Biography:

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Introduction: Global monitoring of SARS-CoV-2 genetic sequences and associated metadata is essential to the COVID-19 response. The Sanger's partial genome sequencing technique was used in Cameroon to monitor circulating variants of SARS-CoV-2.

Methods: Between January 2021 and December 2021, nasopharyngeal specimen was collected from persons suspected of SARS-CoV-2 following the National guidelines. All specimens with threshold cycles (Ct) below 30 after amplification were eligible for sequencing of the partial S gene of SARS-CoV-2 using Sanger sequencing method. Sequences were uploaded into Nextclade (https://clades.nextstrain.org/) to classify them into Pango lineages and WHO clades. Phylogenetic analyses of sequences generated was performed with respect to reference sequences in MEGA version 6.0.

Results: During the study period, 1481 RT-PCR SARS-CoV-2 positive samples were selected for partial sequencing of the S gene of SARS-CoV-2. Amongst these, 878 yielded good sequencing products. There were 647 unassigned variants (73.7%) and 231 probable variants (26.3%). The term 'probable variants' is used here as the full S gene sequence was not performed. Variants were mainly represented by Delta (70.6%), Alpha (15.6%), Omicron (7.4%), Beta (3.5%), Mu (1.7%) and Gamma (0.4%). Phylogenetic analysis of the variants with reference strains confirmed that all prior and current VOCs clustered with their respective reference sequences.

Conclusion: The surveillance strategy implemented in Cameroon, based on partial sequencing of the Spike gene, enabled the identification and distribution of major circulating variants, and contributed to implementing public health measures to control disease spread in the country.

Use of antigen-rapid diagnostic test for detection of COVID-19 cases in university settings in Cameroon

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Biography:

As an infectious diseases' specialist, I am interested in understanding the interaction between pathogens and hosts as well as host, pathogen or external factors that may explain this relationship. It is to achieve this goal that my prior research experience has focused. In my past research experience, I have worked on respiratory pathogens including influenza virus and their genome characterization. This conference is an opportunity to share ideas and network with other scientists in the field.

Background: Robust testing strategies are an essential aspect of preparedness and response to the COVID-19 pandemic. In 2022, most regions were yet to attain the WHO recommended 10 tests/10000 population in Cameroon. The study aimed to scale-up national testing capacity for SARS-CoV-2 by targeting the university setting; and to assess the knowledge, attitude, and practice of this population with regards to COVID-19 infection.

Methods: Six Universities participated in this study from April to November 2022 located in Buea, Douala, Dschang, Maroua, Ngaoundere and Yaounde. Nasopharyngeal swabs were collected from participants and screened for COVID-19 using Ag-RDTs. For all positive cases, high risk contacts were tested as well. A questionnaire was administered to assess the knowledge, attitude, and practice of participants with respect to COVID-19.

Results: Overall, 7006 participants were recruited and 54 (0.8%) were positive for SARS-CoV-2. Regarding close contacts, three out of 61 (4.7%) tested positive. University of Maroua was the only site that had satisfactory testing capacity, achieving the study target of 30 tests/10.000 in 94.1% of weeks. Knowledge of COVID-19 was moderate-to-good among the participants (≥50%). However, about 28% were not sure of the effectiveness of the COVID-19 vaccine; 36% admitted the lack of restrictions on entry into campus without mask and non-respect of social distancing on campus (42.7%). These factors could favor the spread of SARS-CoV-2 in university settings.

Conclusion: The SARS-CoV-2 positivity rate in the university setting was low. Sensitization should be performed in university settings and other training establishment to increase knowledge on SARS-CoV-2.

Viral etiologies, clinical profiles, and association with outcomes of hospitalized children with severe acute respiratory infections: A multicenter study in three Egyptian governorates, November 2022.

Dr Ola Deghedy[1], Dr Manal Fahim[2], Dr Wael H. Roshdy[3], Dr Mohamed K. Khalifa[4], Dr Rabeh El Shesheny[5], Dr Ahmed Kandeil[6], Dr Amel Naguib[7], Dr Salma Afifi[8], Dr Amira Mohsen[9], Dr Amr Kandeel[10], Dr Khaled abdelghaffar[11]

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Biography:

My name is Ola Deghedy. I currently work as the National Focal Point for Influenza and other Respiratory illnesses at the General Department of Epidemiology and Surveillance, Ministry of Health and Population, Egypt. I have a special interest in the surveillance of respiratory infections such as Influenza, COVID-19, and RSV. I have published many Manuscripts in peer-reviewed journals during the last two years.

Background: In late 2022, severe acute respiratory infections (ARI) surveillance reported abrupt increase in non-COVID-19 infections among children after three years of drastic reductions. Signals of increased absenteeism due to ARI among primary and preparatory school children were detected by Event-Based Surveillance. We conducted a hospital-based survey of children who were admitted with ARI to identify the causative pathogen(s) and estimate the burden of infection.

Methods: A survey was conducted among children <16 years in 21 referral hospitals in the three governorates with the highest ARI rates. Patients' demographics, clinical symptoms, and severity were collected from medical records using line list. Patients were swabbed and tested for a panel of 33 respiratory pathogens by RT-PCR at the Central Laboratory in Cairo. Descriptive data analysis was performed for demographic data. Patients' characteristics were compared by causative agents' clinical picture and severity using Chi2 with a $p<0.05$ significance.

Results: Overall, 317 patients were enrolled, 58.3% were ≤1 year of age, 61.5% were males. Of 229 (72.7%) of positively tested patients, viruses caused 92.1% including RSV 63.8%, Rhinovirus 10.0%, Influenza 9.2%, Adenovirus 5.2%, and 1.3% co-infected with two viruses. Bacteria caused 3.5% of cases and 4.4% had mixed viral-bacterial infections. RSV and Rhinovirus had more severe disease courses and outcomes than Adenovirus and Influenza. ICU admission and deaths were significantly higher among patients with mixed infections compared to viral or bacterial infection (60% and 20% vs 31.8% and 1.9% vs 12.5% and 12.5%, $p <0.001$).

Conclusions: Viruses particularly RSV are the leading cause of SARI causing significant health problems among children <16 years in Egypt. Bacterial on top of viral infection can worsen disease courses and outcomes. Studies are required to estimate the ARI burden accurately among Egyptian children and a comprehensive approach tailored to Egypt is necessary to reduce the ARIs burden.

Viral co-infection with human respiratory syncytial virus in suspected acute and severe respiratory tract infections during COVID-19 pandemic in Yaoundé, Cameroon, 2020–2021

Mr Moïse Henri Moumbeket Yifomnjou[1,2], Dr Gwladys Chavely Monamele[1], Mr Mohamadou Njankouo-Ripa[1], Dr Abdou Fatawou Modiyinji[1], Dr Paul Alain Ngoupo[1], Pr Onana Boyomo[2], Pr Richard Njouom[1]
[1]Centre Pasteur of Cameroon, [2]Laboratory of Microbiology, University of Yaounde I

Biography:
I am PhD student in microbiology, medical microbiology option. Motivated, enthusiastic and hardworking, i am doing my research work at Centre Pasteur du Cameroun. I have strong communication, observation and integration, interpersonal and project management skills. I have acquired relevant academic and technical knowledge in microbiology, clinical biology, molecular biology and next generation sequencing. I have acquired expertise in virological diagnostic techniques, mainly for respiratory viruses, as well next generation sequencing methods and in analysis and post-sequencing results interpretation. My research goal is to contribute effectively to fight against infectious diseases which are one major health burdens in my country.

Background: Acute lower respiratory tract infections (ALRIs) are one one of the leading causes of morbidity and mortality among people of all ages worldwide, particularly in low- and middle-income countries (LMICs). The purpose of this study was to determine epidemiological characteristics of respiratory viruses in acute respiratory infection (ARI) patients during the COVID-19 pandemic in Yaoundé, Cameroon.

Methods: Patients were monitored for respiratory symptoms as part of the surveillance of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) and other respiratory viral infections. Patients of all ages with respiratory symptoms less than 5 days were considered. Sociodemographic and clinical data as well as nasopharyngeal samples was collected from patients. Nasopharyngeal samples were tested for SARS-CoV-2, influenza, and respiratory syncytial virus (RSV) using real-time reversetranscription polymerase chain reaction methods. Virus distribution and demographic data were analyzed with R version 2.15.1.

Results: From July 2020 to October 2021, 1120 patients were included. The overall viral detection rate was 32.5%, including 9.5% for RSV, 12.6% for influenza virus and 12.8% for SARS-CoV-2. Co-infections were detected in 6.9% of positive cases. While RSV and influenza virus showed seasonal trends, SARS-CoV-2 was detected throughout the study period.

Conclusion: We found that during COVID-19 pandemic, respiratory viruses play an important role in etiology of influenza-like illness in Cameroon, and this observation was true for patients of all ages.

Co-circulation of Influenza virus and Respiratory Syncytial Virus during the peak of covid19 (2019-2021)

Ms Nakaseegu Joweria[1]
[1]Uganda Virus Research Institute

Biography:

My name is Joweria Nakaseegu. A laboratory Technologist at Uganda Virus Research Institute. I am currently pursuing a Maters Degree in Biomedical Laboratory Science and Management.

I have a passion of being a well known researcher in the future.

Co-circulation of Influenza virus and Respiratory Syncytial Virus during the peak of covid-19 (2019-2021)

Background. Influenza is an important respiratory virus, and its active surveillance is key in Uganda. Additionally, recent literature has indicated raising circulation of RSV in children. The co-circulation of Influenza and Respiratory syncytial virus may rise a concern on the severity of respiratory disease. Since these viruses commonly present with similar symptoms, timely diagnosis for appropriate response is important. To this effect children below 2 years from two sentinel sites were tested for Influenza and RSV during the peak of COVID-19 at the Uganda Virus Research Institute.

Methods. Nasopharyngeal and oral pharyngeal samples were collected from symptomatic children below 2 years. Samples were extracted using the Qiagen kit and run on Reverse Transcriptase-PCR. Samples with a Ct value of less or equal to 36 were considered positive for Influenza. Furthermore, samples with Ct values less or equal to 40 were considered positive for RSV.
Results: From Tororo and Fort portal, a total of 171 samples were tested, 11% (18) tested positive for RSV A, 4% (7) RSV B, 1.75% (3) Influenza B and none tested positive for Influenza A.

Conclusion.
Integrated systems for constant and aggressive surveillance of respiratory viruses' circulation are essential to understand how they might affect morbidity, mortality and resource demand in the healthcare system during any pandemic.

Multiple SARS-CoV-2 variants Circulating in Uganda between June 2020 and February 2023

Mrs Jocelyn Kiconco[1], Mr. John Kayiwa[1], Ms Charity Nassuna[1], Ms Gladys Kiggundu[1], Ms Sophia Mulei[1], Ms Joweria Nakaseggu[1], Ms Esther Amwine[1], Mr. Nicholas Owor[1], Professor Julius Lutwama[1], Professor Pontiano Kaleebu[1]
[1]Uganda Virus Research Institute

Biography:
I work in the Department of Arbovirology Emerging and Re-Emerging Infectious Disease at Uganda Virus Research Institute (UVRI). I am directly involved in doing laboratory research and have played a great role in testing for COVID-19 in Uganda. In the past 16 years that I have acquired excellent skills and knowledge of Molecular technology and virology. Currently I have enrolled as a PhD student in Makerere University where I am investigating Viral Respiratory Co-infections and associations with SARS-CoV2 Epidemiology in Uganda. I also hold a Masters in Public Health and a Bachelors in Science(Majoring in Biochemistry).

Background
Viruses like SARS-CoV-2 continuously evolve as changes in the genetic code (caused by genetic mutations or viral recombination) occur during replication of the genome. SARS-CoV-2 has consistently mutated over the course of the pandemic, resulting in variants that are different from the original SARS-CoV-2 virus.

Methods
Over 300 genome sequences of SARS-CoV-2 strains circulating in Uganda between June 2020 and February 2023 have been analyzed by the Department of Arbovirology, UVRI. Viral RNA was extracted from RT-PCR confirmed COVID-19 cases, followed by sequencing of samples with CTs< 30 using iSeq Illumina platform and analyzed using EDGE COVID-19 pipeline. All the lineage and clade classifications were done using both PANGOLIN (Phylogenetic Assignment of Named Global Outbreak LINeages) and Nextclade software.

Results
Our analyses revealed that the variants in Uganda include Delta (B.1.617.2 first identified in India), Eta (B.1.525), Beta (B.1.351 from South Africa), Alpha (B.1.117 identified in the UK), the local strain, which identified as B.1.617 and Omicron BA.1 . Delta (B.1.617.2) dominated beginning June 2021 through July 2021. In January 2022 to date, Several Omicron sublineage(BA.1, BA.1.1, BA.1.1.4, BA.1.17, B.1.1.529, BA.4.1, BA.2.36, BA 5.2.1 e.t.c) were circulating in Uganda and they are Variants Being Monitored(VBM). In December 2022 to February 2023, the Omicron sublineages are BA.4 , BA.4.6.3, XBB.1, XBB.1.13, XBB.3.2, XBB.2, BQ.1 and BQ.1.1.9.

Conclusion
The findings show that continuous genomic surveillance is important for the country and more data on the circulating lineages will strengthen the current surveillance system for COVID-19 in the country.

Respiratory Syncytial Virus (RSV) infection in children in Southern Mozambique: Incidence of disease, associated mortality, and risk factors

Dr Sérgio Massora[1], MD Leocadia Vilanculos[1], MD Hélio Mucavele[1], BSc Janeta Machai[1], MD Percy Pantoja[2], MSc Elena Marbán-Castro[2], DVM Anelsio Cossa[1], BSc Avertino Benedito[1], BSc Adilson Chiang[1], MSc Alberto Chaúque[1], Dr Aina Casellas[2], Dr Nelson Tembe[3], Dr Quique Bassat[2], Dr Inácio Mandomando[1], Dr Clara Menéndez[2,4], Dr Azucena Bardají[2]
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Biography:
Dr. Sérgio Massora works at Manhiça Health Research Centre, in Maputo Province, Mozambique. He is a Microbiologist and Researcher. Dr Massora obtained his Bacherol degree in Biology from Eduardo Mondlane University-Maputo, Mozambique. He also obtained his Master degree in Clinical Microbiology and Doctoral degree in Medicine and Translational Research from Barcelona University, Spain. Dr Massora interest include the study of respiratory infection, invasive bacterial disease and antimicrobial resistance.

Background and Aims: Respiratory syncytial virus (RSV) is a leading cause of under-5 morbidity and mortality. Low and middle-income countries concentrate most (90%) of the RSV burden. We aimed to determine the incidence of RSV acute lower respiratory infections (ALRI), and associated mortality and risk factors, among African children.

Methods: A health facility-based prospective observational study was carried out in children aged 0-60 months hospitalized with WHO-defined clinical criteria for pneumonia at the Manhiça District Hospital (MDH), in Southern Mozambique. Clinical and demographic data was collected through standardized questionnaires. A nasopharyngeal aspirate (NPA)/swab (NP) was collected from all study children at enrolment. Respiratory samples were analyzed for RSV detection by molecular methods (TaqMan Array). In this area, HIV prevalence in pregnant women attending ANC is high (21%), and 30% of admitted children at MDH are HIV positive.

Results: A total of 283 children admitted with WHO-defined criteria for severe pneumonia were recruited between October 2019 and September 2022. Among 161 NP tested RSV prevalence was 35% (56/161). NP and NPA are being tested at Centro de Investigação em Saúde de Manhiça (CISM) using TaqMan Array Card technology, and primers and probes specific for RSV-A and RSV-B using RT nested PCR. Final analyses of clinical and microbiological data are currently ongoing, and will be presented in September at ANISE 2023.

Conclusion: An RSV maternal immunization strategy is being considered for the prevention of severe disease in infants less than six months of age. In this context, generating data of the burden and RSV infection in African young infants is essential.

First report of molecular characterization of influenza virus in Benin in non-epidemiological period 2022

Miss Sètondji Islamiath Kissira[1], Dr Anges YADOULETON[1,5], Dr Martin FAYE[2]
[1]Laboratoire des Fièvres Hémorragiques et Virales du Bénin, [2]Institut Pasteur de Dakar, [3]Ministry of Health of Bénin, [4]WHO Country Office in Bénin, [5]Ecole Normale Supérieure de Natitingou. Université des sciences, Technologies, Ingénierie et Mathématiques

Biography:

Holder of a master's degree in fundamental and applied microbiology, I am a laboratory technician at the Hemorrhagic and Viral Fevers Laboratory in Benin, involved in the screening of SARS-CoV2 and various viruses responsible for respiratory infections and hemorrhagic and viral fevers. I am also involved in sequencing these viruses and analyzing bioinformatics data. Very passionate about scientific research in virology, I enrolled in a PhD program to achieve further objectives and fight against various infections, epidemics, and pandemics threatening humanity.

Influenza is a highly contagious and deadly respiratory disease that is often neglected in developing countries, even though it remains present in this population. It is important to establish surveillance of this infection in each country that does not yet have a surveillance system. This requires an initial description of the viruses in the population. The present study aims to report the first detection of influenza viruses in the Beninese population during a non-epidemic period.

Methods :100 nasopharyngeal swab samples were taken from participants who tested negative for SARS-COV2 but presented with a temperature above 38°C and a cough for at least 10 days. An RT-PCR was performed to identify influenza, and positive samples were sequenced on the Illumina platform (Myseq). A phylogenetic analysis of the obtained sequences was performed on NCBI, and phylogenetic trees were generated using Figtree software.

Results :The results showed the presence of 8 RT-PCR positive samples, but only two were confirmed to be influenza viruses after analysis of the sequences obtained. The two positive samples showed the presence of Influenza A H3N2 in a 31-year-old participant and Influenza B of the Victoria lineage in a 33-year-old participant, both residing in Cotonou. From the phylogenetic tree, it appears that the H3N2 (influenza A) virus detected in our study is closer to MN716342.1_Influenza A South Africa A255-004-037_2018, while the influenza B virus is closer to OD202394.1_Influenza B_Michigan_01_2022.

This first report of the presence of influenza viruses during a non-epidemic period, following a pandemic during which very strict barrier measures were put in place and respected, reinforces the urgent need for permanent genomic surveillance of these viruses in the population. The study is still ongoing with a larger sample size, and aims to also detect antiviral resistance observed among the participants, in order to establish an effective management.

Genetic diversity of human respiratory syncytial virus during COVID-19 pandemic in Yaounde, Cameroon, 2020-2021.

Mr Moïse Henri Moumbeket Yifomnjou[1,2], Dr Gwladys Chavely Monamele[1], Dr Abdou Fatawou Modiyinji[1], Mr Mohamadou Njankouo-Ripa[1], Pr Onana Boyomo[2], Pr Richard Njouom[1]
[1]Centre Pasteur of Cameroon, [2]Laboratory of Microbiology, University of Yaounde I

Biography:
I am PhD student in microbiology, medical microbiology option. Motivated, enthusiastic and hardworking, I am doing my research work at Centre Pasteur du Cameroun. I have strong communication, observation and integration, interpersonal and project management skills. I have acquired relevant academic and technical knowledge in microbiology, clinical biology, molecular biology and next generation sequencing. I have acquired expertise in virological diagnostic techniques, mainly for respiratory viruses, as well next generation sequencing methods and in analysis and post-sequencing results interpretation. My research goal is to contribute effectively to fight against infectious diseases which are one major health burdens in my country.

Background: Human respiratory syncytial virus (HRSV) is one of the leading viral causes of severe lower respiratory tract disease in people of all ages worldwide. The purpose of this study was to describe for the first time, genetic variability of HRSV in Cameroonian patients living in Yaoundé during the COVID-19 pandemic.

Methods: HRSV-positive nasopharyngeal samples detected in individuals of all ages in Yaoundé were collected from July 2020 to October 2021. Semi-nested RT-PCR, sequencing and phylogenetic analyses of the second hypervariable region of the G gene were performed.

Results: A total of 106 HRSV positive samples were collected during the study period. Of these, 40 (37.7%) could be amplified in the G gene. HRSV group A (HRSV A) and group B (HRSV B) co-circulated in this population at 47.5 and 52.5%, respectively. HRSV A strains clustered in GA2.3.5 genetic lineage, while HRSV B strains clustered in GB5.0.5a genetic lineage.

Conclusion: This study reports for the first time molecular epidemiology data of HRSV in Cameroon during the COVID-19 pandemic. Additional studies are needed to clarify the evolutionary patterns of HRSV throughout sub-Saharan Africa to support antiviral and vaccine development. This work has implications for HRSV vaccine research, as well as for strategies for prevention and control of HRSV infection in humans.

Keywords: Cameroon, Genetic characterization, Human respiratory syncytial virus, Molecular epidemiology, COVID-19 pandemic.

Comparative study of Egyptian Pilgrims Returning from Hajj and Umrah Mass Gatherings in Saudi Arabia in July and May 2022: Changes in SARS-CoV-2 and Influenza Epidemiology and Whole Genome Sequencing

Dr Hala Bahaa Eldin[1], Dr Manal Fahim[1], Dr Ola Deghedy[1], Dr Wael H. Roshdy[1], Dr Mohamed Kamel Khalifa[1], Dr Ahmed Kandeil[2], Dr Rabeh El Shesheny[2], Dr Amel Naguib[1], Dr Salma Afifi[3], Dr Amira Mohsen[2], Dr Amr Kandeel[1], Dr Khaled Abdel Ghaffar[4]
[1]Preventive Sector, Egypt Ministry Of Health And Population, [2]Centre of Scientific Excellence for Influenza Viruses, National Research Centre, [3]Public Health Consultant, Egypt Ministry Of Health And Population, [4]Minister of Health and Population

Biography:
Dr. Hala Bahaa Eldin has served, since 2017, as the coordinator assistant of Egypt's Field Epidemiology Training Program (FETP), under the supervision of the Department of Epidemiology and Surveillance at the Egyptian Ministry of Health and Population.

She began her work serving the preventive sector at the Ministry of Health and Population and currently is focused on working with epidemiology and surveillance investigators on emerging diseases.

Introduction: The Hajj is the largest annual mass gathering made by Muslims in Mecca Saudi Arabia every year. Ramadan Umrah is the second Islamic mass gathering that holds the same religious value as Hajj. We aimed at describing the changes occurred in SARS-CoV-2 and influenza incidence, epidemiology, clinical picture, and prevalent genotypes among the Egyptian pilgrims returning from Hajj in July and Umrah in May 2022.

Methods: Pilgrims were contacted at the airport and invited to participate voluntarily in the surveys. Pilgrims who consented verbally were interviewed using a standardized line list that includes participant demographics, symptoms if any, previous COVID-19 infection, and vaccination information collected from vaccination cards. Participants were asked to provide throat and nasopharyngeal swabs for SARS-CoV-2 and influenza testing by RT-PCR and a sample of isolates was sequenced. Descriptive data analysis was performed, and incidence rates were calculated among a representative sample of Egyptian pilgrims. Rates were compared between Hajj and Umrah surveys using chi2 and t-test with significance level <0.05.

Results: Overall, 3,862 Egyptian pilgrims enrolled, their mean age was 50.5±47, with half of them >50 years of age, 58.2% were males. Of them, 384 (9.9%) tested positive for SARS-CoV-2, and 51(1.3%) for influenza viruses. SARS-CoV-2 incidence and vaccine breakthrough infection rate was significantly higher (9.9 vs 6.7%, p<0.001) with a wide difference between SARS-CoV-2 variants identified among Hajj and Umrah pilgrims. Whereas no significant difference was found in influenza vaccination, incidence, and breakthrough infection rates (26.9 vs 26.8%, 11.7 vs 9.2%, and 1.4 vs 1.1% respectively).

Conclusions: SARS-CoV-2 incidence increased with reduced vaccine effectiveness among Egyptian pilgrims returning from Hajj to Umrah in July and May 2022 suggesting a possible wave of SARS-CoV-2 in the upcoming winter. To ensure vaccine effectiveness, vaccination strategies need to be revised to accommodate the rapidly evolving SARS-CoV-2 virus.

Predictors of severity and prolonged hospital stay of viral Acute Respiratory Infections (ARI) among children under five years in Burkina Faso, 2016-2019

Dr Abdoul Kader Ilboudo[1], Ms Assana Cissé[1], Dr Brice Wilfried Bicaba[2], Dr Jean Charlemagne Kondombo[2], Pr Serge Potandi Diagbouga[1], Pr Zekiba Tarnagda[1]

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Biography:

Abdoul Kader Ilboudo is an epidemiologist and junior researcher for the National Influenza reference laboratory hosted by the institute of research in health sciences of Burkina Faso. He is a medical doctor and hold a master degree in epidemiology and biostatistics. Abdoul Kader got more than ten year experience in severe acute respiratory infection (SARI) and influenza like infection (ILI) surveillance. He is now coordinating the "influenza cooperative agreement project", a five-year program which aims to reinforce the surveillance system of the country.

Introduction

Despite high morbidity and mortality of viral acute respiratory infections (ARIs) little is known on the risk factors of severe cases. We aimed to identify factors associated with increased severity and prolonged hospitalization due to viral severe ARI (SARI) among children under five years in Burkina Faso.

Methods

Data were collected from four SARI sentinel surveillance sites from October 2016 to April 2019. A SARI case was define as a child under five years with an acute respiratory infection, including a history of fever or measured fever ≥ 38°C and cough with onset within the last ten days, requiring hospitalization. An oropharyngeal and/or nasopharyngeal sample was collected and analyzed by multiplex rRT-PCR using FTD-33 Kit (Fast Track Diagnostics). For this analysis, we included only SARI cases with rRT-PCR positive test results for at least one respiratory virus. Sociodemographic and clinical data were collected from each patient. We used simple and mixed logistic regression models to assess factors associated with increased severity and prolonged hospitalization among patients with viral SARI.

Results

Overall, 1159 viral SARI cases were included in the analysis. SARI cases with danger signs or need of intensive care cases were common among children living in urban areas (AdjOR=1.6; 95% CI: 1.2-2.1), those under three months of age (AdjOR=1.7; 95% CI: 1.1-2.6) and coinfection with Klebsiella pneumoniae (AdjOR=1.6; 95% CI: 1.2-2.2). Malnutrition (AdjOR=2.2; 95% CI: 1.1-4.2), hospitalization during the rainy season (AdjOR= 1.71; 95% CI: 1.2-2.5), and infection with human CoronavirusOC43 (AdjOR=3; 95% CI: 1.2-8) were significantly associated with prolonged (>7 days) length of hospital stay.

Conclusion

These findings emphasize the need for preventive actions targeting younger children, childhood malnutrition and illness during the rainy season to control SARI morbidity and mortality.

Key words: Acute respiratory infections, severity, length of stay, predictors, children under five, Burkina Faso

Increased binding and neutralizing antibody titers in heterologous BNT162b2 but not homologous Ad26.CoV.2 boosting

Dr Jinal Bhiman[1,2], Dr Simone Richardson[1,2], Dr Carol Crowther[1,2], Ms Elizabeth Venter[1,2], Ms Frances Ayres[1,2], Ms Haajira Kaldine[1,2], Ms Nelia Manamela[1,2], Ms Nonkululeko Mzindle[1,2], Dr Mashudu Madzivhandila[1,2], Ms Prudence Kgagudi[1,2], Mr Qiniso Mkhize[1,2], Ms Sashkia Balla[1,2], Mr Strauss van Graan[1,2], Ms Tandile Modise[1,2], Dr Thandeka Moyo-Gwete[1,2], Ms Thopisang Motlou[1,2], Ms Zanele Makhado[1,2], Ms Shobna Sawry[3], Mr Jean le Roux[3], Prof Glenda Gray[4], Prof Helen Rees[3], Dr Catherine Riou[5,6,7], Prof Wendy Burgers[5,6,7], Prof Alex Sigal[8,9,10], Prof Lee Fairlie[3], Prof Penny Moore[1,2,5,11]
[1]National Institute for Communicable Diseases of the National Health Laboratory Services, [2]SAMRC Antibody Immunity Research Unit, School of Pathology, University of the Witwatersrand, [3]Wits RHI, Faculty of Health Sciences, University of the Witwatersrand, [4]South African Medical Research Council, [5]Institute of Infectious Disease and Molecular Medicine, University of Cape Town, [6]Division of Medical Virology, Department of Pathology, University of Cape Town, [7]Wellcome Centre for Infectious Diseases Research in Africa, University of Cape Town,, [8]Africa Health Research Institute, [9]School of Laboratory Medicine and Medical Sciences, University of KwaZulu-Natal, [10]Max Planck Institute for Infection Biology, [11]Centre for the AIDS Programme of Research in South Africa, University of Kwazulu-Natal

Biography:
Jinal N. Bhiman obtained a PhD and two post-docs at the NICD (Johannesburg) and Scripps Research (San Diego) in HIV virus-host dynamics and vaccine design. Between 2019-2021, as the Director of the National Influenza Centre, Jinal developed diagnostic assays, assessed surveillance data, performed antigenic characterization and whole genome sequencing for influenza, respiratory syncytial virus (RSV) and severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). Currently Jinal scientifically leads the Global Immunology and Immune Sequencing South Africa (GIISER-SA), focussing on diagnostics and vaccine/infection induced antibody responses to SARS-CoV-2 and RSV.

Despite rapid development and deployment of SARS-CoV-2 vaccines, low-to-middle-income countries had disproportionate access to them. Sero-prevalence studies across Africa reflect high levels of SARS-CoV-2 infection, regardless of the limited vaccine coverage. We investigated the impact of fractional dosing in homologous (2 doses of Ad26.COV2.S) and heterologous (Ad26.COV2.S followed by BNT162b2) vaccine regimens in South Africa.

Immunogenicity was evaluated in 217 participants randomized to receive a full or half dose homologous or heterologous booster vaccination at least 4 months after their Ad26.COV2.S primary dose. Serum was collected at baseline, week 2, 12 and 24 post-booster administration. Anti-nucleocapsid and anti-spike binding antibodies were measured by ELISA. Neutralizing antibodies (NAbs) and antibody-dependent cellular cytotoxicity (ADCC) against D614G, Beta, Delta, Omicron BA.1 and BA.4 were measured using lentiviral spike-pseudotyped and FcγRIIIa cross-linking assays respectively.

At baseline, high levels of hybrid immunity were observed in all arms (85-94% anti-nucleocapsid positivity). Spike binding and NAb titers were also relatively high (median EC50 1:1170 and D614G IC50 1:4114). At week 2, spike binding antibody in the half/full dose BNT162b2 arms increased by 4,6 to 5-fold, while a 1,2-fold increase occurred in the Ad26.COV2.S arms. Median NAb titers against D614G were 5,2 to 8,6-fold higher in the BNT162b2 arms compared to 0,8 to1,5-fold change in the Ad26.COV2-S arms. NAb titers against all other SARS-CoV-2 variants reflected the D614G pattern. ADCC titers, regardless of spike variant, vaccine dosage or platform, were not boosted. By week 12, antibody titers in the BNT162b2 arms waned to baseline levels, and these were maintained in all arms at week 24.

In the context of hybrid immunity, unlike Ad26.COV2.S homologous boosting, BNT162b2 heterologous full and half dose boosting induces higher binding and NAb titers. While the Ad26.COV2.S vaccine is a suitable prime, it may be less optimal for boosting regimens.

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Influenza A virus in pigs in Senegal and risk assessment of Avian Influenza Virus emergence and transmission to human

Mr Mamadou Malado Jallow[1,3], Dr Mamadou Aliou Barry[2], Dr Amary Fall[1], Mrs Ndiende Koba Ndiaye[1], Mr Davy Kiori[1], Mrs Sara Sy[1], Mrs Deborah Goudiaby[1], Dr Niang Mbayame Ndiaye[1], Dr Gamou Fall[1], Pr Malick Fall[3], Dr Ndongo Dia[1]
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Biography:
Mamadou Malado Jallow, born on May 04th, 1993, in New Jeshwang (The Gambia), graduated from the Senegalese High School in Banjul in 2012. Subsequently, I was admitted at the University Cheikh Anta Diop de Dakar with a cooperation scholarship to pursue a degree in Biology. In 2015, I was selected to pursue a Master degree in Parasitology after achieving my BSc with a distinction. As part of my thesis, I joined the Pasteur Institute in Dakar in July 2017 and contributed in several research projects. Currently I am working on the burden of influenza at the human/animal interface.

Pigs carry receptors for both avian and human adapted influenza viruses and have previously been proposed as a mixing and amplification vessel for influenza. Therefore, in pigs, possibilities to generate influenza reassortants are real. Until now, there has been no investigation of influenza viruses within animal in Senegal. So here, we investigated the epidemiology and genetic characteristics of IAVs as well as serological evidence of AIV infections in pigs at interfaces with human populations in Senegal.

This study was carried out between September 2018 to December 2019 in the single pig slaughterhouse in Dakar. Samples were collected on a weekly basis and IAVs were diagnosed by qRT-PCR. A subset of positive samples for H3 and H1 subtypes were selected for full genome amplification and NGS sequencing. The serum samples were tested by HI assay for the presence or not of antibodies, recognizing four AIVs.

Overall, 1691 swine nasal swabs were collected and tested. IAV was detected in 30.7%, and A/H1N1pdm09 virus was the most commonly identified subtype accounting for 38.07%, followed by A/H1N2 (16.3%) and A/H3N2 (5.2%). Phylogenetic analyses of all eight gene segments revealed that the isolated IAVs were closely related to human IAV strains belonging to A/H1N1pdm09 and seasonal H3N2 lineages. Several mutations, including D204 and N241D in the receptor binding site, S31N in the M2 gene and P560S in the PA protein were found. Serological analyses revealed that 83.5% of the 1636 sera collected were positive for the presence of antibodies against either A/H9N2, A/H5N1, A/H7N7 or A/H5N2. Influenza A/H7N7 (54.3%) and A/H9N2 (53.6%) were the dominant subtypes detected in Senegalese pigs.

Given the co-circulation of multiple subtypes of influenza viruses among Senegalese pigs, the potential exists for the emergence of new hybrid viruses of unpredictable zoonotic and pandemic potential in the future.

SARS-CoV-2 and RSV detection through the framework of influenza surveillance in Niger, 2020-2023

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Biography:
Dr Adamou Lagare is a virologyst heading the virology unit in CERMES and also the laboratory focal point for influenza surveillance in Niger. His main area of research is focused on respiratory viral infections. He has more than 10 years experience on influenza and contribute strongly to document influenza and other respiratory virus epidemiology in Niger.

Introduction
Acute respiratory infections (ARI) cause more than four million deaths particularly among children annually, with the overwhelming majority occurring in developing countries. Influenza and respiratory syncytial virus accounted as major viral pathogens of ARI. However, with the advent of Covid-19 pandemic, SARS-CoV-2 has become a serious threat. In Niger, part of influenza sentinel surveillance, SARS-CoV-2 and RSV have been monitored to determine predominating strains and coinfections.

Methodology
From January 2020 to April 2023, nasopharyngeal swab samples were collected from the eight sentinel sites located in three regions according to the WHO case definition for Severe Acute Respiratory Infections (SARI) and Influenza Like Illness (ILI) patients. Influenza and SARS-CoV-2 virus were detected by qRT-PCR using the CDC Influenza SARS-CoV-2 Multiplex Assay (RUO) kit. RSV was detected using specific primers and probe.

Results
A total of 7,664 suspected influenza cases were sampled during the study period from which 4,268 (55.7%) were SARI cases. The average age was 3.6 years with predominance of male 4,229 (55.2%). Influenza types A and B viruses were detected in 612 (7.8%) cases. H1N1pdm and H3N2 accounted respectively 260/433 (60.0%) and 151/433 (34.9%). Influenza B Victoria was the only lineage detected with 201/214 (93.9%). Covid-19 and RSV infections were confirmed among 194 (2.5%) and 612 (8.0%) cases. 33 cases of co-detections involving either two viruses were recorded with SARS-CoV-2/RSV and influenza/RSV predominating

Conclusion
Although the impact of the pandemic on the health system, influenza sentinel surveillance in Niger contributed to monitor both Covid-19 and RSV infections. These data sustain the new WHO strategy for integrated surveillance of influenza and other respiratory pathogens including Covid-19.

Resurgence of Influenza and respiratory syncytial virus in Egypt following two years of decline: outpatient survey of infants and children less than 16 years old, October 2022

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Biography:

Dr.Manal Labib Fahim Morcos: Medical Epidemiologist, consultant tropical medicine, graduated from Egyptian fellowship on applied epidemiology 2009, Field epidemiology training program (FETP) 2007, Master degree Tropical medicine 1996, currently I'm the Director of Department of Epidemiology and Surveillance (DES) preventive sector- MoHP, Egypt,

National Focal person of Influenza and acute respiratory illness surveillance. also FETP mentor

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Introduction: Two years after unprecedented low rates of circulation of non-SARS-CoV-2 respiratory viruses, the Egyptian ARI surveillance system detected an increase in acute respiratory infections (ARIs), especially among school children. A one-day survey was carried out in 98 governmental outpatient clinics distributed all over the country to identify the viral causes of ARI among children <16 years of age and estimate their burden.

Methods: The four largest referral hospitals in each of the 26 Egyptian governorates where most of the ILI patients seek care were selected. Using the WHO case definition, the first five patients <16 years of age with influenza-like illness (ILI) symptoms visiting the selected outpatient clinics on the survey day were enrolled. Basic demographic and clinical data of patients were collected using a linelist. Patients were swabbed and tested for SARS-CoV-2, influenza, and Respiratory Syncytial virus (RSV) by RT-PCR at the Central Laboratory in Cairo.

Results: Overall, 530 patients enrolled, their mean age was 5.8±4.2, 57.1% were males, and 70.2% reside in rural or semi-rural areas. Of all patients, 134 (25.3%) had influenza, 111 (20.9%) RSV, and 14 (2.8%) coinfections. Influenza-positive children were older compared to RSV, (7.2±4.1, 4.3±4.1, $p<0.001$), with more than half of them (53.0%) being school students. Dyspnea was reported in RSV more than in influenza (62.2% vs 49.3%, $p<0.05$). Among RSV patients, children <2 years had a higher rate of dyspnea than others (86.7% vs 53.1%, <0.001).

Conclusions: A resurgence of influenza and RSV was detected in Egypt in the 2022-2023 winter season. Influenza caused a higher rate of infection than RSV, while RSV caused more severe symptoms than influenza. Monitoring a broader range of respiratory pathogens is recommended to estimate the ARI burden and risky groups for severe disease in Egypt.

Keywords: influenza viruses, Respiratory Syncytial virus, acute respiratory infection

Estimating the national burden of Influenza-associated Severe Acute Respiratory illness in Egypt,2016 -2019

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Biography:

Walaa A. Attia is an epidemiologist and surveillance officer working in the preventive sector of the Ministry of Health in Egypt. She has been working in this field since 2016 and has made significant contributions to public health in the country.

Attia was born and raised in Egypt and received her undergraduate degree in pharmaceutical science from October University. Then she completed the Field Epidemiology Training Program (FETP) in Egypt, which gave her the skills and knowledge necessary to work in disease surveillance.

Attia is passionate about public health and has a particular interest in one health topics.

Background: Estimation of influenza-associated severe acute respiratory illness (influenza-SARI) is needed particularly in developing countries for resource allocation and promotion of influenza vaccination. This study aims to estimate the national number and rates of influenza- SARI by level of severity and deaths among different age groups.

Methods: We conducted retrospective study using data of two sentinel sites surveillance in two different governorates during 2016-2019. Age-specific rates of (influenza-SARI) were estimated and adjusted for Egypt based on the prevalence of risk factors for pneumonia and healthcare-seeking behavior of Sexually transmitted infections as a proxy for ARI healthcare-seeking behavior using the 2014 Demographic and Health Survey. Influenza Pyramid Tool was used to estimate the burden of (influenza-SARI)

Results: Overall, 8,188 patients were hospitalized with SARI in the selected governorates. (influenza-SARI) accounted for 15.1 %, 17.3 % among patients aged <5 and 14.0 % in those aged ≥5 years. SARI cases in the two sentinel sites were 1,017 with Influenza accounted for 143 (14.1%). the estimated mean annual rate of (influenza-SARI) was 37.9 /100 000 population, 64.7 in patents aged<5 and 29.3in those aged ≥5 years. Children aged <5 years accounted for 41.6 % of the total (influenza-SARI). Estimated influenza-associated mild/moderate number of cases, hospitalizations, critical cases, and deaths were 13,929,088 and 36,639nand 8,016 and 2,153 respectively and influenza death rate was 2/100,000 population.

Conclusion: WHO method was useful for estimation of influenza burden using sentinel surveillance data. The study indicated that Egypt has heavy burden of influenza-associated morbidity and mortality. There is urgent need for interventions to reduce influenza burden in Egypt, in particular among the most vulnerable groups.

Genetic characterization of influenza A(H1N1) pdm09 and A(H3N2) viruses circulating in Mauritius, 2017- 2019.

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Biography:

Mrs Ramuth Magalutcheemee is a Senior Clinical Scientist in the National Virology Department, Central Health Laboratory, Ministry of Health and Wellness, Mauritius.

She forms part of the focal team for viral outbreak investigations nationally. She is involved in Influenza surveillance in Mauritius NIC and has played a key role in establishing Sequencing of SARS-CoV-2 in Mauritius using the Oxford Nanopore Sequencer with the support of WHO and Africa CDC. She collaborates with international centers (Francis Crick Institute) and South Africa (NICD and KRISP)and Kenya (ILRI) for the establishment of genomic surveillance for other viral pathogens in Mauritius.

Background: Mauritius, a tropical island to the East of Africa experience circulation of influenza with no distinct pattern and data on circulating strains are limited. In this study, we describe the genetic and evolutionary characteristics of influenza A(H1N1) pdm09 and A(H3N2) strains that circulated in Mauritius from 2017 to 2019.

Methods: Influenza A virus isolates (N=118) were obtained by viral culture of polymerase chain reaction (PCR) positive specimens from National Influenza Surveillance Programs, 2017-2019. Influenza A(H1N1)pdm09 accounted for 77.1% (91/118) and A(H3N2) for 22.7% (27/118) of isolates. We used reverse transcription-PCR to amplify all eight genome segments in a single reaction followed by Oxford Nanopore sequencing. Genome Detective Virus tool was used to assemble gene segments, Nextclade to align sequences, built trees and to perform mutational analysis.

Results: Among 51.6 % A(H1N1)pdm09 (47/91) 6B subclades with varying annual dominance were: 6B.1(13/16, 2017), 6B.1A.5a (5/12, 2018) and 6B.1A.5a (14/19, 2019). HA mutational analysis identified two amino acid substitutions A232E, D239G involved in host cell receptor binding. Influenza A(H3N2) viruses (70.4%, 19/27) belonged to 3C and subclades with varying dominance: 3C.2(4/6, 2017), 3C.2a1b.1 (7/10,2018) and 3C.2a1b.2b (2/3, 2019). Over the 3 years the number of N-linked glycosylation sites (PNGs) in HA of A(H1N1)pdm09 were mostly 7 (44/47) and more variable among A(H3N2) sequences. Four A(H1N1)pdm09 strains had the D151E mutation and 2 A(H3N2) viruses had the D151N mutation in NA which is associated with reduced sensitivity to neuraminidase inhibitors. The number of PNGs across NA protein sequences of A(H1N1)pdm09 (46/47) and A(H3N2) (14/19) remained fairly constant at 8.

Discussion and Conclusions: In Mauritius A(H1N1)pdm09 6B subclades vary with 6B.1A.5a emerging and dominating in 2018 and 2019. For 2017 to 2019 A(H3N2) 3C.2 dominance changed from 3C.2 > 3C.2a1b.1 > 3C.2a1b.2b. Mutations affecting sensitivity to neuraminidase inhibitors were limited.

The need to strengthen the Sentinel Surveillance system for Influenza and other respiratory pathogen; lessons from COVID 19 pandemic.

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[1]Uganda Virus Research Institute

Biography:

Health researcher at the Uganda Virus Research Institute for over 10 years with back ground in Data management pursuing Laboratory and Bioinformatics

Background

Influenza is a severe respiratory disease caused by Influenza A, B and C virus characterized by sudden onset of fever, cough and severe aches. Other respiratory infections with similar symptoms are caused by other respiratory pathogens including respiratory syncytial virus, coronavirus.
The Influenza sentinel surveillance systems has been operational since 2006 but with the COVID-19 outbreak in March 2020 and increase in samples and cases from all over the country, there was need to urgently expand diagnostic capacities to other facilities and Laboratories.

Methods

From 16 health facilities in various regions of the country, Nasopharyngeal/oropharyngeal swabs were collected from Patients reporting with symptoms matching the WHO case definition of Influenza Like Illnesses (ILI) at Outpatient clinics and Severe Acute Respiratory Infection (SARI) on admission. Samples transported to the Uganda Virus Research Institute Laboratory were only tested for Influenza viruses but later for SARS-CoV and Respiratory Syncytial Virus (RSV) by RT-PCR, subtyping. Demographic and clinical information were obtained by interviewing patients at the hospitals.

Results

Of the 10,862 patients, 8,847 (81.45%) were at outpatient clinics (ILI) and 2,015 (18.55%) inpatients (SARI), 7,427 (68.54%) were Female and 3,409 (31.46%) were Males. Among the positives, 798 (7.35%) for SARS-CoV, 526 (4.8%) for influenza and 507 (4.6%) for RSV. 23 (0.2%) for Influenza/SARS-CoV coinfections, 50 (0.4%) Influenza/RSV coinfection, 37(0.34%) SARS-CoV/RSV coinfection. Influenza subtypes include A/H3 (2.02%), Influenza-B (1.6%) and H1/pdm09 (1.14%) and these infect more of the children more than the adults.

Conclusions: With the unstable healthcare systems and neglect of other infections during outbreaks, sustaining and strengthening the existing integrated surveillance and response systems through capacity and infrastructure building in both urban and rural community health setup would enhance timely case identification and reporting while monitoring and responding to outbreaks emergencies in the Uganda.

Clinical outcomes of patients admitted with respiratory illnesses associated with viral pathogens among people living with HIV and not living with HIV in Western Kenya

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Biography:
Dr Ben Andagalu is a medical doctor and clinical researcher currently serving as a Senior Public Health Specialist with the Influenza Program at the US CDC Kenya Country Office in Nairobi. He is currently supporting the implementation of several influenza surveillance projects in Kenya, including two cohort studies.

Background
Acute respiratory infections are major causes of morbidity and mortality among people living with HIV (PLWH). This study aimed to describe the prevalence of respiratory virus infections, clinical characteristics, and outcomes among PLWH admitted with respiratory illness at a referral hospital in western Kenya.

Methods
We analyzed hospital-based surveillance data from patients aged 13 years and above admitted to Siaya County Referral Hospital between January 2014 and November 2016 with a respiratory illness, defined as cough or difficulty in breathing. TaqMan Array Cards were used to detect the pathogens of interest in biological samples. HIV status was determined through medical and laboratory record review – patients with HIV test records were thus classified as PLWH or as not living with HIV. Those with no record were excluded. Inpatient follow-up was conducted to determine the outcome of the admission. Chi-squared tests were used to assess differences in severe outcomes by HIV status.

Results
A viral pathogen was detected in 376 out of 1,545 (24.3%) cases of respiratory illness, with no significant difference observed by HIV status. Rhinovirus (71/376, 18.9%), influenza A/B (22/376, 6.0%), enterovirus (13/376, 3.5%), respiratory syncytial virus (9/376, 2.4%), and human coronavirus OC43 (8/376, 2.1%) were the most prevalent viruses. Among patients with at least one virus detected, PLWH were more likely to stay longer (more than 7 days) in the hospital (34.1% vs 14.0%; $p<0.001$) or die during the admission (18.2% vs 8.5%; $p=0.005$) compared to people not living with HIV. No significant differences by HIV status were noted in the need for oxygen supplementation (7.4% vs 6.0%; $p=0.590$) or referral for ICU admission (4.0% vs 2.5%; $p=0.416$).

Conclusions
PLWH hospitalized with viral respiratory illness more frequently have poorer clinical outcomes. This underscores the importance of implementing routine respiratory viral diagnostics to inform patient management among PLWH.

Hemagglutinin stalk-specific Fc effector functions are associated with protection after vaccination with trivalent inactivated influenza vaccine

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Biography:

Boitumelo holds a Master of Science from Rhodes University, South Africa. She is currently in her final year of PhD research at the Antibody Immunity Research Unit of the National Institute for Communicable Diseases (NICD) and at the University of the Witwatersrand. Her research focuses on characterizing antibody Fc-mediated functions induced by influenza vaccination, in the context of HIV infection. Understanding the contribution of these Fc functions to influenza immunity in HIV infected individuals may improve the vaccine design for high risk groups.

Background

Several universal influenza vaccine candidates are aimed at eliciting antibodies targeted towards the conserved hemagglutinin (HA) stalk domain. Furthering our understanding of the protective mechanism of these antibodies, which elicit potent Fc effector functions, is critical.

Objectives

We examined the association between HA (H1 subtype) stalk-specific Fc-mediated functions and protection against confirmed influenza virus illness following vaccination with trivalent inactivated vaccine (TIV) in pregnant women.

Methods

Pregnant women were enrolled in a maternal influenza (MatFlu) vaccination trial (138 TIV and 145 placebo recipients) in which influenza virus illness was confirmed by PCR (11 group 1 A/H1N1 and 12 non-group 1 illnesses (6 A/H3N2; 2 B/Victoria and 4 B/Yamagata) within 6 months of vaccination. Plasma samples were tested for H1 stalk-specific antibody-dependent cellular phagocytosis (ADCP), complement deposition (ADCD) and cellular cytotoxicity (ADCC) at enrolment and 1-month post-vaccination; and associations were determined by logistic regression analysis.

Results

We observed significantly lower ADCP and ADCD activity ($p<0.0001$) among vaccine (n=5) and placebo (n=18) recipients with confirmed influenza, irrespective of the infecting subtype, when compared with participants that did not display symptoms of influenza (127 placebo and 133 vaccine) 1-month post- vaccination. We found that high levels of ADCP, in the absence of infection, reduced the odds of A/H1N1 infection by 83% (odds ratio (OR); (95% confidence interval (CI)) 0.11; (0.01-0.67)). Against non-group 1 infections, the odds of infection decreased as the ADCP activity increased but the association was not significant. High ADCD was significantly associated with >84% protection (OR; (95% CI) 0.10; (0.01-0.57)) against both A/H1N1 and non-group 1 infections. ADCC was not associated with protection against influenza.

Conclusion
HA stalk-specific Fc-mediated functions correlate with protection against influenza following seasonal TIV. These findings inform future broadly protective HA stalk-based vaccine strategies by indicating the mechanisms through which HA-stalk antibodies protect following vaccination.

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Coinfections with SARS-CoV-2 variants and influenza virus during the 2019 Coronavirus disease pandemic in Burkina Faso: A surveillance study

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Biography:
Biologist in National Influenza reference Laboratory(NIRL), Engineer of research, PhD Student in Université Nazi Boni of Burkina Faso, works in NIRL since 2010. I have experiences in Inflenza and others respiratory pathogen detection by RT -PCR, SARS-CoV-2 séquencing. I 'm NIRL Management quality responsible , and have experience in biosafety /biosecurity

Background
Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) particularly the variants of concern coinfections with influenza is a public health concern in Africa. We aimed to characteri the SARS-CoV-2 variants and determine the rate of coinfections with influenza in Burkina Faso.

Methods
COVID-19 surveillance study was conducted between August 2021 and January 2022 using reverse transcription polymerase chain reaction (RT-PCR). Three multiplex real-time qualitative RT-PCR kits, the SNPsig® SARS-CoV-2 (EscapePLEX), The SNPsig® VariPLEX (COVID-19) and SARS-CoV-2E Spike Delta/Omicron TaqMan Typing were used on positive specimens for rapid and presumptive detection of the SARS-CoV-2. The multivariant panel kits assays targeting some of the most widespread mutations. In addition, influenza virus strains were detected by RT-PCR in SARS-CoV-2 positive specimens using the CDC primers, probes, and protocols.

Results
Of 324 specimens assessed, the Omicron and Delta variants of SARS-CoV-2 were the most prevalent with 27.2% [95% confident interval (CI): 22.5–32.4] and 22.2% [95% CI: 17.9–27.2], respectively. The Beta and Gamma variants were detected in 4.3% [95% CI: 2.4–7.1] and 0.3% [95% CI: 0.0–1.7], respectively. Coinfections of Omicron and Beta variants were reported in 21.3% [95% CI: 17.0–26.2], Omicron and Delta variants in 1.2% [95% CI: 0.3–3.1] of specimens, and the Omicron–Gamma variants' coinfections in 0.6% [95% CI: 0.1–2.2]. One COVID- 19 specimen with an undetected SARS-CoV-2 variant was also tested positive for the seasonal influenza A (H3N2) virus. No cases of pandemic influenza A (H1N1) pdm09, seasonal A/H1N1, and influenza B were detected.

Conclusion
The current World Health Organization SARS-CoV-2 variants of concern were prevalent and their coinfections with influenza were uncommon. Continuous surveillance of both pathogens is, however, needed because of their public health implications.

Keywords : Burkina Faso, COVID-19, influenza, mutation, SARS-CoV-2, variant

Burden of COVID-19 Cases and Deaths in Ethiopia: Findings from the Analysis of the Nationally Representative Surveillance and Response Data

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Biography:

I earned my medical doctorate (MD) from Hawassa University School of Medicine in 2013 and MPH in Field Epidemiology from Saint Paul Hospital Millennium Medical College in 2019.

Currently I am the lead for Respiratory Viral Diseases Surveillance and Response Case Team in Ethiopian Public Health Institute. I am also the surveillance lead of the COVID-19 Relief Act project and co-lead of the national COVID-19 Vaccine effectiveness study and AFI Surveillance project and section chief for Major Outbreaks Surveillance and Response Section. Involved in designing, development, and coordination of surveillance and response programs for SARS-CoV-2, influenza, RSV.

Background: The COVID-19 pandemic is one of the most devastating public health emergencies of international concern (PHEIC) to have occurred in the past century. To ensure a safe, scalable, and sustainable response, it is imperative to understand the burden of disease, epidemiological trends, and responses to activities that have already been implemented.

Methods: COVID-19 data were captured from October 01, 2021 to September 30, 2022, in 64 systematically selected health facilities throughout Ethiopia. The number of health facilities included in the study was proportionally allocated to the regional states of Ethiopia. Data were captured by standardized tools and formats. A descriptive analysis of COVID-19 testing performed, cases detected, and deaths registered by region was carried out.

Findings: Overall, 18,964 cases out of 215,024 tests (9.0%, 95% CI: 8.9% – 9.1%) were positive. Out of the confirmed and reported cases, 534 resulted in deaths with a CFR of 2.8% (95% CI: 2.6% – 3.0%), and 21% were hospitalized patients. Out of 664 healthcare workers (HCWs) infected, eight (1.2%, 95% CI: 0.37% – 2.03%) died. Out of 12,813 index cases identified through contact tracing, 9,323 (72.8%) were tested and 1095 (11.7%, 95% CI: 11.1% - 12.4%) were found to be positive.
Interpretation: The high burden of COVID-19 cases and deaths underscores the need for concerted efforts to strengthen COVID-19 preventive measures, especially targeting the surveillance system. To ensure effective integration, it is critical to remain vigilant and keep the momentum of active case detection and provision of optimal response.

Evaluation of the Influenza Sentinel Surveillance System in Kenya, January 2019–April 2023

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Biography:
I am a Medical laboratory officer at the Ministry of Health, Division of Disease Surveillance and Response. I have specialized in medical microbiology and epidemiology. My duties include conducting disease surveillance activities at the national level for Influenza to prevent the spread of influenza viruses. I am involved in collecting, analyzing, and interpreting data related to influenza outbreaks and coordinating with various healthcare institutions, collaborating partners, and other government agencies to ensure effective surveillance and response. I also conduct public awareness about influenza through educational campaigns and public outreach programs, as well as research and surveillance system improvement.

Background: The influenza sentinel surveillance system in Kenya has been operational since 2007. The World Health Organization recommends periodic evaluation of influenza surveillance systems to identify areas for improvement and allows evidence-based decision-making. There is limited information on the performance of influenza surveillance in Kenya. We aimed to assess the usefulness of the influenza sentinel surveillance system in Kenya and determine if the system meets its objectives.

Methods: We conducted a retrospective review of influenza surveillance system data in Kenya from January 2019 through April 2023. We interviewed the surveillance focal persons to establish the description and operating procedures of the system. Furthermore, we evaluated the system's attributes using the United States Centers for Disease Control and Prevention guidelines for evaluating public health surveillance systems. We developed specific indicators for each system attribute and used quantitative and qualitative methods to describe them. The performance of each system attribute was scored on a 5-point scale, ranging from very poor to excellent performance.

Results: We obtained 14,826 Influenza Like Illness (ILI) and Severe Acute Respiratory Illness (SARI) records from eight sentinel surveillance sites in Kenya. Children below 12 were the majority at 94.1% (7167/14,826). We calculated a predictive value positive of 11.8% from 12,969 laboratory analyses conducted, and 68% (1,045/1,536) of the laboratory-confirmed cases tested positive for Influenza A. The system was timely, with 80.4% (10,532/13,105) of laboratory results available within seven days. Although the data quality audit performance was good, with a 91% completion rate, influenza vaccination entry records had gaps. The interoperability of epidemiological and virological data was limited.

Conclusion: The overall system performance was satisfactory and useful in providing reliable and timely data about influenza virus circulation. We recommend expanding influenza surveillance population coverage in the country and making the system interoperable to improve data quality, representativeness, and simplicity.

Circulation of endemic respiratory viruses during the COVID-19 pandemic in urban and rural Malawi

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Biography:

Dr Elen Vink is a Clinical Research Fellow at the MRC-University of Glasgow Centre for Virus Research and an Infectious Diseases/Microbiology registrar at NHS Lothian. Her research interests lie in the clinical epidemiology and genomics of emerging infections and her current research focuses on the interactions between SARS-CoV-2 and other respiratory viral infections in the UK and Sub-Saharan Africa. She collaborates with the ISARIC and COG-UK Consortiums. Dr Vink gained her medical degree from the University of Edinburgh, a BSc (hons) from the University of St. Andrews, and a Diploma in Tropical Medicine and Hygiene from the University of Liverpool.

Background

Non-pharmaceutical interventions (NPIs) during the COVID-19 pandemic have disrupted endemic respiratory virus transmission. Virus circulation patterns in Malawi during this time are unknown due to significant constraints on healthcare infrastructure and resources.. Malawi employed less stringent NPIs than most and the impact of this is unclear. Our aim was to investigate circulation patterns of endemic respiratory viruses during the COVID-19 pandemic in Malawi.

Methods

The COVSERO study is a prospective longitudinal cohort study of randomly selected households in an urban (Area 25, Lilongwe) and rural community (Karonga) in Malawi, carried out between February 2021 and April 2022. Comprehensive metadata were collected 3 monthly. SARS-CoV-2 PCR and multiplex RT-PCR testing for endemic respiratory viruses were performed on self-obtained upper respiratory tract samples (URT).

Results

PCR was performed on 1626 URT samples from 945 participants in 542 households; 7.5% of samples tested positive for respiratory viruses, with SARS-CoV-2 (4.4%) and Rhinovirus (2.0%) the most frequently detected. No influenza A virus was detected; Influenza B and RSV were rare. Significantly higher virus positivity was detected in Karonga. Virus positivity declined over the study period. Co-infections were infrequent (0.2%).

Conclusion

Endemic respiratory viruses continued to circulate in the community in Malawi during the COVID-19 pandemic however influenza and RSV were rare. Distinct differences were seen in virus positivity and demographic factors between urban and rural cohorts. Respiratory virus surveillance data from African countries is scarce and further studies are needed to monitor the ongoing impact of co-circulation of SARS-CoV-2 with endemic respiratory viruses.

Barriers towards seasonal influenza vaccine among pregnant women in Tunisia

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Biography:
Hind is an assistant professor in epidemiology and public health working at the Tunisian Ministry of Health, with experience in infectious disease surveillance, epidemic preparedness and response and field epidemiology. She has been involved in influenza surveillance for many years with research mainly in evaluation of influenza surveillance system, influenza modelling, and influenza vaccine uptake. During the COVID-19 pandemic, she participated in the national response including the analysis of national surveillance data, risk assessment, monitoring of the international situation as well as weekly epidemiological reporting and various COVID-19 research activities.

Introduction

Pregnant women (PW) remain the highest priority group for influenza vaccination, especially in countries planning to initiate or expand their influenza vaccine (IV) programs. Although known as effective and safe, IV uptake is particularly low among this high-risk group. Many factors are suspected to affect vaccine acceptance and vary with the setting and context.
This study aimed to explore barriers to seasonal influenza vaccine uptake among PW in Tunisia.

Methods

We conducted a qualitative study based on 10 focus group discussions (FGD) among PW from five governorates across the country (north, center, and south) between March and June 2019. Participants were selected with the collaboration of healthcare workers (HCWs) in each region, both in rural and urban settings. All data were recorded, transcribed in the local language and translated in English. Data analysis was based on a thematic approach and NVivo Software was used. Written consent was required from all participants.

Results

In total, 86 PW participated in the 10 FGDs. Lack of information about being at high-risk of influenza and mistrust against the vaccine composition were the main factors affecting IV uptake. Participants noted the fear of several potential side effects and complications; the strongest one was a belief that it could cause cancer. Besides, some PW believed that medication including the vaccine can affect the immune system and that the body needs to defend itself. Advice against taking medication including the vaccine by HCWs was also reported as well as issues in availability and access to the vaccine.

Conclusion

Our study provided a better understanding of PW perception and barriers towards IV uptake in Tunisia. These findings will guide decision makers to adapt policy recommendations and strategies regarding the vaccination of PW with the final aim to improve vaccine uptake among this target group.

Comparing performance of facility based year-round and campaign-mode influenza vaccination strategies among children aged 6-23 months in Kenya: 2019 – 2021

Dr Jeanette Dawa[1], Rose Jalang'o, Harriet Mirieri, Rosalia Kalani, Doris Marwanga, Kathryn E. Lafond, Mary Margaret Njenga, Joyce Ejoi, Faith Chiguba, Shem Patta, Patrick Amoth, Emmanuel Okunga, Collins Tabu, Sandra S. Chaves, Malembe S. Ebama, Philip Muthoka, Virgina Njenga, Elizabeth Kiptoo, Isaac Jewa, Raphael Mwanyamawi, Joseph Bresee, M. Kariuki Njenga, Eric Osoro, Lucy Mecca, Gideon O. Emukule
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Biography:

Jeanette Dawa is a medical epidemiologist based at the Washington State University – Global Health Program in Nairobi, Kenya. She has several years' experience in disease surveillance research and epidemiology. Her special interests include the use of analytic methods to enhance the utility of research surveillance data in decision making, especially in regard to respiratory viruses, and has used respiratory illness surveillance data to fit an influenza virus dynamic transmission model to influenza activity in Kenya. She also supports implementation of public health programs in Kenya including influenza vaccination among children and healthcare workers.

Introduction: In 2016, the Kenya National Immunization Technical Advisory Group requested additional programmatic data to inform the choice of strategy for a national influenza vaccination program among children aged 6 to 23 months of age. In response, we conducted an influenza vaccine demonstration project to compare the performance of a year-round versus campaign-mode vaccination strategy. Findings from this demonstration project will help identify essential learning lessons for a national program.

Methods: We compared two vaccine delivery strategies: (i) a year-round vaccination strategy where influenza vaccines were administered throughout the year at health facilities. This strategy was implemented in Njoro sub-county in Nakuru (November 2019 to October 2021) and Jomvu sub-county in Mombasa (December 2019 to October 2021), (ii) a campaign-mode vaccination strategy where vaccines were available at health facilities over four months. This strategy was implemented in Nakuru North sub-county in Nakuru (June to September 2021) and Likoni sub-county in Mombasa (July to October 2021). We assessed differences in coverage, dropout rates, vaccine wastage, and operational needs.

Results: We observed similar performance between strategies in coverage of the first dose of influenza vaccine (year-round strategy 59.7%, campaign strategy 63.2%). The coverage obtained in the year-round sub-counties was similar (Njoro 57.4%; Jomvu 63.1%); however, more marked differences between campaign sub-counties were observed (Nakuru North 73.4%; Likoni 55.2%). The campaign-mode strategy exceeded the cold chain capacity of participating health facilities, requiring thrice monthly instead of once monthly deliveries, and was associated with a two-fold increase in workload compared to the year-round strategy (168 vaccines administered per day in the campaign strategy versus 83 vaccines administered per day in the year-round strategy).

Conclusion: Although both strategies had similar coverage levels, the campaign-mode strategy was associated with considerable operational needs that could significantly impact the immunization program.

Seeking novel SARS-COV-2 variants among patients meeting Influenza Like Illness and Severe Acute Respiratory Illness case definitions — Zambia,2021-2023.

Mr Paul Simusika[1], Mr Jay Sikalima[4], Dr Jonas Hines[2], Miss Taonga Banda[1], Mr Keith Kabegengle[3], Miss Miniva Mwanza[1], Miss Agness Mushabati[1], Mrs Chilala Jere[1], Mr Reuben Mwanza[1], Mr Edward Chentulo[1], Dr Justin Chileshe[3], Miss Lombe Kampamba[3], Dr Daniel Owusu[2], Ms Leah Mukwaza[1], Ms Dorren Shempela[4], Dr Nyambe Siyange[5], Dr Davie Simwaba[5], Dr Muzala Kapina[5], Dr Samuel Yingist[2], Dr Aaron Samules[2], Dr Mwaka Monze[1]

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Biography:

My Name is Paul Simusika, I will be presenting this Scientific work. I hold Master of Science Degree in Medical Virology from the University of Manchester ,United Kingdom. Iam a receipient of the prestigious Chevening Schoarship from the UK'S foreigne office.I have over 10 years experince working in influenza surveillance in Zambia with various publications in Influenza and related Viruses.

BACKGROUND

Tracking SARS-CoV-2 genomes is important to monitor for emergence of new variants of concern (VOCs). Zambia has been sequencing SARS-CoV-2 since 2020. We aimed to describe detection and molecular characterization of SARS-COV-2 VOCs from patients in the influenza-like illness / severe acute respiratory infection (ILI/SARI) sentinel surveillance system in Zambia.

METHODS

From January 2021 through April 2023, patients with ILI (temperature 38°C and cough 10 days) or SARI (admitted cases with 38°C/reported fever and 10-day cough) were recruited from 10 sites. The CDC multiplex assay for influenza/SARS-COV-2 was used for initial screening. Using version 3 primer pools created by ARTIC Network, SARS-COV-2-positive samples with a cycle threshold of <25 were sequenced using next-generation whole genome sequencing (NGS) on Illumina platforms with version 3 primer pools designed by ARTIC Network.Sequences were aligned using MAFFT 7.1 and Pango lineage nomenclature (Nextclade) was used for VOC classification. Maximum likelihood (ML) phylogenetic analysis was done using MEGA 7.0.

RESULTS

Of 9,271 persons recruited into the ILI/SARI system from 2021 to 2023; 926 (10.0%) were SARS-COV-2 positive. Of these, 450 (48.6%) were submitted for NGS with 254 (56.4%) sequences obtained. Based on the ML analysis, our samples grouped into Beta, Delta, and Omicron variants, these grouped into 3 distinct waves: Beta (20.6%) during January -March 2021, Delta (19.4%) during (June-August 2021) and Omicron (60.0%) during (January -December 2022). For Omicron, the evolution occurred as follows: BA1 (46.5%) and BA2 (24.5%) in the first half of 2022, later BA.4 (21.3%) and finally in 2023, XBB (7.1%).

CONCLUSION

The ILI/SARI surveillance system was able to identify SARS-CoV-2; from which it was possible to identify VOCs that matched those discovered in other nations. The ILI/SARI system offers a long-term platform to detect new and circulating SARS-CoV-2 variants, which can help Zambian policymakers.

KEYWORDS: SARS-CoV-2/genetics, sentinel surveillance, Zambia

Epidemiology and genetic evolution of Influenza B viruses circulating in the DRC from 2015 to 2019: implication of vaccination.

Docteur Edith Nkwembe[1]
[1]Inrb

Biography:

Medical doctor and specialist in Microbiology and Virology in particular. Associate of higher and university education at the Faculty of Medicine of the University of Kinshasa and expert in the molecular diagnosis of respiratory viruses including influenza viruses

Head of the respiratory virus laboratory at the INRB and responsible for the biological monitoring of influenza viruses and Sars CoV-2 in the DRC as part of sentinel surveillance.

President of the laboratory commission in the fight against covid-19 in the DRC; she leads the activities of the response against the covid-19 pandemic in the laboratory.

Background:
Influenza A and B viruses are responsible for severe acute respiratory infections worldwide with a morbidity of 5 million and mortality of 29,000-650,000 deaths per year. In DRC, the genomes of the influenza A viruses have already been characterized. However, the influenza B viruses remain unknown. The purpose of this study is to examine the genetic and dynamic evolution of influenza B viruses circulating in the DRC over a period of 5 years.

Method:
Samples were collected from suspected outpatients with influenza-like illness (ILI) and in all hospitalized patients with SARI. Molecular analysis was done to determine influenza type and subtype, then segments encoding the HA of Flu B of the Yamagata and Victoria influenza B viruses were performed.

Results:
Of 4894 samples tested, 416 (8.5%) were positive for influenza viruses, including 268 (64.4%) for influenza A viruses and 148 (35.5%) for influenza B viruses among which 52 were sequenced including 25 B/Yamagata and 27 B/Victoria. By comparing with the reference viruses, the HA genes of influenza B viruses circulating in the DRC show deletions in the HA1 region. Molecular analysis of influenza B viruses reflects genetic diversity of influenza B/Yam clades alternating with influenza B/Victoria clades. Yamagata B viruses had circulated in 2015, 2016 and 2018 and Victoria in 2017 and 2019. An interlineage reassortment between B/Yam and B/Vic was detected in 2016. The phylogenetic analysis of these B strains shows compatibility with the corresponding vaccine strains for each influenza season. They were all sensitive to the usual antivirals

Conclusion:
This study highlights the importance of continuous surveillance of influenza viruses to better understand the epidemiology and evolutionary dynamics of influenza B viruses in the DRC for the fight and control of influenza.

Key words: Epidemiology, genetic evolution, Influenza B viruses, DRC

Resilience of the Biological Sentinel Surveillance network of Madagascar during the first wave of COVID-19 in 2020

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Biography:
Responsible for establishing and managing the biological sentinel surveillance network in Madagascar, tracking all progress, learning outcomes, health agent engagement, and ensuring that the surveillance system being consistently and systematically tracked and reported. Collaborates with the Ministry of Health to provide feedback on data collection and indicators; analyzes data reported from lab; and supports training of health agent in quality assurance methods: epidemiologic data and biological samples collection.

Introduction: Since February 2019, the biological sentinel surveillance (BSS) network led by Referral Centers for Biological Surveillance (CSB_R) has been used by the Ministry of Public Health (MoH) to reinforce the “electronic integrated disease surveillance and response” (e-IDSR). Here, we report the challenges encountered to manage the BSS network during the first wave of COVID-19.

Methods: Seven CSB_Rs located in urban area or harbour town, were implicated in the passive surveillance of arboviral and respiratory diseases using fever as the main criteria to collect specimens. They performed appropriate biological sampling and sent them to IPM for diagnosis.

Results: As soon as the first case of COVID-19 was identified, the government first set-up a national lockdown from week 12 to 32 and followed by a partial lockdown from week 33 to 42 of 2020. During these periods: the number of outpatient visits at CSB_R decreased by 45% thus the average of the monthly outpatients visits was 2,168 vs 1,191. The transportation of samples from CSB_Rs to IPM was disturbed with the median time of transportation increased by 6 days (IQR: 3-7) to 7 days (IQR: 4-9). Nevertheless, from week 01 to 42, IPM received and analyzed 641 nasopharyngeal samples from patients presenting influenza like illness for respiratory diseases surveillance and 182 acute blood samples for arbovirus diagnosis. All samples met quality and safety requirements. DENV-1 and 2 were identified in 3/7 CSB_Rs: Nosy Be (week 02 to 25), Mahajanga I (week 18 to 26) and Antsiranana I (week 20 to 22), with a global positivity rate of 37.4% (68/182).

Conclusion: These results highlight the fact that the BSS network was still able to monitor dengue circulation even in a degraded context. So, BSS network is a key to prompt survey epidemic prone disease in Madagascar and must maintain for pandemic preparedness.

Molecular characterisation of influenza A(H1N1)pdm09 virus and antigenic drift from the seasonal vaccine strain in South Africa in 2022

Ms Dikeledi Kekana[1], Ms Anele Mnguni[1], Ms Noxolo Ntuli[1], Ms Amelia Buys[1], Ms Alexandra Moerdyk[1], Ms Ayanda Nzimande[1], Mr Boitshoko Mahlangu[1], Ms Buhle Ntozini[1], Ms Josie Everatt[1], Ms Fahima Moosa[1], Ms Nadine Stock[1], Ms Thulisile Dlamini[1], Ms Valencia Petje[1], Ms Sibongile Walaza[1,3], Ms Cheryl Cohen[1,2], Ms Anne Von Gottberg[1,2]

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Biography:

Dikeledi Kekana is a Medical Scientist (Bioinformatics) who completed her honours degree at Nelson Mandela University, majoring in Physiology. Her research project focused on the neuroinflammation in rats prenatally exposed to a high-fat diet. Kekana completed a Master's in medicine, infectious diseases and clinical microbiology from the University of the Witwatersrand investigating a neonatal Candida auris outbreak using bioinformatics methods. Kekana works as a Bioinformatics Scientist at the National Institute of Communicable Diseases located in Johannesburg, South Africa. She focuses on next-generation sequencing (NGS) data analysis of Viral genomes.

Introduction

Influenza A viruses evolve through substitutions that may change antibody binding sites directly or through the acquisition/loss of glycosylation sites on the haemagglutinin (HA) protein (antigenic drift). As a result, seasonal vaccines are reviewed annually to include recently circulating viruses. We aimed to describe the genotypic and phenotypic characteristics of the A(H1N1)pdm09 viruses circulating in 2022.

Methods

Influenza-positive specimens were collected through syndromic respiratory illness surveillance. Phylogenetic analysis of HA genes (n=88) obtained from GISAID on 09/04/2023 was achieved using RAxML v8.2.12. Clades were designated using NextClade, while N-glycosylation (NLG) sites were predicted using NetNGlyc1.0. The haemagglutinin inhibition (HAI) assay was performed using antisera raised against A/Indiana/02/2020 (same clade (5a.2) as the 2022 vaccine strain). Only sequences with available HAI results were used for the NLG analysis (n=60/88).

Results

Of the 88 sequences, 58% (51/88) clustered within the 6B.1A.5a.2a.1 (5a.2a.1) clade while 25% (22/88) and 17% (15/88) belonged to 6B.1A.5a.1 (5a.1) and 6B.1A.5a.2a (5a.2a) clades respectively. Vaccine antisera showed good recognition of strains belonging to the 5a.1 clade (94%, 16/17) and reduced recognition to 5a.2a (40%, 4/10) and 5a.2a.1 (24%, 8/33). Nine potential N-glycosylation sites were identified at positions 27, 28, 40, 104, 179, 293, 304, 498, 557. All sites, except 293, were conserved across all clades. Clades 5a.1 and 5a.2a possessed the sequon (a sequence of consecutive amino acids) NTTC on site 293 while clade 5a.2a.1 had the NATC sequon. Additionally, clade 5a.2a.1 possessed the P154S substitution that might have contributed to the reduced antibody recognition. The substitution is located within an immune epitope which allows evasion of antibodies targeting the Ca2 antigenic region.

Conclusion

Three clades of A(H1N1)pdm09 co-circulated in South Africa in 2022. Furthermore, antigenic drift through amino acid substitutions and N-glycosylation was observed and resulted in poor recognition of clade 5a.2a.1 viruses against vaccine-like antisera.

Integrating COVID-19 and influenza sentinel surveillance – Experience from Togo

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Biography:
Dr Issaka Maman is graduated as PhD in molecular Microbiology and Immunology of University of Lomé (Togo). He is currently working as Head of Molecular biology laboratory and Head of National Influenza Center (NIC) in Togo at the national reference laboratory in Togo (Institut National d'Hygiène). He is teaching Genomic and molecular biology course at the University of Lomé Sciences Faculty and in high school of food and biology technology (ESTBA).

Background

Togo established influenza sentinel surveillance in 2010, with a total of 6 sentinel sites for influenza-like-illness (ILI) and severe acute respiratory infection (SARI) distributed across the country. As the COVID-19 pandemic hit, Togo started facing challenges with influenza surveillance recording a substantial reduction in the number of ILI and SARI cases and of specimens collected at sentinel sites. The integration of SARS-CoV-2 surveillance into the influenza sentinel surveillance is important to maintain its routine activities.

Methods

Strategies used to understand the low circulation of influenza virus due to the presence of SARS-CoV-2 virus include 1) sentinel site visit in July 2020 and May 2021. Meetings with clinicians, site focal point, laboratory staff, data manager and the site director were organized to discuss the challenges and find potential solutions 2) investigation of outbreak in January 2021. Based on findings, a new surveillance approach was validated with the integration of SARS-CoV-2 into the influenza sentinel surveillance.

Results

This new approach helped strengthening biosafety and biosecurity measures at sentinel sites with the provision of consumables and PPE for sample collection; improved collaboration with the COVID-19 rapid response team and redefined patients and samples pathways; ensured daily transportation of samples by leveraging the transport means used for SARS-CoV-2 samples; and ensured testing simultaneously for influenza and SARS-CoV-2 using the new CDC Flu-SARS-CoV-2 protocol. A new protocol of integrated sentinel surveillance of influenza and SARS-CoV-2 was validated by October 2021. By the end of 2021, the number of samples collected increase of approximately 20% in comparison to 2020.

Conclusions

The integrated approach has been successfully implemented in all the six sentinel sites. For the sustainability of the influenza surveillance program, SARS-CoV-2 and other respiratory virus should be integrated into influenza surveillance.

Key words: COVID-19, Influenza, Integration

Repurposing an integrated national influenza platform for genomic surveillance of SARS-CoV-2 in Ghana: a molecular epidemiological analysis

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Biography:

I am a young researcher specializing in infectious diseases, particularly respiratory viruses, and HIV, with a passion for unraveling mechanisms of transmission and pathogenesis of these diseases to develop innovative therapies and improve patient outcomes. My work has been published in reputable journals and actively contributes to scientific discourse. I am committed to expanding my knowledge, networking with experts, and making a lasting impact in the field. Attending ANISE 2023 is a pivotal step in my academic career, providing valuable opportunities for collaboration and growth. I aspire to become a leading figure in infectious disease research and global health initiatives.

Background: Genomic surveillance of SARS-CoV-2 is crucial for monitoring the spread of COVID-19 and guiding public health decisions, but the capacity for SARS-CoV-2 testing and sequencing in Africa is low. We integrated SARS-CoV-2 surveillance into an existing influenza surveillance network with the aim of providing insights into SARS-CoV-2 transmission and genomics in Ghana.
Methods: We collected SARS-CoV-2 test data from 35 sites across 16 regions in Ghana from Sept 1, 2020, to Nov 30, 2021, via the Ghanaian integrated influenza and SARS-CoV-2 surveillance network. SARS-CoV-2-positive samples collected were sequenced with Oxford Nanopore Technology and the ARTIC tiled amplicon method. The sequence lineages were typed with pangolin and the phylogenetic analysis was conducted with IQ-Tree2 and TreeTime.

Results: During the study period, 5495 samples were submitted for diagnostic testing through the national influenza surveillance network. Additionally, 2289 samples were obtained from travelers who arrived in Accra and had a positive lateral flow test; 1626 were confirmed as SARS-CoV-2 positive. Co-circulation of influenza and SARS-CoV-2 in Ghana was detected, with increased cases of influenza in November 2020, November 2021, and January, and June, 2021. We detected four waves of SARS-CoV-2 infections in Ghana; each wave was driven by a different variant: B.1 and B.1.1 were the most prevalent lineages in wave 1, alpha (B.1.1.7) was responsible for wave 2, delta (B.1.617.2) and its sub-lineages were responsible for wave 3, and omicron variants were responsible for wave 4.

Conclusion: This study shows the value of repurposing existing influenza surveillance platforms to monitor SARS-CoV-2. Influenza continued to circulate in Ghana in 2020 and 2021 and remained a major cause of severe acute respiratory illness. Investment in strengthening national influenza

surveillance platforms in low- and middle-income countries has the potential for monitoring of SARS-CoV-2 and future pandemics.

Keywords: Integrated influenza platform, Genomic surveillance, SARS-CoV-2, Ghana

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Estimation of influenza attack rate using PCR and serology within a community cohort (PHIRST), South Africa, 2016

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Biography:

I am a 36-year-old highly motivated Medical Scientist with over 5 years of experience in diagnostic, public health research and surveillance in Medical Virology. I was trained as a Medical Scientist at the National Institute for Communicable Diseases, and I work in the Centre for Respiratory Diseases and Meningitis in the section of Influenza serology and virus Isolations. I hold BSc honours degree (University of Limpopo), MSc Virology (University of Limpopo) and PhD Microbiology degree (University of Pretoria).

Background

Influenza causes substantial morbidity, and mortality worldwide. Here, we compared the influenza attack rate using serology versus rRT-PCR in a household community cohort study.

Methods

Household members from randomly-selected households were enrolled in Klerksdorp (urban) and Agincourt (rural) settings in May 2016 and followed for six months. Nasopharyngeal swabs were collected twice weekly regardless of symptoms and tested and subtyped by PCR. Blood specimens were collected at the beginning and end of the follow-up period, corresponding to before and after the influenza season (May-August), and tested by hemagglutination inhibition assay against circulating viruses with a ≥4-fold rise in antibody titre considered seroconversion. Proportions were compared using chi-squared test.

Results

Overall, 420/542 (77.5%) individuals from 122 enrolled households had pre-and post-season serology results. The serological attack rate was 42.9% (180/420): 16.4% (69/420) against A(H1N1) pdm09,

3.3% (14/420) against A(H3N2), 18.1% (76/420) against B/Victoria, and 5.0% (21/420) against B/Yamagata. A total of 43/420 (10.2%) persons seroconverted against two subtypes/lineages with 34.9% (15/43) seroconverting against A(H1N1) pdm09 & B/Victoria. The attack rate by PCR [31.2% (131/420)] was lower than by serology ($p<0.001$); with 11.9% (50/420), 3.3% (14/420), 15.2% (64/420), and 0.7% (3/420) testing positive for A(H1N1) pdm09, A(H3N2), B/Victoria, and B/Yamagata, respectively. Among individuals who seroconverted, 11.6% (8/69) A(H1N1) pdm09, 28.6% (4/14) A(H3N2), 27.6% (21/76) B/Victoria, and 47.6% (10/21) B/Yamagata were not detected by PCR. Among PCR-positive individuals, 12.0% (6/50) A(H1N1) pdm09, 28.6% (4/14) A(H3N2), 18.8% (12/64) B/Victoria, and 33.3% (1/3) B/Yamagata did not seroconvert.

Conclusion

A significantly higher number of individuals seroconverted compared to PCR-documented infection. In addition, a substantial proportion of PCR positive individuals did not seroconvert. These findings indicate that serology may be important in detecting cases missed by PCR and the utility of using both serology and PCR for determining attack rate and refining burden of disease estimates.

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Integrating SARS-CoV-2 into Global Influenza Surveillance System: the Experience of WHO African countries in the Context of the Pandemic

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Biography:

Employed by World Health Organization's (WHO) Headquarters Global Influenza Programme as a technical officer. Medical doctor trained as a laboratory physician. Started the career in 2007 as a Biosafety Officer at the National Microbiology Reference Laboratory (NRL) in Riga, Latvia, and worked as a Virologist in the WHO-recognized NIC-Riga. From 2013-2015, was employed by the ECDC European Public Health Microbiology Training (EUPHEM) program and was based at the Robert Koch Institute in Berlin, Germany. Then worked as a Laboratory Consultant at the WHO Regional Office for Europe from 2015-2021 (both full-time and part-time) and was head of NRL/Latvia 2019-2023.

Background

Following the COVID-19 pandemic, the Global Influenza Surveillance and Response System network rapidly escalated the ILI/ARI and SARI sentinel surveillance to integrate SARS-CoV-2 (SC-2) testing in sentinel health facilities to monitor the spread and intensity of COVID-19.

Methods

Data was collected from FluNet, the WHO data platform for influenza virological surveillance, between March 30, 2020, to March 30, 2023, and analyzed by year for consistency, adequacy, and timeliness, according to WHO guidance criteria. Countries reported SC-2 results from different sources (sentinel, non-sentinel, undefined).

Results

Of the 47 Member states of the WHO African Region, 30 (64%) countries reported virological surveillance data to FluNet, of which 25 (83%), 28 (93%), and 29 (97%) countries reported during the first, second, and third year, respectively. Only two, five, and seven countries reported timely during years one, two, and three, respectively. Results of sentinel or undefined SC-2 specimens tested were reported by 15 (60%), 23 (82%), and 25 (86%) countries in the 1st, the 2nd, and the 3rd year respectively. The number of countries reporting consistently (>30 weeks and more) was 5 (20%), to14

(50%), and 22 (76%) in years 1, 2, and 3, respectively. We noted that 1(4%), 6 (21%), and 12 (41%) countries tested and reported at least 50 specimens per week during 30 weeks or more.

Conclusions
We have observed a consistent increase in the number of countries that have reported their integrated SC-2 surveillance data to FluNet. However, the number of countries that regularly report sentinel data in a timely manner is still low, with some countries within the region not reporting their data to FluNet. These gaps in reporting underscore the need for continued efforts to improve the detection and reporting of surveillance data related to respiratory viruses that can potentially cause epidemics and pandemics.

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Epidemiological aspects of co-infection of Influenza and coronavirus 2 viruses from severe acute respiratory syndrome during pandemic to coronavirus-19 disease in Yaoundé, Cameroon.

Mr Mohamadou Leopold Njankouo Ripa[1], Dr Gwladys Chavely Monamele[1], Mr Moïse Henri Moumbeket Yifomnjou[1], Dr Serges Tchatchouang[1], Mr Landry Messanga[1], Dr Abdou Fatawou Modiyinji[1], Dr Paul Alain Tagnouokam Ngoupo[1], Pr Richard Njouom[1]
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Biography:
I am a laboratory technician trained at the Centre pasteur du Cameroun since 2003. I have been working in the virology department of this institution since 2009, in charge of detecting influenza and other respiratory viruses. I also work on other viral topics. I have co-authored several scientific articles. I have been a very active member of the COVID-19 response in Cameroon. I have also participated in the training of several medical analysis technicians and in the technical supervision of several Masters and Thesis students.

COVID-19 caused by the severe acute respiratory syndrome–corona virus 2 (SARS-COV-2) is a respiratory syndrome with symptoms and epidemiology similar to those of influenza. These two viral infections are responsible for a great burden of respiratory disease worldwide. It is therefore important to study the circulation of influenza viruses and SARS-COV-2 to provide evidence to guide policies on the surveillance of these viruses. The aim of this study was to describe the epidemiology of influenza virus and SARS-CoV-2 infections during the COVID-19 pandemic in Yaoundé.

In a prospective cross-sectional study, nasal and nasopharyngeal swabs were collected from patients presenting with influenza-like illness during the period from July 2021 to February 2022 in Yaoundé, Cameroon. These samples were analyzed at the virology laboratory of the Centre Pasteur du Cameroun using the real-time triplex Reverse Transcriptase-Polymerase Chain Reaction technique, which detects both influenza viruses (Influenza A and B) and SARS-CoV-2. Influenza A and B positive cases were subtyped using a multiplex RT-PCR developed by the Centers for Disease Control and Prevention.

A total of 767 samples were collected and results showed that 107 (14%) were positive for SARS-CoV-2, 129 (16.8%) for influenza viruses. Influenza A virus was the predominant virus identified accounting for 83.7% of all influenza viruses (108/129). On subtyping influenza viruses, 74 (57.4%) were A/H1N1pdm09; 34 (26.4%) A/H3N2 and 20 (15.5%) B/Victoria viruses. The unique case (0.6%) of co-infection involved influenza A/H3N2 subtype and B/Victoria lineage. No case of co-infection between Influenza and SARS-CoV-2 viruses was identified.

The results of this study show co-circulation of Influenza and SARS-CoV-2 viruses during the COVID-19 pandemic. However, no cases of co-infection between the two viruses were identified. Analysis on a larger scale and representative sample of the population are necessary to confirm these results.

Influenza, SARS-CoV-2, COVID-19, RT-PCR, Co-infection, Cameroon

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First identification of the XBB.1.5 sublineage among indigenous Covid-19 cases detected through the influenza sentinel surveillance system in Niger

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[1]Centre de Recherche Medicale et Sanitaire (CERMES)

Biography:

Head of Virology unit at CERMES withmore than 10 years experience on influenza surveillance

The emergence of Omicron variant in November 2021, has incredibly cause panic worldwide due to the rapid evolution and the ability of the virus to escape the immune system. Since, several Omicron sublineages (BA.1 to BA.5) and their descendent recombinant lineages have been circulating worldwide. Furthermore, in December 2022, a new Omicron subvariant XBB.1.5 characterized by unusual mutation in the spike protein evolved in the United States and rapidly spread to the other continents. Our study reports on the first cases of XBB.1.5 sublineage among indigenous SARS-CoV-2 positive cases detected through the influenza sentinel surveillance system in Niger. All influenza suspected cases were tested for both influenza and SARS-CoV-2 using the CDC Influenza SARS-CoV-2 Multiplex qRT-PCR Assay. SARS-CoV-2 positive samples with cycle threshold ≤28 were selected for whole genome sequencing subsequently using the Oxford Nanopore Midnight protocol with rapid barcoding on MinIon MK1B device. A total of 51 SARS-CoV-2 positive samples were confirmed between December 2022 and March 2023. We successfully obtained 19 sequences with a predominance of the XBB.1/XBB.1.5 sublineages (73.7%). In addition, a recombinant XBD sequence was also first-ever identified in early March 2023. Our findings support the need to strengthen the influenza sentinel surveillance for routine Covid-19 surveillance and SARS-CoV-2 variants monitoring in Niger.

Demonstration projects to estimate the burden of disease from RSV infection in select African countries

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Biography:

Eva Leidman, PhD MSPH, leads the Epidemiology and Operational Research Team within the Centers for Disease Control and Prevention's (CDC) Global Respiratory Virus Branch. She holds an adjunct appointment at the Hubert Department of Global Heath at the Emory Rollins School of Public Health. Current work focuses on surveillance of coronaviruses (particularly SARS-CoV-2), Respiratory Syncytial Virus (RSV), and other respiratory viruses including characterizing burden of disease and vaccine effectiveness.

Background: Respiratory syncytial virus (RSV) vaccine candidates have advanced to late-stage human trials and regulatory approval. To support public health and inform vaccination introduction, national and global initiatives aim to catalyze efforts to estimate RSV disease burden.

Methods and Results: Coordination of surveillance activities in Kenya and Zambia aim to support burden of disease estimation – characterizing the contribution of RSV to hospitalizations (Tier 1 burden of disease), more severe disease (Tier 2) as well as incidence of medically attended RSV in the population (Tier 3). In Zambia, universal testing of all children two years of age and younger presenting to intensive care (IC) and/or with acute onset respiratory infection at two pediatric referral hospitals, will allow for monitoring the proportion of IC admissions due to RSV. Universal testing will additionally allow for evaluation of sensitivity and feasibility of applying the World Health Organization proposed case definition for RSV surveillance. In Kenya, a longstanding Population-Based Integrated Disease Surveillance (PBIDS) platform will be leveraged to estimate incidence of RSV in sites in three regions: Siaya, Nairobi, and Isiolo. PBIDS maintains rigorous vital registration, via active house-to-house surveillance, and health facility-based surveillance. Available data will allow for estimating incidence by disease severity and care seeking behaviors among children and older adults. Both Siaya and Nairobi have hospitals planning to integrate RSV testing into ongoing influenza sentinel surveillance, providing an opportunity to triangulate findings. In all pilot studies, respiratory specimens from eligible individuals will be tested by rtPCR using a multiplex assay that allows for typing of RSV A and B.

Conclusions: The pilots will leverage existing RSV surveillance efforts, including a pilot integration of RSV into the Global Influenza Surveillance and Response System (GISRS+) and previous studies in both countries, to inform plans for future vaccine introduction and strengthen regional surveillance platforms.

Genetic evolution of seasonal influenza A(H3N2) in South Africa spanning the COVID-19 pandemic, 2018-2022

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Biography:

Anele Mnguni is a Medical Scientist at the National Institute for Communicable Diseases (Centre of Respiratory Diseases and Meningitis). Anele is a wet-lab scientist for Centre's Whole Genome Sequencing Team which forms part of the National Influenza Centre. They characterize Influenza, SARS-CoV-2 and RSV pathogens using sequencing methodologies. Part of her interests includes optimizing new sequencing work-flows for respiratory pathogens and facilitating teaching and training for other African countries. She obtained a MSc. in Genetics at the University of KwaZulu Natal.

Background
Influenza A(H3N2) accumulates substitutions in hemagglutinin(HA), a surface glycoprotein, that leads to novel sub-clades every 2-6 years and may affect susceptibility to neutralizing antibodies from vaccination or previous infection. Currently-circulating sub-clades branch from clade 3c.2. We aimed to describe the genetic evolution of A(H3N2) during 2018-2022, spanning the COVID-19 pandemic during which there was limited influenza activity.

Methods
Influenza polymerase chain reaction (PCR)-positive nasopharyngeal specimens were collected through sentinel, syndromic respiratory illness surveillance in South Africa from 2018-2022, and characterized using whole genome sequencing. A(H3N2) sequences with complete HA genes were downloaded from GISAID on 9 May 2023 (N=108). Phylogenetic analysis was performed using RAxML. Sub-clades were identified on NextClade. Maximum Clade Credibility tree was created using BEAST v1.10.4. Periods of circulation were defined as 2018-2019 (prior), 2020-2021 (during), and 2022 (post-pandemic).

Results
We sequenced 19% (43/225) prior, 63% (25/40) during and 28% (40/143) post-pandemic A(H3N2) samples. Nine sub-clades of 3c.2a circulated from 2018-2022. Sub-clade 3c.2a1b.2a.2c was not identified prior to the pandemic (0/43) but accounted for 36% (9/25) of sequences in 2020-2021 and 80% (32/40) in 2022. Substitutions were detected in the HA1 subunit; HA2 remained conserved. Sub-clade 3c.2a1b2a.2b (20%, 8/40) was only detected post-pandemic, 3c.2a1b.1 and 3c.2a1b.1b only circulated prior (21% (9/43), 5% (2/43)) and during (8% (2/25), 20% (5/25)) the pandemic at low levels. Genomes that diverged from 3c.2a.1 had E62G and T128A substitutions. Sub-clade 3c.2a1b.1a was only detected in 2020-2021 (36%, 9/25) with additional substitutions observed in 2021 compared to 2020 strains. In 2018-2020, circulating strains were closely related to vaccine strains, however circulating viruses from 2021-2022 were more divergent.

Conclusion
Despite limited circulation during the COVID-19 pandemic, influenza A(H3N2) viruses continued to evolve and undergo antigenic drift, which may affect vaccine effectiveness. Continued genomic surveillance is important to monitor changes relative to vaccine strains.

ETIOLOGICAL PROFILE OF OTHER RESPIRATORY VIRUSES DURING THE 2020-2021 COVID-19 PANDEMIC

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Biography:

She is Doctor of medicine, and in the course of specialization in medical biology option microbiology.

She works as a scientist in the laboratory of respiratory viruses including influenza at the INRB and has acquired expertise in the diagnosis of respiratory viruses. She is preparing for the defense of her master's degree in virology.

Background

The emergence of SARS CoV-2 in the Covid-19 pandemic has sparked interest in the role of others respiratory viruses in respiratory infection which are a major cause of morbidity and mortality worldwide.

As part of sentinel surveillance of influenza in the DRC, the laboratory had extended detection to other respiratory viruses circulating in the same way as SARSCoV2.
The purpose of this study is to monitor the other viral etiologies of acute respiratory infections during the 2020-2021pandemic.

Methods

Samples were collected from suspected outpatients with influenza-like illness (ILI) and in all hospitalized patients with SARI seen at sentinel influenza surveillance sites in Kinshasa.
Molecular analysis was done to detect the following respiratory viruses like influenza A and B viruses, SARS Cov2, RSV, MPV, PIV, RV, AdV

Results

Of 1665 samples received and tested , 757 (45%) were positive for respiratory viruses including 324 (43%) SC2 ,112 (15%) influenza including 70% Flu A and 30% Flu B, 93 (12%) RSV, 88 (11.6%) RV, 51 (6%) PIV3, 32 (4.2%) ADV, 31 (4%) MPV; and remainder is divided between PIV4 (1.4%), PIV1 (1.3%) and PIV2 (1%).
12 % of coinfections were noted between SARS CoV-2 with other respiratory viruses such as PIV1 , PIV4, Flu (A/ H3N2) and RSV .
40% viral respiratory infection were an outpatient and 45% were hospitalized associated at 14% SarsCoV2, 10% RSV and 4% MPV.
A/H3N2 was predominant than A/H1N1pdm among flu A and B/Victoria more important than B/Yamagata among Flu B.

Conclusion

Respiratory viruses play a key role in respiratory pathology.
Hence the importance of strengthening surveillance of respiratory viruses in the influenza system particularly those associated with disease severity including RSV and MPV in addition to influenza viruses and SarsCoV2.

Evaluation of Point of Care device and antigen kits for diagnosis of seasonal influenza infection in Ghana

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Biography:
Esinam Amenuvor is a young research scientist with a keen interest in studying the spread, diagnosis and treatment of infectious diseases, predominantly of viral origin that pose public health threats. Esinam has a background in biochemistry with a working experience in molecular identification and characterisation of respiratory pathogens. It is from this she has gained interest to further her career in medical microbiology and public health. She also has skills in molecular techniques, data management, and quality management systems.

Background
Rapid diagnosis of influenza is essential for early treatment and the institution of control measures. We evaluated the sensitivity, specificity, and feasibility for point-of-care use of the UniCare Influenza A/B Antigen test kits and UniKoReader Smart Analyzer using archived (collected between 2018 and 2021) and freshly collected nasopharyngeal swabs (taken between April to August 2022).

Method
A total of 300 archived samples with influenza infection status previously determined by reverse transcription quantitative polymerase chain reaction (RT-qPCR) assays (influenza A, n = 120; influenza B, n = 120; negative samples, n = 60) and 1241 (influenza A, n = 258; influenza B, n = 1; negative samples, n = 982) freshly collected nasopharyngeal swabs from patients experiencing respiratory symptoms were tested.

Results
The sensitivity of the UniCare kit was higher for the freshly collected nasopharyngeal swabs (66%, 171/259) than for the archived samples (48%, 115/240) [p-value<0.001]. In archived samples, sensitivity was 57% (68/120) for influenza
A and 39% (47/120) for influenza B. With freshly collected samples, sensitivity was 64% (166/258) for influenza A, and 100% (1/1) for influenza B. Specificity was 83% (50/60) for archived samples and 77% (759/982) for the freshly collected samples (p-value=0.281).

Conclusion
Field observations indicated that the kits and analyzer were user-friendly and had a long battery-life. We conclude that the UniCare kit and UnikoReader analyzer can be used as a screening tool for the diagnosis of influenza in field settings.

Surge in influenza and COVID-19 cases in Ghana within the first two months of 2023

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Biography:

Obed Ofori Bangdome is an author of the book titled "Qualitative Study on Delivery Care Services in Bibiani Anhwiaso Bekwai". He is young researcher who graduated from the University of Ghana and currently works as the Influenza Coordinator for Ghana. His passion is developed skills to build expertise in infectious diseases prevention to improve human health.

Background

Respiratory tract associated infections are responsible for significantly high morbidity and mortality especially during pandemics and seasonal episodes. In Ghana, routine and sentinel surveillance for respiratory pathogens has been established. This report describes the surge of influenza and SARS-CoV-2 infections in Ghana within the first two months of 2023.

Methods

We analyzed data and test results on samples sent from sentinel and non-sentinel sites during epidemiological weeks 1-9, 2023. Data was analyzed as detection rates, trends, and regional distribution.

Results

Influenza detection for processed samples was significantly higher in the first 9 weeks of 2023 (11%, 198/1766) vs the same period in 2022 (0.7%, 4/519) [p-value<0.001]. However, SARS-CoV-2 detection was higher in 2022 (144/519) vs 2023 (5%, 75/1766) [p-value<0.001]. For influenza related infections 94% (187/198) were influenza A(H1N1) pdm09 with the majority of cases detected among the 5-14 year age group. Majority of the influenza detections were from patients with ILI (83.4%, 166/198) compared with SARI (16.7%, 33/198). Geographically, the highest positivity rates for influenza were observed in Greater Accra (24%) and Ashanti (18%) regions while Northern and Savannah regions recorded 14% and 12% positivity rate for SARS-CoV-2. Although SARS-CoV-2 and influenza co-circulated, influenza driven by A(H1N1) pdm09 significantly contributed to the surge in respiratory infection in Ghana compared to the previous year. Similar situations have been recorded in Ghana’s neighboring countries.

Conclusions

These observations underscore the importance of maintaining surveillance systems such as these.

Evaluation of the Illumina Respiratory Pathogen ID/AMR Enrichment Panel (RPIP) as a pandemic preparedness tool

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Biography:

Ayanda Nzimande is a Medical Scientist in the Centre for Respiratory Diseases and Meningitis at the National Institute for Communicable Diseases of the National Health Laboratory Service, South Africa. She is also involved in surveillance, genomics and viral diagnostics research for public health. Ayanda currently holds a Master's degree in Applied Sciences: Biotechnology.

Background

Avian influenza outbreaks continue to occur among wild birds and poultry, with increasing reports of spill-over into humans. We evaluated multiplex hybridisation capture sequencing to characterise influenza (including avian subtypes), as a pandemic preparedness tool in the event of unknown respiratory pathogen outbreaks.

Methods

Influenza PCR-positive nasopharyngeal specimens (cycle threshold value <30, n=18) from individuals enrolled in sentinel syndromic surveillance for influenza-like illnesses and severe respiratory illness in South Africa were sequenced using Respiratory Pathogen ID/AMR Enrichment Panel (RPIP) kit (Illumina® Inc, San Diego, CA, USA) on the Illumina NextSeq1000. We tested RNA extracts of avian influenza subtypes H4N8, H11N2, H6N2, H3N6, H7N1 (n=5). Sequencing data was analysed with the Explify RPIP Data Analysis tool on BaseSpace (quality criteria of 80% coverage, 100x median depth and ≥500 RPKM [Reads Per Kilobase of targeted sequence per Million reads] of the whole genome) and the Iterative Refinement Meta-Assembler (IRMA) pipeline.

Results

For seasonal influenza, high quality whole genomes were obtained for 100% (4/4) A(H1N1)pdm09, 82% (9/11) A(H3N2) and 100% (3/3) B/Victoria samples, with >90% coverage and median depth ≥9095x (77148 RPKM), ≥22698x (66850 RPKM) and ≥310x (14203 RPKM), respectively. Two A(H3N2) samples had <80% coverage: subtype was determined, but whole genome data had insufficient quality. Explify did not detect avian influenza, however, using IRMA viruses were detected and subtyped. High coverage for 80% (4/5) avian influenza samples, with average coverage at 10x depth of 85% for HA and 100% for NA, PA, PB1, PB2, NS, NP and MP gene segments was produced. For H7N1, all 8 segments had average coverage <50%.

Conclusion

RPIP accurately detects seasonal influenza, but avian influenza subtypes were only detected when used together with the IRMA pipeline. RPIP may serve as a useful tool to investigate unknown respiratory disease cases, but may require additional analysis tools.

Keywords: RPIP, Pandemic preparedness, Influenza, Avian influenza, Sequencing

Differences in clinical presentation between respiratory syncytial virus and influenza infected children — global respiratory syncytial virus surveillance project, 2017–2022

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Biography:
Dr Shang is a consultant for WHO Global Influenza Program since 2022 Nov. Previously she worked as an epidemiologist in WHO Papua New Guinea Country Office and Cambodia Office during 2018-2022. Before joining WHO, Dr Shang worked in Immunization Service Division and Influenza Division of CDC (2010-2018).

Background: Respiratory Syncytial Virus (RSV) and influenza are two important causes of pediatric acute respiratory infections (ARI) and hospitalizations. Since 2017 WHO has piloted a surveillance strategy for RSV in 25 countries across the 6 WHO regions that leverages the Global Influenza Surveillance and Response Systems.

Methods: Children aged <5 years and met ARI case definition that did not require fever at the sentinel hospitals were swabbed and tested with RT-PCR for RSV and influenza. Data were collected on clinical symptoms, severity, and pre-existing conditions. We compared RSV and influenza percent-positivity across 5 age groups and clinical presentations in RSV positive children with influenza positive children using random effect logistic regression controlling for age and country cluster.
Results: Among 49,478 children tested during 2017–2022, 27% had RSV, 5% had influenza, 0.42% had co-infections. The percent-positivity of RSV was higher than influenza in children aged 0–2 months, 3–5months, 6–11 months, 12–23 months, 24–59 months (32% vs 2%, 38% vs 3%, 27% vs 6%, 20% vs 7% and 13% vs 10% respectively, $P < 0.01$). RSV infected children were less likely to have fever (OR: 0.53, 95% CI:0.47–0.60), Integrated Management of Childhood Illness danger signs (OR: 0.73, 95% CI:0.56–0.95), low oxygen saturation (OR:0.59, 95% CI:0.46–0.76), but more likely to have tachypnoea (OR: 1.63, 95% CI: 1.45–1.85), wheeze (OR:2.27, 95% CI: 1.91–2.70), shortness of breath (OR: 2.45, 95% CI: 2.10–2.92) than influenza infected children. We did not observe difference in ICU admission and/or ventilatory support needs (OR: 0.93, 95% CI: 0.75–1.18).

Conclusions: RSV infection was more common than influenza infection among young children especially those aged <2 years. This analysis highlighted focused attention for young children with ARI symptoms irrespective of fever to minimize the risk of severe outcomes.

Genomic Sequencing Capacities in Africa during the COVID-19 Response

Dr Obadiah Mfuh Kenji[1], Dr Siddhivinayak Hirve[1], Dr Sebastian Maurer-Stroh[3], Dr Belinda Louise Herring[2], Dr Sergejs Nikisins[1], Dr Dmitriy Pereyaslov[1], Dr Wenqing Zhang[1]
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Biography:

Dr. Kenji Obadia is a highly accomplished professional with a diverse medical microbiology, molecular biology, and public health background. Kenji has made significant contributions to the field with an MPH and Ph.D. in Medical Microbiology. Previously, Kenji was the Lead Scientist for Clinical Genomics at Illumina USA, Manager of Infectious Disease and Esoteric Testing at Stanford Medicine USA, and Medical Lab Director Consultant. Kenji has demonstrated expertise in molecular diagnostics and Genomic surveillance. Kenji is a consultant for the Global Influenza program at the World Health Organization (WHO), leveraging his extensive knowledge for integrated respiratory virus surveillance.

Background: The COVID-19 pandemic has highlighted the crucial role of genomic sequencing in understanding viral transmission, detecting emerging variants, and guiding public health interventions. Africa, experiences a disproportionate infectious diseases burden and regionally utilization of genomic sequencing technologies has been limited. The COVID-19 pandemic offered an opportunity to strengthen genomic sequencing capacities across Africa.

Methods: We reviewed SARS-CoV-2 genomic sequencing data (GSD) submitted to GISAID, the global data science initiative, from September 2020 to August 2022.

Results: During the study period, 12,898,815 SARS-CoV-2 GSD submissions were made to GISAID, with countries in the WHO African Region accounting for 125,912 (0.97%) of these submissions. There were 34,018 submissions from the WHO African Region between September 2020 and August 2021, 91,893 submissions between September 2021 and August 2022, an increase of 170%. Globally, the Global Influenza Surveillance and Response System (GISRS) laboratories contributed 28% of sequence submissions. Contributions by GISRS laboratories in each of the 6 WHO Regions were 24.7% 35.8%, 2.2%, 26.3%, 8.7%, and 12.6% from the WHO African Region, WHO Regions of the Americas, Eastern Mediterranean, Europe, Southeast Asia, and Western Pacific Regions respectively. The timeliness of GSD submission globally improved with the median time from sample collection to deposition decreasing from a range of 8 to 147 days in the last 6 months to a range of 8 to 79 days in the most recent 3 months.

Conclusion: Genomic sequencing capacities improved significantly globally during the COVID-19 pandemic as seen by the increased submissions and improved timeliness of genomic sequence data. It is important to sustain and further strengthen sequencing capacities in all WHO Regions for other pathogens as part of WHO Global Genomic Surveillance strategy.

Keywords: Genomic sequencing, Africa, COVID-19, Capacity building

Using Community health workers to capture COVID-19 suspect cases and other Acute Respiratory Illnesses in Rural areas of Mozambique through a digital platform (AfyaData)

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Biography:

I am a Senior Researcher at the Instituto Nacional de Saúde – Ministry of Health – Mozambique, PostDoc Fellow in occupational Health at BICMINS Program from INS, coordinator of the Acute Febrile Illness Surveillance for The Emerging Infectious Disease, coordinator of the One Health Platform of Mozambique, In 12 years of vast experience working in a multidisciplinary environment, Under this umbrella, I participated in several research projects on pathogen surveillance, emergence, and health systems improvement, COVID-19 surveillance platform and ARI surveillance.

Background
Community Health Workers (CHWs) are members of the community deployed to deliver basic health care and education in their communities mainly in developing countries. Despite, their little technical, scientific, and technological skills, their contribution is unquestionable. However, how the CHWs deal with emerging diseases is unclear. This work aimed to assess the viability of the digital platform and CHW approach in community surveillance of the pandemic COVID-19.

Methods
An implementation study was carried out in the Chókwè district, based on surveys applied to eligible households between May and September 2021 with the help of 26 CHWs trained to use the AfyaData platform to identify COVID-19 and acute respiratory illnesses cases. Descriptive statistics and regression analysis were calculated.

Results
The AfyaData platform was able to capture 1801 suspected cases of COVID-19 compared to 1376 captured through hospital-based routine surveillance, of which, 301 were laboratory confirmed (r=0.709). The cases reported by CHW were located between 3 km and 15 km from a health facility. Of the suspected cases, 67.5% were female and 36.4% were under 18 years old. Family farmers and students were the most predominant with 38.8% and 16.5% respectively. Most of the participants claimed to have had contact with confirmed cases of COVID-19 in social gatherings, funerals, and public transport. The six most reported symptoms showed an alternating pattern. Most of the patients sought conventional treatment 97.8% and among those 27.3% performed self-medication.

Conclusion
The results suggest that a combined surveillance model using CHW and digital platforms such as AfyaData creates an opportunity for early reporting of cases and hence early detection of diseases such as COVID-19 and ARI at the community level. Social gatherings and funerals were the main sources of disease transmission. There is a need for planning interventions for proper Self-medication within the community.

Co-circulation of Influenza and SARS-COV-2 in Tunisia, season 2022-2023

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Biography:

Hind is an assistant professor in epidemiology and public health working at the Tunisian Ministry of Health, with experience in infectious disease surveillance, epidemic preparedness and response and field epidemiology. She has been involved in influenza surveillance for many years with research mainly in evaluation of influenza surveillance system, influenza modelling, and influenza vaccine uptake. During the COVID-19 pandemic, she participated in the national response including the analysis of national surveillance data, risk assessment, monitoring of the international situation as well as weekly epidemiological reporting and various COVID-19 research activities.

Background:
Circulation of respiratory viruses has changed substantially since the dissemination of SARS-COV-2 in early 2020. Following the low influenza activity reported during the first two years of the pandemic, influenza viruses seem to circulate again on a similar pre-COVID trend. Our objective was to describe the circulation of influenza viruses and SARS-COV-2 in Tunisia during 2022-2023 season.

Methods:
We conducted a descriptive analysis of the national sentinel surveillance data from week 40/2022 to week 18/2023. Nasopharyngeal samples were collected from sentinel Influenza-like illness (ILI) and Severe acute respiratory infection (SARI) and tested by multiplex rRT-PCR in the National Influenza Center. Data were entered in the national influenza electronic platform and analysis was using Epi-Info 7.2.

Results:
Out of the 1807 samples analyzed over the season, 380 were positive for influenza (overall positivity rate: 21%). Of these, 262 were type A, mainly A (H1N1) pmd09 virus (n=175; 66.79%). Circulation of influenza viruses started from W42-2022. From W46, influenza positivity rate increased to reach a peak in W49. After a predominance of the A(H1N1)pdm09 subtype, influenza activity decreased with a higher circulation of type B (subtype Victoria) since W5-2023. The overall SARS-CoV-2 positivity rate was 5.92%. During the first three months, SARS-COV-2 was detected at low levels with a general upward trend from W6-2023. Seven cases of co-infection of influenza and SARS-COV-2 were detected and 2 cases of co-infection of two influenza types.

Conclusion
After high SARS-COV-2 activity in 2020-2022, there was a significant circulation of influenza viruses since the beginning of the 2022-2023 season in Tunisia. This co-circulation can result in increasing pressure on the health system. Improving preparedness and awareness of preventive measures is highly recommended for the next season, especially among vulnerable groups.

Key words: influenza, virology, surveillance

Severity of seasonal influenza in Tunisia during 2022-2023 season

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Biography:

Hind is an assistant professor in epidemiology and public health working at the Tunisian Ministry of Health, with experience in infectious disease surveillance, epidemic preparedness and response and field epidemiology. She has been involved in influenza surveillance for many years with research mainly in evaluation of influenza surveillance system, influenza modelling, and influenza vaccine uptake. During the COVID-19 pandemic, she participated in the national response including the analysis of national surveillance data, risk assessment, monitoring of the international situation as well as weekly epidemiological reporting and various COVID-19 research activities.

Background:

Although most infections are mild, influenza can cause serious illness and death in people at high risk. The world has witnessed considerable changes in influenza virus circulation due to the COVID-19 pandemic. Our study aimed to describe the epidemiological and virological characteristics of severe acute respiratory infections (SARI) during the 2022-2023 season in Tunisia.

Methods:

We conducted a descriptive analysis of data collected from the SARI Sentinel Sites and the National Influenza Center. Influenza surveillance started from week 40/2022 to week 18/2023. All samples were tested for influenza viruses, SARS-CoV-2 virus and other respiratory viruses by multiplex rRT-PCR. We used the WHO case definition of SARI. The national influenza electronic platform was used for data entry and Epi-Info 7.2 for data analysis.

Results:

The total number of reported SARI cases was 1019. The highest number of SARI hospitalization was reported in W7, and 70% of the cases occurred between W48 and W11. The majority were males (58.6%) and aged more than 65 years (34%). Comorbidities were reported in 63.2% of the cases. Most cases were not vaccinated against influenza (98.02%). Influenza viruses were detected in 138 SARI cases (positivity 13.5%), mainly A(H1N1)pmd09 (58.7%). The overall SARS-CoV-2 positivity rate among SARI cases was 6.08%. A total of 100 SARI cases died (lethality rate 9.8%), of which 15 cases were positive for influenza; A (H1N1)pmd09 in 6 cases, A(H3N2) in 6 cases and influenza B in 3 cases.

Conclusion

After a predominant SARS-COV-2 circulation the past two years, influenza season was considerably severe in 2022-2023 in Tunisia, with similar patterns as the pre-pandemic seasons. Men, old people and those with comorbidities were the most affected. This highlights the need to target these groups by appropriate preventive measures, especially increasing influenza vaccination coverage which remains low.

Key words: influenza, severity, surveillance

Impact of the covid-19 pandemic on the epidemiology of others viral infections in the ICU

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Biography:

- *Professor of Medicine*
- *Medical Resuscitator (intensivist)*
- *Head of Department at the Tunis Faculty of Medicine*
- *President of the "UR22SP01" research unit*
- *President of the Tunisian Resuscitation Association (ATR)*
- *Spokesperson for the scientific committee to combat COVID-19*
- *Head of the Intensive Care Unit of Abderrahmane Mami Hospital*
- *Member of various committees at the Ministry of Health of Tunisia*
- *Coordinator of the CEC "Respiratory assistance in hospital and at home" at faculté de médecine Tunis since 2016*

Background:

Over the past 100 years, the world has seen the emergence of several viruses that have been responsible for several pandemics, the most recent being that of covid-19. the seriousness of these viral infections lies in the fact that they cause severe acute respiratory infections (SARI) leading to hospitalizations in intensive care and excess mortality. these SARI were dominated by infections secondary to influenza and coronavirus. The objective of this study was to analyze the impact of the covid-19 pandemic on the epidemiology of other viral infections in intensive care units.

Methodology

Single-center retrospective study from January 2015 to May 2023 including 7 seasons.
Were included all patients admitted to the intensive care unit of the Abderrahmane Mami hospital, meeting the SARI definition, and having had a nasopharyngeal swab for viral analysis.

Results

The study included a total of 2129 patients, 771 before covid-19 pandemic, 599 patients during the pandemic (March 2020 to December 2021), and 759 hospitalized patients from January 2022 to May 2023.
Before the pandemic, the rate of isolated virus was 11.94%, and the predominant respiratory viruses were influenza viruses, including H1N1 at 7.78%.
During the pandemic no other viruses were isolated.
After the year 2021, the rate of isolated virus was 31.33. SARS-COV was predominant with a rate of 17.26% especially during the first half of 2022, followed by rhinovirus at 5.4% and H1N1 at 2.63%.
Viruses other than influenza and SARS-COV2 represented 10% of the isolated viruses.

Conclusion

In addition to the clinical and socio-economic impact, covid-19 pandemic has led to an upheaval in the ecology of respiratory viruses and in the management of the resulting pathologies

Results from WHO GISRS Global External Quality Assessment Programme 2020-2022 for molecular detection of SARS-CoV-2 in the WHO African Region

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[1]WHO Global Influenza Programme, [2]WHO Collaborating Centre for Reference and Research on Influenza, [3]WHO Health Emergency Programme, World Health Organization Regional Office for Africa, [4]Centre for Health Protection, Department of Health

Biography:

Belinda Herring is a technical officer working on influenza at the WHO Health Emergency Programme, World Health Organization Regional Office for Africa, Republic of Congo.

Background: In 2020, the External Quality Assessment Programme (EQAP) for the Detection of SARS-CoV-2 Virus by RT-PCR was rapidly launched to assess the proficiency of laboratories in the molecular detection of SARS-CoV-2, building on the existing WHO coordinated Global Influenza Surveillance and Response System (GISRS) EQAP.

Methods: Since 2020, a total of 60 laboratories (National Influenza Centres and/or National SARS-CoV-2 Reference Laboratories) from 47 countries, areas or territories from the WHO African Region were invited to participate. From 2020-2022, validated panels of virus samples containing SARS-CoV-2 wild-type and variants of concern, as well as human coronaviruses, were distributed to these laboratories, accompanied by a survey to identify concerns in launching/implementing molecular detection of SARS-CoV-2.

Results: During 2020-2022, 71.1%-80.8%. of participating laboratories reported results on time. Of the results returned, 95.6%, 74.4% and 91.7% of laboratories reported all correct results in 2020, 2021 and 2022, respectively. In most cases, further assay validation/to enhance sensitivity was required improvement measures.
According to survey responses, the biggest concerns for implementing detection of SARS-CoV-2 were the need for specific staff training, insufficient primers/probes/testing reagents, and establishing procedures/guidelines/protocols on specimen collection/shipping/storage and standard virus detection methods. In 2022, an increased proportion of respondents (+7.3% compared to 2021) indicated no major concerns (10% total). In 2022, ~30% and ~40% of laboratories reported detecting variants of concern by real-time RT-PCR and/or next generation sequencing, respectively.

Conclusions: Our results indicate that laboratories are performing well in the molecular detection of SARS-CoV-2. In 2022, 60% of responding participants reported that both detection of SARS-CoV-2 and influenza are being implemented. Integrated sentinel surveillance of influenza and SARS-CoV-2 is now a primary objective of GISRS; the WHO GISRS EQAP is important to ensure and maintain quality assurance of laboratories and support countries in the molecular detection and enhanced genomic surveillance of SARS-CoV-2.

Findings from the third WHO External Quality Assessment panel for the molecular detection of respiratory syncytial virus in the Africa Region

Dr Belinda L. Herring[1], **Dr Fernando Motta**[4], Dr Thomas Williams[2], Dr Mei Shang[4], Dr Sanjiv Rughooputh[3], Dr Siddhi Herve[4], Dr Wenqing Zhang[4]
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Biography:

Fernando Motta holds a PhD in microbiology with a specialization in Virology from the Federal University of Rio de Janeiro, Brazil. Since 2000, he has been dedicated to researching respiratory viruses and developing improved techniques for virus detection and characterization, with a focus on public health. Presently, he serves as a consultant for the WHO RSV Network within the Global Influenza Program.

Background: The WHO launched the Global RSV Surveillance Project in 2016 to improve global knowledge of RSV infection. The success of this Project relies heavily on the RSV detection methods. Considering this, three EQA panels have been distributed, evaluating the capacity of participating laboratories by assessing the RSV molecular diagnostic protocols used in their routine. This study describes the results obtained by WHO RSV Project laboratories from the Africa region in the 3rd WHO RSV EQA, conducted between 2021 and 2022.

Methods: The 3rd WHO RSV EQA panel, constituted of 12 blinded samples, was distributed to 81 laboratories across all WHO Regions, 13 from Africa. These laboratories tested the panel for RSV using their routine RT-PCR protocols. The results and Ct values obtained were reported online in an anonymized manner. A scoring system with four tiers was used to classify laboratory performance and enable comparison of results across other participants. Technical aspects such as turnaround time (TAT), nucleic acid extraction technology, real-time platform, and detection/subtyping protocol were also analysed.

Results: Eleven out of the 13 African laboratories that received the panel were enrolled in the WHO RSV Project. Ten laboratories (77%) submitted their findings within an average turnaround time of 64,2 (± 22,5) days. Most countries employed manual extraction and CDC protocols to identify and subtype RSV. Seven laboratories received a top score, all participating in the WHO project. The average obtained Cts matched the expected values in 5 out of 9 positive samples.

Conclusions: 77% of African laboratories reported their results, with 6 responding after the average TAT. This result highlights the pandemic's negative impact on the region's laboratory response. Similar protocols were used among participants, therefore, differences in Ct are due to unaccounted factors. Only one African lab reported a false positive result, demonstrating excellent overall performance.

Prevalence of Respiratory Syncytial Virus infection and associated factors among under five years children with severe acute respiratory illness and Influenza like illness in Ethiopia

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[1]Ethiopian Public Health Institute, [2]World Health Organization, [3]World Health Organization, [4]Addis Continental Institute of Public Health

Biography:

Adamu Tayachew is a researcher working for Ethiopian Public Health Institute(EPHI) since the last 8 years. He was among the very frontline COVID-19 responders in Ethiopia played a critical role in leading and coordinating the COVID-19 laboratory pillar in the national incident management system. Currently, he is coordinating the NIC Ethiopia which is WHO recognized lab under his fellow lab and surveillance coleagues and higher EPHI leadership. He is also perusing his PhD degree in Tropical and infectious diseases from Addis Ababa University (ALIPB) and undertaking his research entitled with Molecular and Sero-epidemiology of respiratory viruses among ILI/SARI cases, Ethiopia.

Abstract

Background: Acute respiratory illnesses are among the major global public health problems. It can be caused by a wide variety of micro-organisms and respiratory syncytial viruses (RSV) is considered as among the major pathogens. The prevalence of RSV infections and associated factors are not well understood among under five children in Ethiopia.

Objective: To assess the prevalence and associated factors RSV infection among under five children with ILI and SARI using influenza sentinel surveillance sites in Ethiopia.
Method: A cross-sectional study design was employed utilizing ILI/SARI data from Jan 2021 to Dec 2022 at Ethiopian Public Health Institute. Descriptive statistics were used for categorical variables including the prevalence. Binary logistic regression and multi-variable analysis were done to assess the association of variables with RSV RT-PCR positivity rate. Variables with a P-value below 0.05 in the multi-variable analysis were considered to have statistically significant association.
Result: A total of 2234 cases were included in to the analysis. The overall RSV positivity rate was 16.2%. The RSV positivity was highest among children under one year of age (22.8%) and during the spring season (24.8%). The RSV positivity rate was significantly association with age, under 1 years [AOR 2.8, 95% CI (1.89-4.15)] and 1-2 years [AOR 1.9, 95%CI (1.26-2.73). Additionally, spring season was significantly associated with RSV test positivity [AOR 1.67, 95% CI (1.17-2.38)].

Conclusion and Recommendation: The study revealed that considerably large RSV positivity was detected among children under five years of age in Ethiopia. Prevention and control of RSV infection and case management procedures should be targeted to minimize respiratory tract infection among children. Moreover, further studies on the RSV viral genotype, clinical characteristics and diseases outcome need to be conducted for better understanding of the virus and disease caused outcome.
Key words: RSV, Epidemiology, SARI/ILI, Ethiopia

SARS-CoV-2 seroprevalence in two communities in South Africa (HUTS-3), January-March 2023

Miss Michaela Davids[1], Miss Wilhelmina Strasheim[1], Miss Caitlyn Slabbert[1], Dr Sibongile Walaza[1,2], Dr Jocelyn Moyes[1,2], Dr Jackie Kleynhans[1,2], Dr Susan Aiken[3], Tamika Fellows[3], Cherie Cawood[4], Dr Anne van Gottberg[1,5], Dr Cheryl Cohen[1,2], Dr Nicole Wolter[1,5]

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Biography:

I have obtained a master's degree in Medical Virology at the University of Pretoria in 2020 working with enteric viruses. As an early researcher with more than 2 years of experience in the molecular field of virology, I recently found a new interest in serology. As a result, I am currently entry medical scientist at the Centre for Respiratory Diseases and Meningitis at the National Institute for Communicable Diseases, working on the serology aspects of respiratory viruses i.e Influenza, SARS-CoV-2 and RSV. I look forward to achieving more career endeavors in this field, becoming an experienced researcher.

Background

South Africa experienced five COVID-19 waves; the last Omicron BA.4/5-driven wave ending June 2022. Subsequently, the number of reported cases remained low, primarily due to decreased testing. The second SARS-CoV-2 Healthcare Utilisation and Seroprevalence survey, conducted during the fifth wave (HUTS-2; April-June 2022), showed an overall seroprevalence for anti-spike(S) and/or anti-nucleocapsid(N) antibodies of 97.3% (90.9% anti-N and anti-S, 6.2% anti-S only and 0.1% anti-N only). We conducted a third survey (HUTS-3) that aimed to describe seroprevalence in the post-pandemic period in two communities (Pietermaritzburg, KwaZulu-Natal and Mitchell's Plain, Western Cape), where pneumonia and influenza-like illness (ILI) surveillance are conducted.

Methods

Individuals living in randomly-selected HUTS cohort households were enrolled from January-March 2023, and demographic information were collected by questionnaire. Sera were collected and tested for SARS-CoV-2 total antibodies against N and S proteins using the commercial Roche Elecsys®Anti-SARS-CoV-2 assays. Individuals were considered seropositive if positive for anti-N and/or anti-S antibodies. Proportions were compared using the chi-squared test.

Results

A total of 4966 individuals from 1282 households were enrolled; 51.1% (2536/4966) from Pietermaritzburg and 48.9% (2430/4966) from Mitchell's Plain, which 87.3% (4337/4966) individuals had results. The median age of enrolled participants was 35 years (interquartile range 22-50 years). Overall SARS-CoV-2 seroprevalence (anti-N and/or anti-S) was 97.3% (4218/4337); 98.0% (1942/1982) in Pietermaritzburg and 96.6% (2276/2355) in Mitchell's Plain ($p=0.007$). Seropositivity was 90.8% (3936/4337) for anti-N and anti-S, 6.4% (277/4337) anti-S only and 0.1% (5/4337) anti-N only. Seroprevalence (anti-N and/or anti-S) was 96.1% (842/876) in children (≤18 years), 95.7% (3030/3166) in adults (19-64 years) and 94.8% (346/365) in elderly (≥65years) ($p=0.050$).

Conclusion

Seven months after the last COVID-19 wave in South Africa, SARS-CoV-2 seroprevalence remained high, with almost all individuals positive for anti-S and/or anti-N SARS-CoV-2 antibodies, similar to that observed in HUTS-2 survey conducted during the pandemic period.

Seroprevalence, SARS-CoV-2, HUTS

Influenza attack rates before and during the COVID-19 pandemic in a community cohort in South Africa (PHIRST)

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Biography:

I am a young medical scientist at the Centre for Respiratory Diseases and Meningitis, National Institute for Communicable Diseases of the National Health Laboratory Services. I have over 3 years of experience in diagnostics, surveillance, and research of respiratory pathogens in molecular and serology fields. I hold a BSc in Biomedicine and a BHSc Honours in Clinical Microbiology and Infectious Diseases. As a researcher, I believe that my work may be of public health importance.

Introduction

Influenza transmission in South Africa changed during the COVID-19 pandemic, with little activity in 2020 and atypical summer activity in 2021. We aimed to describe influenza attack rates before and during the pandemic period.

Methods

Sera, collected during cohort studies in randomly-selected households in an urban and rural community before (April-May 2018) and after (October-November 2018) the 2018 season (dominated by A(H1N1)pdm09) and before (July-August 2021, lockdown-level 3/4) and after (March-April 2022, lockdown-level 1) the 2021 season (dominated by A(H1N1)pdm09), were tested using haemagglutination inhibition against circulating influenza viruses. A ≥4-fold titre increase between paired sera was considered to indicate infection. Chi-squared test was used to compare proportions. Among 1758 participants, 22 who received influenza vaccine and 500 without paired sera were excluded.

Results

We included 339(2018) and 919(2021) participants with median age 17 years (interquartile range (IQR) 9-37) in 2018 and 15 years (IQR 8-36) in 2021. Pre-season seroprotective antibodies (titre ≥1:40) for 2018 and 2021 against subtypes/lineages were 52.2% (177/339) vs. 37.1% (341/919) for A(H1N1)pdm09; 70.8% (240/339) vs. 13.1% (120/919) for A(H3N2); 27.1% (92/339) vs. 6.2% (57/919) for B/Victoria; and 40.1% (136/339) for B/Yamagata(2018 only). Attack rates in 2018 were 27.1% (92/339) and in 2021 were 44.7% (411/919) (P<0.001), with 6.8% (23/339) and 9.8% (90/919) of individuals seroconverting against >1 subtype/lineage, respectively. In 2018, A(H1N1)pdm09 accounted for 35.2% (43/122) of infections, followed by B/Victoria (32.8%, 40/122), B/Yamagata (19.7%, 24/122), and A(H3N2)(12.3%, 15/122). In 2021, A(H1N1)pdm09 accounted for 44.6% (229/514) of infections, followed by B/Victoria (30.4%, 156/514), and A(H3N2) (25.1%, 129/514).

Conclusions
Pre-season seroprotection was higher in 2018 than 2021. Despite being an atypical season, infection attack rates in the first season following SARS-CoV-2 emergence were higher than during a typical pre-COVID-19 pandemic season. Higher attack rates may have resulted from a lack of exposure during COVID-19 restrictions.

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Genomic analysis of respiratory syncytial virus circulating in South Africa, 2021 - 2023

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Biography:
I always had an interest in how mircoorganisms affected the human body , this curiosity led me into my career path.

I started at the National Institute for Communicable Disease (Centre for Respiratory Diseases and Meningitis) in 2020 during the height of the CoViD-19 pandemic where we began genomic surveillance for SARSCoV-2. Then we started genomic surveillance for respiratory syncytial virus (RSV) and influenza.

As an emerging researcher I am interested in how RSV will evolve after the CoViD-19 pandemic. I think in these uncertain times, the One Health initiative is important for communicable disease surveillance.

Background
The annual RSV season in South Africa normally occurs between February and May, with severe disease most common in young children. However, RSV circulation was disrupted during the COVID-19 pandemic. We aimed to genetically characterise circulating RSV during and after the pandemic period.

Methods
Nasopharyngeal samples were collected through sentinel syndromic surveillance for influenza-like illness and severe respiratory illness. RSV PCR-positive samples were subtyped, and those with a cycle threshold (Ct) value ≤30 were randomly sequenced using the Illumina platform. Genomes were assembled using viral-ngs (v2.1.20.0). The ectodomain of the G-gene was used to assign lineages according to Goya nomenclature (https://cacciabue.shinyapps.io/resvidex/).

Results
RSV-A made up 51.8% (266/514), 36.2% (323/892), and 76.9% (416/541) of RSV-positive specimens for 2021, 2022 and 2023 (Jan-Apr) respectively, while RSV-B made up 46.9% (241/514), 61.7% (550/892), and 20.7% (122/541) for each year.

Of 297 RSV-A samples sequenced, 61.3% (182/297) could be assigned a lineage. In all three years the predominant lineage was GA.2.3.5 (87.8%, 43/49; 78.6%, 33/42; 81.3%, 74/91, respectively). In 2021, only two additional lineages were observed (GA.2.3.2b and GA.2.3.4, 1). However, in 2022, four other lineages were observed (GA.2.3.2b, GA.2.3.3, GA.2.3.4 5 and GA.2.3.6b), three of which have also been observed in 2023 (GA.2.3.3, GA.2.3.4 and GA.2.3.6b).

Of 125 RSV-B samples sequenced, 57.6% (72/125) could be assigned a lineage. The dominant lineage for all three years has been GB.5.0.5a (85.2%, 23/27; 96.9%, 31/32; 84.64%, 11/13, respectively). In 2021, only two additional lineages were observed (GB.5.0.0 and GB.5.0.4a). While one additional lineage for 2022 (GB.5.0.0) and 2023 (GB.5.0.4a) were observed.

Conclusion
RSV continued to circulate during the COVID-19 pandemic. RSV-A and RSV-B were dominated by lineages GA.2.3.5 and GB.5.0.5a, respectively. It is important to continue to monitor RSV genotypes as interventions such as vaccination and long-acting monoclonal antibodies become available in the near future.

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Evolutionary analysis and characterisation of the RSV F-gene over the January 2021 - March 2023 period in South Africa: Implications for monoclonal antibody use and vaccine development

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[1]Centre for Respiratory Diseases and Meningitis, National Institute for Communicable Diseases of the National Health Laboratory Service, [2]Centre for HIV and STIs, National Institute for Communicable Diseases of the National Health Laboratory Service, [3]SAMRC Antibody Immunity Research Unit, School of Pathology, University of the Witwatersrand, [4]School of Public Health, University of the Witwatersrand, [5]School of Pathology, University of the Witwatersrand, [6]Faculty of Health Sciences, University of Cape Town

Biography:
Buhle Ntozini is a Medical Scientist (Bioinformatics) at the Centre for Respiratory Diseases and Meningitis at the National Institute for Communicable Diseases. Her work is focused on sequencing data analysis for respiratory pathogens including Respiratory Syncytial Virus (RSV) and SARS-CoV-2.

She obtained her BMedSc(Hons) degree at the University of Cape Town (UCT), majoring in Human Genetics, and her MSc(Med) in Clinical Microbiology and Infectious Diseases at the University of Witwatersrand (WITS). Her masters research project was focused on whole genome-based characterization of invasive Streptococcus agalactiae in South Africa.

Introduction
Respiratory syncytial virus (RSV) is a major cause of severe lower respiratory tract infections in infants and young children, globally. Efforts to combat disease include monoclonal antibodies and advances in vaccines, most of which target the fusion (F) protein. This study aimed to identify mutations in the F-gene among circulating RSV strains in South Africa, focusing on those emerging in the six antigenic sites (Ø, I-V) during and post COVID-19 pandemic.

Methods

Nasopharyngeal samples (n=21,804) were collected (2021-2023) from individuals of all ages enrolled in sentinel syndromic surveillance for influenza-like and severe respiratory illness. RSV-positive samples (n=1947) were detected and subtyped using real-time reverse transcription polymerase chain reaction. A convenience sample of specimens (n=398) with a PCR cycle threshold (Ct) value ≤30 was sequenced using the Illumina platform. Genomes were assembled with viral-ngs v2.1.20.0, aligned with Nextalign, curated in AliView, and translated to identify amino acid substitutions, relative to GISAID references (EPI_ISL_412866 and EPI_ISL_1653999 for RSV-A and RSV-B, respectively).

Results

Sequencing produced 251 (168 RSV-A, 83 RSV-B) genomes with ≥50% coverage of the F gene. In RSV-A, substitutions were observed at 46 sites, including all six antigenic sites. I384T (site I) and S190N (site III) were most prevalent, accounting for 46.4% (39/84; 2021 and 2022) and 16.3% (20/123; 2022 and 2023) of sequences, respectively. For RSV-B, substitutions were observed at 28 sites, including antigenic sites Ø, I, and V; S389P (site I) was most prevalent (38.3%, 23/60; 2022 and 2023), followed by R209Q (site Ø, 21.7%, 5/23; 2021).

Conclusion

RSV F-gene evolution in key antigenic sites may have important public health implications for use of monoclonal antibodies and vaccines and highlights the importance of genomic surveillance for this virus. Our analysis shows that in SA, new mutations have been detected in antigenic sites in recent years.

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Evaluation of a Rapid Chromatographic Immunoassay as an Alternative Method for Detecting Influenza A and B Growth in Virus Cultures

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Biography:

My name is Thulisile Dlamini, I am a 32-year-old Medical Technician. I have been working with the NICD at the Centre of respiratory Diseases for over 2 years.

My work includes serology with a focus on Influenza and RSV.

Background: Detection and characterisation of circulating influenza strains are important for monitoring antigenic evolution and guiding annual vaccine composition. Traditional methods such as indirect fluorescence antibody assay (IFA) are used for confirming virus growth. However, limited availability can be problematic in resource-limited settings. We explored a more easily available method for confirming growth in virus cultures.

Methods: We assessed a rapid, qualitative chromatographic immunoassay (Flu A+B+RSV, Certest Biotec S.L, Zaragoza, Spain). Ten influenza polymerase-chain reaction (PCR)-positive specimens (cycle threshold<30) (4 A(H1N1) pdm09, 3 A(H3N2) and 3 B/Victoria) were cultured in Madin-Darby canine kidney (MDCK) cells with trypsin/bovine serum albumin in Eagle’s minimal essential medium for up to 72 hrs. We calculated sensitivity and specificity compared to IFA (Light Diagnostics SimulFluor, Chemicon International, Temecula, CA) as the gold standard.

Results: Using IFA 9/10 (90%) PCR-positive specimens had viral growth with observed cytopathic effect, with 1+(2), 3+(2), and 4+ (5) grading. The immunoassay correctly identified viral growth in 8/9 influenza cultures (2/3 A(H1N1) pdm09, 3/3 A(H3N2) and 3/3 B/Victoria viruses), demonstrating high concordance with the IFA results. One influenza A culture with an IFA grading of 1+ tested negative using the immunoassay, likely due to poor viral growth. The sensitivity of the immunoassay was determined to be 89% (8/9), while the specificity was 100% (1/1).

Conclusion: An immunochromatographic assay was shown to be a sensitive alternative to IFA for detecting influenza A and B growth in virus cultures. Given its ease of use, rapidity and availability, this assay has the potential to be widely used in settings where IFA reagents are not readily available. Further investigations with a larger sample size are ongoing.

Keywords: influenza A, influenza B, virus culture, immunochromatographic assay, rapid diagnostic test.

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Prenatal Exposure to SARS-CoV-2 Infection during Pregnancy and Neurodevelopmental Outcomes among Infants in Western Kenya at 6 months of age

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Biography:
Nancy has 17 years of experience of leading epidemiologic research and public health in the field of infectious disease research and prevention, especially related to respiratory diseases and maternal-child health. She combines a basic science background (Biology and Chemistry), with advanced training in Applied Epidemiology and Biostatistics, Project Management and doctorate training in Project Monitoring and Evaluation. For 10 years, she managed and continues to support the national sentinel surveillance system for influenza and other respiratory pathogens. She has designed, managed, and continue to provide technical oversight to maternal and child health research and surveillance programs in western Kenya.

Background
Diagnosis of COVID-19 during pregnancy is associated with adverse pregnancy and neonatal outcomes. However, knowledge on the effect of exposure to COVID-19 during pregnancy on infant development is limited. We assessed the risk of developmental delay at 6 months of age in infants exposed to COVID-19 during pregnancy.

Methods
We enrolled pregnant women (under 31 weeks of gestation) and contacted them weekly through telephone to identify cases of COVID-like illness (CLI). We followed them until delivery, and their infants for 6 months. Nasopharyngeal and oropharyngeal swabs were obtained from patients with CLI and tested for SARS-CoV-2 by real-time reverse transcription polymerase chain reaction. We performed growth and developmental evaluations for infants at 6 months using Caregiver Reported

Early Development Instruments (CREDI), assessed through four domains: cognitive, language, motor and socio-emotional. Failure was flagged when -2< z-score >2. Differences in developmental outcomes by maternal prenatal COVID-19 exposure were assessed using chi-square tests. Further assessment, and with Baileys, will be conducted at 12, 18 and 24 months.

Results
Between February 1-December 2, 2022, we enrolled 1,988 pregnant women, median gestational age (IQR) 21.0 (17.0-26.0); and 1641 (82.5%) gave birth. Of the 1,641 women, 360 (22.2%) reported CLI during pregnancy; 345 (95.8%) were tested for SARS-CoV-2; and 54 (15.7%) were positive. Of the 345 infants whose mothers had been tested for SARS-CoV-2 during pregnancy, 156 (45.2%) had their CREDI assessment done at 6 months; 26 (16.7%) were born to mothers who had COVID-19 during pregnancy. Infants whose mothers had COVID-19 during pregnancy were more likely to have delays in cognitive (11.5% vs 2.3%; p-value=0.03) and socio-emotional development (15.4% vs 4.6%; p-value=0.04).

Conclusion
Maternal prenatal COVID-19 exposure was associated with lower CREDI cognitive and socio-emotional scores in infants at 6 months. Further analyses are needed to determine if these findings persist through toddlerhood.

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MOLECULAR CHARACTERIZATION OF SARS-CoV-2 IN YAOUNDE, CAMEROON: GENETIC DIVERSITY

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Biography:
Degree in Medical Analysis

Master's Degree in Health Science, Immunology option

PhD Student in Clinical Biology

Background:
From 30 December 2019 to 10 October 2022, WHO estimated, 620,878,405 cases of COVID-19 and 6,543,138 deaths worldwide, of which 9,340,399 cases were from Africa. According to the Cameroon COVID-19 situation report, 124 328 cases and 1 965 deaths were recorded as of March 2023. The resurgence of worrying variants that the world is experiencing is the result of the various mutations that the SARS-CoV-2 genome is undergoing. This study aimed to study the molecular epidemiology of SARS-CoV-2 in Cameroon between 2020 and 2022 during the COVID-19 pandemic.

Methods:
Nasopharyngeal samples were collected between 2020 and 2022 in the Central region of Cameroon in the framework of the COVID-19 response. COVID-19 diagnosis was performed at the Centre Pasteur of Cameroon using RT-PCR assay. Positive samples were further subjected to SARS-COV-2 Variants Of Concern (VOC) specific mutation screening using Single Nucleotide Polymorphism (SNP) followed by Whole Genome Sequencing and analysis on NGS platforms.

Results:
Our data show a diversity and temporal distribution of variants of SARS-CoV-2 between 2020 and 2022 in Cameroon. Delta and omicron were the predominant in 2021 and 2022, respectively that is 53, 3% (113/212) for delta and 95% (111/117) for omicron. In 2022, several omicron sub-lineages: 21K (14%), 21L (11%) 21M (1%), 22A (4%), 22B (62%) and 22E (8%) were identified (total 111). According to the epidemiology of SARS-CoV-2 during the study period, other VOCs were as well determined at lower frequencies: alpha 12, 3% (26/212) and beta 2, 3% (5/212).

Conclusion:
Alpha, beta, delta and omicron were identified in Yaounde, Cameroon between 2020 and 2022. The variants that dominated in the last two years of the COVID-19 epidemic were delta and omicron variants respectively in 2021 and 2022.

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Impact of HIV Infection and Malaria Parasitemia on Immunogenicity of Inactivated Influenza Vaccine in Pregnant Women and on Mother-to-Child Vaccine-induced Antibody Transfer

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Biography:
Nancy has 17 years of experience of leading epidemiologic research and public health in the field of infectious disease research and prevention, especially related to respiratory diseases and maternal-child health. She combines a basic science background (Biology and Chemistry), with advanced training in Applied Epidemiology and Biostatistics, Project Management and doctorate training in Project Monitoring and Evaluation. For 10 years, she managed and continues to support the national sentinel surveillance system for influenza and other respiratory pathogens. She has designed, managed, and continue to provide technical oversight to maternal and child health research and surveillance programs in western Kenya.

Background
Vaccinating pregnant women with seasonal influenza vaccines is recommended by the World Health Organization. However, impact of HIV infection and malaria parasitemia on the immunogenicity of inactivated influenza vaccines and trans-placental transfer of antibodies has not been well-explored.

Methods
At two hospitals in western Kenya, immune responses to influenza vaccination and vertical antibody transfer were assessed in three groups of pregnant women (at <31 weeks gestation): 1) HIV-positive; 2) malaria positive with parasitemia at enrolment (malaria(+ve)); and 3) HIV-uninfected without malaria parasitemia (comparison group). All women received trivalent inactivated influenza vaccine. Hemagglutination inhibition assay (HAI) antibody titers were measured at enrolment and vaccine administration (day 0), day 16 post-vaccination (range 14-24 days), and at delivery. For infants, HAI titers were measured in cord blood, at week 16 and 24 weeks post-delivery. Seroconversion against

each virus subtype was defined as four-fold rise in HAI titer with post-vaccination titer ≥1:40, and vaccine-induced antibody transfer as infant HAI titers ≥1:40.

Results

Between June 2018 – January 2020, 355 pregnant women were enrolled and vaccinated against influenza (89 HIV+, 77 malaria(+ve) and 189 HIV-/malaria(-ve). Two to four weeks post-vaccination, all three groups achieved >86% protective HAI titers (≥1:40) against A/H1N1pdm09 and >83% against A/H3N2; lower proportions achieved titers ≥1:40 against influenza B/Victoria: HIV+ (53%), malaria(+ve) (56%) and HIV-/malaria(-ve) (71%). A/H1N1pdm09 was the most immunogenic subtype and most women (>77%) had HAI titers ≥1:40 at delivery. Trans-placental antibody transfer was similar across groups of women. At birth, 84%, 75% and 56% of newborns had HAI titers ≥1:40 against A/H1N1pdm09, A/H3N2, and B strains.

Conclusion

This study provided additional evidence of immunogenicity of influenza vaccination during pregnancy among HIV-infected and malaria-infected women, high levels of vertical antibody transfer in all groups and potential protection of infants during the first six months of life.

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World Health Organization’s Unity Studies: a preparedness and readiness framework of investigations and studies of emerging respiratory pathogens of pandemic potential to inform evidence-based action in the Africa Region

Mrs Hannah Lewis Winter[1], Dr Nicki Boddington[1], Dr Elise Farley[2], Dr Sophie von Dobschuetz[1], Dr Lorenzo Subissi[1], Dr Joshua Mott[1], Dr Maria Van Kerkhove[1], Dr Wenqing Zhang[1], Dr Isabel Bergeri[1], Dr Joseph Okeibunor[2], Dr Belinda Herring[2]

[1]WHO Health Emergencies Programme, World Health Organization Headquarters, [2]Regional Office for Africa, World Health Organization

Biography:

Hannah Lewis is a senior epidemiologist with over 15 years experience in international health emergency preparedness and response. She currently works at WHO HQ. As part of the Unity Studies team for SARS-CoV-2, she co-ordinated study implementation in the Africa region between 2020-2022 . Previously she worked at the Robert Koch Institute, Germany (2013-2019), WHO Lao PDR Country Office (2008-2012), Statens Serum Institut, Denmark (2006- 2008), Public Health England (2004-2006) and the Department of Health, England (1999-2003). Hannah holds a Master of Public Health from Kings College, University of London (2005) and is an EPIET Alumna (2008).

Background

The World Health Organizations’ (WHO) Unity Studies provides a generic preparedness and readiness framework for conducting detailed investigations and studies critical for risk assessment of emerging respiratory pathogens of pandemic potential. During the COVID-19 pandemic, the initiative produced standardized protocols and supported countries to generate robust and comparable data. Twenty-seven African member states undertook at least one investigation aligned with COVID-19 protocols. We describe the activities planned globally and in the Africa Region to ensure preparedness for timely and robust investigations and studies during future pandemics.

Methods

WHO is developing the Unity Studies 2.0 ‘at the ready’ international framework initiative. This will address both disease-specific aspects, such as pandemic influenza and coronaviruses, and also other respiratory pathogens of pandemic potential. This work is being co-ordinated through two workstreams: architecture and governance; and the operationalization of the framework. In the

Africa Region, workstreams and the related activities will be tailored to the specific context of, and lessons learned in, the region.

Results
Standardized, disease specific protocols have been revised and implementation tools have been developed. A global network, based on regionally operational networks of sites, primed to conduct studies, is being developed. In the Africa Region, the target is to have two sites operational by 2025 and six sites by end 2029. Future plans include the development of protocols fit-for-purpose for any respiratory virus of pandemic potential, additional supporting implementation tools, and an acceptable architecture for a timely results repository as well as exercising during seasonal outbreaks/epidemics.

Conclusions
Revising standardized protocols and developing supporting tools will ensure preparedness and response readiness for the early and ongoing characterization of emerging respiratory pathogens in Africa. This is being conducted in a globally coordinated and collaborative manner through the Unity Studies 2.0 network.

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An updated Pandemic Influenza Severity Assessment (PISA) framework

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[1]World Health Organization

Biography:
Holly Sadler is a consultant with the Global Influenza Programme at the World Health Organization headquarters in Geneva. She works within the epidemiology team on several projects, most notably on severity assessments for influenza. Prior to this, she completed her doctorate in influenza virology and vaccine development at the University of Oxford.

Background
The pandemic influenza severity assessment (PISA) framework was developed by the World Health Organization (WHO) to help countries understand and communicate national influenza activity and inform public health preparedness and response needs. Current influenza activity is qualitatively assessed relative to in-country historical levels for three indicators: transmissibility, seriousness of disease and impact. Since it was piloted in 2014, the number of WHO Member States participating in PISA has grown year-on-year to 28 in 2019. However, participation dropped during the COVID-19 pandemic due to disruptions to surveillance systems.

Methods
Through a Member State survey, a web literature review, and expert technical working groups in four key areas (PISA Concept, Threshold Setting, Modelling, Global Assessments), WHO collated best practices and lessons learned to update and broaden the PISA guidance.

Results
The list of suggested parameters has been expanded to reflect the diversity of suitable approaches across countries. The use of hospital data to assess morbidity and mortality and the impact of this on healthcare capacity is emphasized, as this was found to be useful in many countries during the COVID-19 pandemic. The value of syndromic as well as influenza-specific assessments, particularly for monitoring health care capacity impact and the need for public health interventions, is addressed. Various threshold setting methods are proposed, including using non-statistical thresholds where historical data is limited. Input from investigation, studies, modeling and forecasting has been

substantial for severity assessment during the COVID-19 pandemic, however, there remain many challenges. Better preparing for data needs and including new sources might overcome some.

Conclusions
The updated PISA guidance uses country experiences from the COVID-19 pandemic to improve its applicability during pandemics. This framework may be of great use to countries for evaluating the severity of influenza during both seasonal and pandemic periods and informing risk communication and decision making.

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Illness outcomes of in-and-out patients co-infected with SARS-CoV-2 and Malaria, 2020-2022

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Biography:
Jorim Opiyo Ayugi is a Data Analyst with 5 years of work-experience with KEMRI. He is currently undertaking a masters' degree program in Epidemiology and Biostatistics. He's got solid background knowledge in Statistics, mathematics and surveillance.

Background
There is paucity of data on the impact of co-infection of severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) and malaria on illness outcomes, especially in Sub-Saharan Africa where malaria is common. We assessed illness outcomes among inpatients presenting with respiratory illness who were infected with SARS-CoV-2 or malaria compared to those coinfected with SARS-CoV-2 and malaria.

Methods
We analyzed data collected from eight severe acute respiratory illness (SARI) and influenza like illness (ILI) sentinel surveillance sites in Kenya. SARI was defined as hospitalization with a cough and fever (reported or documented) with 10 days onset, whereas ILI was defined as presentation with cough and measured fever ≥ 38o C with 10 days onset. Severe outcomes were defined as either death, intensive care unit (ICU) or acute care unit (ACU) admission, or use of supplemental oxygen. SARS-CoV-2 infection was confirmed through reverse transcription polymerase-chain reaction (rtPCR) while malaria infection was confirmed through microscopy or rapid diagnostic tests (RDT). Differences in severe outcomes were assessed using Odds ratios (OR).

Results
During the period March 2020 to December 2022, we enrolled 4922 patients (4000 inpatients and 922 outpatients); of which 3880 (78.8%) were aged <5 years and 2702 (54.9%) were males. The prevalence of SARS-CoV-2 infections was 7.7 % (381/4922): 6.1% (238/3880) and 13.7% (143/1042) among patients aged <5 and ≥5 years, respectively. Malaria was detected in 25.4% (1252/4922) of the patients: 23.7% (921/3880) among children <5 years and 31.8% (331/1042) among older patients. Co-infections of SARS-CoV-2 and malaria were detected in 1.5% (76/4922) of the patients. Co-infected inpatients were more likely to die during admission as compared to those infected with malaria alone (11.79 (2.59-53.67), p<0.01).
Conclusion
Understanding the effect of SARS-CoV-2 and malaria co-infection is important in advising effective patient management practices. Co-infected patients require more attention and should be prioritized.

Innovative surveillance to expand influenza vaccine effectiveness estimates: Home-based testing for influenza, SARS-CoV-2 and respiratory syncytial virus (RSV) Coughcheck, South Africa 2022

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Biography:

I am a medical doctor with training and experience in infectious diseases epidemiology. I have conducted various research projects in the last 18 years including cohort studies, clinical trials in HIV prevention, surveillance and vaccine effectiveness case-control studies. At present I am a senior staff member in the Centre for Respiratory Disease and Meningitis at the National Institute for Communicable Diseases (NICD) in South Africa. I have worked in my present position in influenza, respiratory syncytial virus (RSV) and other infectious disease surveillance for 15 years.

Background

Surveillance programmes for influenza and other respiratory pathogens are important to for vaccine effectiveness (VE) estimates and to inform vaccine composition. We aimed to explore the feasibility and acceptability of home-based testing.

Methods

In 3/9 provinces in South Africa, we established a self-referral system for individuals (aged ≥ 18 years) with respiratory symptoms ≤ 10 days duration. Following electronic consent, participants booked an appointment for delivery of swab collection material and completed a questionnaire with self-reported confirmation of vaccination status. PCR testing for influenza, SARS-CoV-2 and respiratory syncytial virus (RSV) was conducted at a local laboratory. Results were delivered by text message to participants within 24 hours. A reference laboratory performed influenza and RSV subtyping. Participants received an acceptability questionnaire. Descriptive statistics were applied to describe demographics, symptoms reported, vaccine coverage and acceptability indicators. A test negative methodology was used to estimate influenza VE.

Results

Adult participants (N=1469) were enrolled 1 December 2021 through 31 August 2022. The median age was 37 years (interquartile range (IQR) 28-51 years). Median duration of symptoms at enrolment was 2 days (IQR 1-4 days). 158 (11%) individuals had received influenza vaccination in 2022. SARS-CoV-2, influenza and RSV were detected in 339 (27%), 76 (5%) and 38 (3%) participants respectively. Of the sample available for subtyping, the dominant influenza strain was A(H1N1)pdm09 (38%,16/42). The VE adjusted for age and in season cases was 15% (95% confidence interval (CI), -1% to -65%) and 69% (95% CI, -20% to 87%) for A(H1N1)pdm09. Of the completed acceptability questionnaires, 123/127 (97%) would make use of the service again. Successful marketing was through the testing centre's webpage 46/127 (36%) and social media 17/127 (13%).

Conclusions

Home-based swabbing was feasible and acceptable. We accessed a vaccinated population and estimated an influenza VE. Virus circulation was similar to other surveillance programmes.

Digital Participatory Surveillance for Influenza-Like Illness and COVID-19 in South Africa and linkage to Home-Based Testing - A Pilot Study

Mr Mvuyo Makhasi[1,2], Dr Jocelyn Moyes[1], Prof Stefano Tempia[3], Dr Daniela Paolotti[4], Mr Phiwokuhle Ntombela[1], Dr Mignon du Plessis[1,5], Dr Nicole Wolter[1,5], Mrs Fahima Moosa[1,5], Prof Anne von Gottberg[1,5], Dr Sibongile Walaza[1,2], Prof Cheryl Cohen[1,2]

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Biography:

I am currently the Data Manager for the Centre for Respiratory Diseases and Meningitis, at the National Institute for Communicable Diseases (NICD). I am responsible for the national pneumonia surveillance data and platform development, and various data systems for specialized research studies. I have a background in electrical and information engineering, with specific interest in applied research and application of Big Data to health data and respiratory disease surveillance/epidemiology. I am doing my PhD in public health, using digital participatory surveillance for real-time syndromic surveillance for influenza-like illness and COVID19 in South Africa

Digital participatory surveillance (DPS) platforms provide important insights on non-medically attended influenza-like illnesses (ILI) cases. We assessed the feasibility and acceptability of a web-application for syndromic surveillance for ILI and COVID-19 and linking eligible participants to home-based testing for laboratory confirmation.

We enrolled an online cohort of volunteers aged ≥18 years in all provinces. Seasonal influenza and COVID-19 vaccination status were collected through baseline questionnaires. Participants completed a weekly respiratory symptoms questionnaire from March through October 2022. We described reported cases of ILI and COVID-19 symptoms and compared the proportion weekly reported cases to weekly ILI consultations rates from sentinel surveillance data using Pearson correlation. We linked participants reporting symptoms in three provinces to self-administered nasal swabs for real-time reverse transcription polymerase chain reaction (rRT-PCR) testing for influenza and SARS-CoV-2, and determined the overall positivity.

Of 954 volunteers who accessed the platform, 249(26%) enrolled in the study. The largest age group was 30-39 years (93/249(37%)); 178/249(71%) were female and 210/249(84%) were employed. Among participants, 62(25%) reported seasonal influenza vaccine receipt in 2022?? and 212(85%) had received at least 1 dose of COVID-19 vaccine. The correlation for reported ILI and COVID-19 with the weekly ILI consultation rates was 0.126 (small correlation) and 0.555 (small to moderate correlation), respectively. A total of 88/249(36%) participants were eligible for home-based testing, and 81/88(92%) were successfully enrolled. We detected 6/81(7%) influenza and 26(32%) SARS-CoV-2 infections.

Although the number of enrolled individuals was low, the study demonstrated the potential of obtaining data on non-medically attended ILI and COVID-19 cases. The poor correlation was due low numbers and inconsistent participation. Linkage to home-based testing was successful and demonstrates the potential for self-swabbing and real-time detection of influenza and COVID-19. This platform could complement sentinel surveillance to provide a better estimate of the community epidemiology of respiratory illness.

Longitudinal serosurveillance study of severe acute respiratory syndrome coronavirus 2 in urban and rural cohorts in Malawi: characterising population exposure and protective immunity to variants using pseudotyped virus neutralisation assays

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Biography:

Mhairi McCormack is a 2nd year PhD student at the Centre for Virus Research (CVR), University of Glasgow. Her research focuses on SARS-CoV-2 seroepidemiology in rural and urban Malawi, specifically looking at neutralising antibodies generated post infection or vaccination. Prior to this, she completed a BSc (Hons) in Microbiology with a specialism in Virology at the University of Glasgow.

Background

The extent of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) exposure and transmission in Malawi remains unclear due to a high proportion of mild/asymptomatic infections, and limited diagnostic capacity. Existing SARS-CoV-2 seroprevalence studies have been cross-sectional, utilising enzyme-linked immunosorbent assays (ELISAs) and convenience samples (e.g. blood donors). Here, we employed pseudotyped virus neutralisation assays for SARS-CoV-2 neutralising antibody measurement, to assess community exposure and protective immunity afforded by natural infection and vaccination.

Methods

Sera were obtained from participants in rural (Karonga, n=1,005) and urban (Lilongwe, n=1000) communities in Malawi, at 3-monthly intervals (February 2021-April 2022). Median age was 23 years (IQR 12-40). Human immunodeficiency virus (HIV)-based SARS-CoV-2 pseudotypes were employed to evaluate neutralisation of B.1, B.1.1.7, B.1.351, B.1.617.2, BA.1 and BA.2. Positive samples identified from fixed-dilution screening were titrated by serial dilution (titre at 50% reduction in infectivity). ELISAs targeting the nucleocapsid protein were performed on vaccinated participant sera to distinguish those solely vaccinated from those also naturally infected.

Results

Seroprevalence increased over time and differed by location (Survey 1-Karonga 6.5%, Lilongwe 11.7% ($p<0.001$); Survey 4-Karonga 45.4%, Lilongwe 68.6% ($p<0.001$)). Variant exposure also differed with site and time, with novel variants emerging in Lilongwe. Neutralisation-positive, unvaccinated participants aged ≥60 years exhibited lower neutralising activity compared with those aged <60 years (Survey 1-B.1.351, 88.0% vs. >90% ($p=0.0013$)). Vaccinated participants displayed their highest neutralisation activity against ancestral virus and Alpha, while a single dose of ChAdOx1-S/nCoV-19 vaccine induced stronger neutralisation than the Janssen vaccine ($p<0.05$). Individuals who were both vaccinated and infected had significantly higher antibody titres compared with those solely vaccinated or infected ($p<0.05$).

Conclusions

SARS-CoV-2 seroprevalence increased over time, with novel variants emerging earlier in Lilongwe, the densely populated travel hub. Considering the lower neutralising antibody levels in individuals aged ≥60 years, vaccination campaigns should prioritise this at-risk group.

Human immunodeficiency virus (HIV)-based pseudotype assays overestimate neutralising activity of severe acute respiratory syndrome coronavirus 2 in sera from areas of HIV prevalence

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Biography:

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Background

Estimating functional immunity requires measurement of neutralising antibodies. As live virus assays require high containment level laboratories, pseudotyped virus neutralisation assays (PVNAs) offer a practical, low containment alternative. Human immunodeficiency virus (HIV)-based PVNAs are widely used, however, these systems have not been widely performed in high HIV prevalence populations. We assessed HIV-based PVNA use to quantify severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) neutralisation in HIV-infected sera.

Methods

HIV(SARS-CoV-2) pseudotypes bearing B.1, B.1.351, B.1.617.2 and BA.1 spikes assessed SARS-CoV-2 neutralisation in sera collected from a longitudinal cohort in Malawi. Sera from HIV-infected participants (4.9% of cohort, n=99) were re-tested using vesicular stomatitis virus (VSV)-based SARS-CoV-2 pseudotypes (VSV(SARS-CoV-2)). HIV(VSV-G) pseudotypes, bearing the VSV-G protein, were used to confirm interference with the HIV base. Lastly, live virus neutralisation assays were performed to compare the accuracy of HIV- or VSV-based SARS-CoV-2 PVNA neutralisation in HIV-infected participants.

Results

In HIV-uninfected participants, SARS-CoV-2 neutralisation seroprevalence ranged between 8.1-54.5%. Seroprevalence was significantly higher in HIV-infected participants (85.5-93.9%) ($p=0.006$). VSV(SARS-CoV-2) PVNAs estimated lower seroprevalence (5.6-65.2%) in HIV-infected individuals, suggesting over-reporting using HIV(SARS-CoV-2) PVNAs. HIV-infected participant sera inhibited HIV(VSV-G) pseudotypes (observed in 75.0-87.9% of HIV-infected samples), confirming interference with the HIV base. For HIV-infected individuals, VSV(SARS-CoV-2) PVNA results correlated highly with live virus assay findings ($r>0.5$), while HIV(SARS-CoV-2) PVNAs correlated poorly ($r<0$). For HIV-uninfected individuals, both assays correlated well with live virus assays. Among HIV-infected participants, there was no significant difference in HIV- or VSV-based seroprevalence by antiretroviral therapy (ART) status ($p>0.05$).

Conclusions

HIV(SARS-CoV-2) PVNAs overestimated neutralisation seroprevalence from HIV-infected participant sera, which was independent of ART. The underlying mechanism of assay interference requires further investigation. HIV-based pseudotyped virus assays should therefore not be used in high HIV prevalence cohorts. Protective immunity to many viruses estimated by HIV-based assays is likely over-reported in high HIV prevalence populations.

The optimization of the epidemic thresholds to determine impact of influenza seasons: Comparing the performance of the Moving Epidemic Method and WHO Average Curve Method in South Africa, 2015-2019.

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Biography:

Thendo Micheal Ramaliba, BSc Microbiology, and Biochemistry, Bsc Hons Microbiology, MSc Public Health (Epidemiology and Biostatistics), is a Epidemiologist at the Centre for Respiratory and Meningitis. Mr. Ramaliba obtained his MSc from the University of Venda, South Africa, and currently pursuing a doctorate in Epidemiology and Biostatistics with the University of Kwazulu-Natal, South Africa. He coordinated and manage data for the South African National HIV Prevalence Survey (SABSSM) project and a South African National TB survey. Mr. Ramaliba has published articles in indexed journals. He has join the CRDM and contribute to the epidemiology of respiratory infection

Background:

Using appropriate methods for determining the impact of seasonal influenza is an essential component of epidemic and pandemic preparedness. We aimed to evaluate the Moving Epidemic Method (MEM) and WHO Average Curve Method (ACM) to determine the annual impact of influenza using sentinel, syndromic surveillance data.

Methods

We used influenza sentinel surveillance data (i.e., using smoothed, 3-week moving average of percentage influenza positivity) among patients hospitalized at 11 hospitals with severe respiratory illness (SRI) during 2015–2019 to determine the threshold for influenza impact using ACM and MEM. The 40, 90, and 97.5 percentiles were used to calculate the moderate, high, and extraordinary thresholds, respectively. ACM and MEM thresholds were applied to the 2022 SRI data.

Results

The ACM influenza positivity impact thresholds were <6.8% for below seasonal threshold, ≥ 6.8% to <16.8% for low, ≥16.8% to < 22.0% for moderate, ≥22.0% to <24.6% for high and ≥24.6% for extraordinary. The MEM impact thresholds were <5.6% for below sessional threshold, ≥5.6% to <13.1% for low, ≥13.1% to <18.3% for moderate, ≥18.3% to <21.1% for high, and ≥21.1% for extraordinary. In 2022, the moving average influenza positivity crossed the ACM low level threshold in week 19 (7.3%), and crossed the MEM low level threshold in week 18 (6.6%). In week 26, the moving average peaked at 14.0%, coinciding with the ACM low level and the MEM moderate level. In week 29, the moving average proportion positive (4.9%) dropped below the seasonal threshold in both methods.

Conclusion

Although the MEM and ACM methods use different algorithms to determine the seasonal thresholds, the MEM thresholds occur at lower levels potentially leading to assessment of flu seasons being of greater impact compared to ACM. Evaluation of data from additional years and other impact indicators could help inform whether this pattern is observed consistently.

Design and Initiation of a Demonstration Project to Leverage President's Emergency Plan for AIDS Relief Supported Clinics to Increase Influenza Vaccination Coverage Among Prioritized Populations within South Africa

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Biography:

Noah Kojima, MD, currently serves as an Epidemic Intelligence Service Officer in Centers for Disease Control and Prevention's Influenza Division. He co-led an investigation of early season influenza activity in Tennessee and conducted respiratory virus surveillance in many networks in the United States.

Prior to joining CDC, he lived in South Africa, from 2013–2014, where he led research projects as a U.S. National Institutes of Health Fogarty Fellow on HIV and other sexually transmitted infections among pregnant women and newborns.

Dr. Kojima received his Doctor of Medicine and training in Internal Medicine from University of California Los Angeles.

Background: In 2016, only 5% of the estimated 23 million South Africans prioritized for influenza vaccination (which includes people living with HIV [PLHIV] and health care workers [HCWs]) were vaccinated. In 2022, the Provincial Departments of Health purchased approximately 690,000 influenza vaccine doses; only 78% were utilized. In December 2022, President's Emergency Plan for AIDS Relief (PEPFAR) released a 5-year strategy with a new pillar aiming to leverage existing PEPFAR capacity to strengthen public health systems and security.

Methods: This prospective demonstration project for KwaZulu-Natal, South Africa will assess whether low-cost interventions leveraging the PEPFAR-supported platform increase vaccine utilization among PLHIV and HCWs. Thirty-six PEPFAR-supported clinics will be purposively selected to ensure inclusion of the following strata: urban/rural setting, and high/low performance metrics. Restricted randomization to intervention or comparator (1:1 allocation) will be used to ensure balance between arms. In intervention clinics, influenza educational materials and trainings will be introduced into routine PEPFAR-supported health literacy interventions, including posters and handouts, peer-to-peer education, and HCW training during the 2024 influenza season. Routine clinic-reported influenza vaccine administration data will be compared between intervention and comparator clinics by strata prospectively. A costing analysis will be conducted to assess cost per additional vaccination.

Results/Conclusions: Assessment protocol, educational materials, and data capture instruments are being finalized. Clinic visits have been initiated to optimize intervention strategies into patient flow, and 2023 influenza season vaccine administration data are being captured to inform clinic selection and pre/post-assessments. Interventions are planned for March–September 2024. If influenza vaccine utilization is increased at low cost per additional vaccination, this methodology can be explored in other provinces and countries as an innovative approach for increasing influenza vaccination among priority populations.

Influenza infection attack rate during the COVID-19 pandemic: HUTS Community Cohort Study, South Africa, 2021-2022

Miss Nokuthula Linda[1], Amelia Buys[1], Cayla Reddy[1], Lorens Maake[1], Thulisile Dlamini[1], Valencia Petje[1], Alexandra Moerdyk[1], Wilhelmina Strasheim[1], Sibongile Walaza[1,4], Jackie Kleynhans[1,4], Jocelyn Moyes[1,4], Aaron M Samuels[5], Sue Aitken[2], Tamika Fellows[2], Sarah Magni[2,4], Cherie Cawood[6], Anne von Gottberg[1,3], Cheryl Cohen[1,4], Nicole Wolter[1,3]
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Biography:
Medical scientist at the Centre for Respiratory Diseases and Meningitis, National Institute for Communicable Diseases (NICD) with over five years experience in the laboratory and research activities. Currently involved in serological studies and working with SARS-CoV-2, RSV and influenza pathogens. Previous experience includes working at the Centre for Healthcare-associated infections, Antimicrobial Resistance & Mycoses at the NICD and Rainbow Veterinary laboratory in Hammarsdale. My interest is to gain and improve scientific knowledge on topics related to public health.

Background:
Influenza circulation was significantly depressed during the COVID-19 pandemic in South Africa. An increase in activity was observed from September to December 2021. We describe influenza infection attack rates in two communities during a period when limited influenza circulation was detected in respiratory illness surveillance.

Methods:
Paired sera were collected from 702 participants enrolled in community-based representative household surveys in March-April 2021, after the second COVID-19 wave, and in April-June 2022, after the fourth COVID-19 wave, in KwaZulu-Natal and Western Cape Provinces. Haemagglutination inhibition assay testing was performed using representative circulating influenza viruses; a ≥four-fold rise in titre between surveys was considered indicative of infection. Whole blood collected from the first collection was tested for HIV using ELISA or PCR in infants. Chi-squared test was used to compare proportions.

Results:
Participant median age was 38 years (interquartile range 24.5-53.5 years), and overall HIV prevalence was 18.7% (126/673). HIV status was unknown for 29 (4.1%) participants. Overall influenza attack rate was 47.0% (330/702). People living with HIV had an attack rate of 46.0% (58/126) compared to 47.4% (259/547) attack rate for non-HIV infected individuals (P=0.789). The attack rate was slightly higher among individuals aged ≤18 years (49.1%, 53/108), followed by adults aged 19-64 years (47.0%, 247/525) and the elderly (≥65 years, 41.5%, 30/69) (P=0.767). Among 330 infected individuals, there were 416 infections detected, with 19.7% (65/330) and 3.0% (10/330) individuals having been infected with two or three different subtypes/lineages, respectively. A(H1N1)pdm09 accounted for 52.5% (220/416), A(H3N2) for 27.4% (114/416) and B/Victoria for 19.7 % (82/416) of all infections.

Conclusions:
During atypical summer influenza activity in 2021, after easing of COVID-19 restrictions, almost half of individuals in the community were infected with influenza of which the majority were A(H1N1)pdm09, and 22.7% of individuals infected with more than one subtype/lineage.

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The changing genetics of the highly pathogenic avian influenza H5Nx outbreaks in South Africa from 2017-2023

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[1]ARC-Onderstepoort

Biography:
Dr. Rotherham completed a PhD studentship (at the University of Pretoria) focusing on the development of a rapid human TB diagnostic assay. After completion of her PhD, she joined the ARC-OVR in 2013 as a postdoctoral fellow with a focus on Foot-and-Mouth Disease research. In 2015, she joined was appointed as a researcher with a research focus on avian influenza and Newcastle disease. A large part of her research focuses on full genome sequence analysis of circulating strains of these viruses. Dr. Rotherham also forms part of the research support to the PCR and Virology diagnostic laboratories for avian influenza.

Highly pathogenic avian influenza (HPAI) viruses of the H5 subtype remain a serious concern for poultry and human health. An H5N8 virus was first detected in poultry in China in 2010; by 2014, this virus had caused multiple outbreaks among ducks, chickens, geese, and wild birds in South Korea and subsequent outbreaks in Japan, China, Europe, and North America. H5N8 viruses belong to the 2.3.4.4 clade of H5 subtype AI viruses. There are two distinct clusters within this particular clade, namely group A and group B. Group A viruses have been detected in China (early 2014) and later in South Korea, Japan, Taiwan, Canada, the United States and Europe. Group B viruses were first detected in China (2013) and South Korea (2014); in May 2016 a novel reassortment of group B viruses was detected in wild birds in Siberia. This novel reassortment of group B viruses has since spread throughout Europe, the Middle East and Africa. This recent group B reassortment virus was detected in several SADC countries in recent years. Full genome analysis of the viruses from 2017 – 2023 have indicated that there are several subclades of the clade 2.3.4.4 B viruses within the South African isolates that have caused different outbreaks. These viruses, however, share a recent common ancestor with viruses that were isolated in Egypt, Nigeria, Korea and India, which prompted the need to determine how these viruses are changing and if the changes are due to new introductions or reassortments of the current strains. To date there have been no human cases reported and sequence data suggests that the receptor binding site of this virus is restricted to avian species. There is currently also no evidence to suggest that under field conditions, this virus is undergoing mutational changes that would enable it to infect mammals.

Genomic epidemiology of human metapneumovirus in Cote d’Ivoire

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Biography:
Dr. Herve KADJO has been working on influenza and other respiratory viruses for more than twenty years at the Pasteur Institute of Côte d'Ivoire. He played a significant role in establishing an influenza surveillance system and laboratory diagnostic capacity (viral isolation, molecular diagnosis and sequencing) for respiratory infectious pathogens at national and sub-regional levels. recently he coordinated molecular diagnostics activities as part of the national response to the COVID-19 pandemic. Dr KADJO is a member of the French Society of Microbiology, the French Society of Virology and the European Society of Clinical Microbiology and Infectious Diseases.

Background: Human metapneumovirus (hMPV) was described as a causative agent of acute respiratory infection (ARI). In Côte d'Ivoire hMPV was first detected in 2010. To date, little data is available to understand the epidemiology of ARI related to hMPV, no molecular data to unveil its genetic diversity and transmission dynamics. Objectives: This study aims to address the lack of knowledge on viral molecular evolution by reconstructing its evolutionary history and transmission patterns.

Material and Methods: The study focused on the analysis of epidemiological data and biological samples from the influenza sentinel surveillance network. Sanger sequencing of surface and attachment glycoprotein genes (F and G) was done. The datasets were aligned using MAFFT v7.409 and subsequently manually inspected in AliView v1.25. After editing the alignments, maximum-likelihood (ML) trees were inferred using RAxML v7.2.6 incorporating a general time reversible (GTR) model of nucleotide substitution with a gamma-distributed (Γ) rate variation among sites. We investigated the temporal signal of the datasets using TempEst. Phylogenetic relationships were inferred for each of the “gene: clade” datasets separately, with a Bayesian phylogenetic approach using MCMC available via the BEAST v1.10.4 package.

Results: The analysis of 3899 data, allowed to show a prevalence of more than 6% of hMPV. We observed a continuous transmission of hMPV throughout the year with an increase in the number of cases during two periods from February to March and from July to September. Two large groups of genotypes A and B subdivided into subgenotypes A2b, B1 and B2 have been identified. Spatial-temporal patterns of the Côte d’Ivoire epidemic showed that the epidemics were characterized by multiple introductions into the country throughout the year from different locations.

Conclusion: Continuous genomic and epidemiological surveillance of hMPV in Cote d’Ivoire and globally would be essential for the prompt and precise identification of viral introductions

Integrated epidemiology and genomic surveillance of influenza viruses and SARS-coV-2 in Côte d'Ivoire from 2020 -2022

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Biography:
Dr. Herve KADJO has been working on influenza and other respiratory viruses for more than twenty years at the Pasteur Institute of Côte d'Ivoire. He played a significant role in establishing an influenza surveillance system and laboratory diagnostic capacity (viral isolation, molecular diagnosis and sequencing) for respiratory infectious pathogens at national and sub-regional levels. recently he coordinated molecular diagnostics activities as part of the national response to the COVID-19 pandemic. Dr KADJO is a member of the French Society of Microbiology, the French Society of Virology and the European Society of Clinical Microbiology and Infectious Diseases.

Background: In Côte d'Ivoire, an influenza surveillance network has been in place since 2007 with a WHO reference laboratory (NIC). This laboratory is also the national reference laboratory for SARS-CoV-2. In November 2020, in the face of the COVID-19 pandemic, the World Health Organization (WHO) created interim guidance on how to integrate testing for SARS-CoV-2 into existing influenza surveillance systems. Objectives: This article aims to show the results of implementation of integrated influenza and COVID-19 surveillance.

Material and methods: Samples from sentinel surveillance were sent with an epidemiological form containing the patient's biometric data, medical history and clinical symptoms. The samples are analyzed by real-time multiplex PCR targeting the genes of the influenza virus and SARS-CoV-2 using CDC Flu SC2 multiplex kits. All SARS-CoV-2 positive specimens with Ct values less than or equal to 28 are collected for sequencing with MinION Mk1c device according to ARTIC protocol. The influenza positive samples were sent to WHOCC in Atlanta for sequencing.

Results: Over the 3 years, 11,599 samples were analyzed, 52% of which were SARI cases. The positive rates over the period were 4% for influenza and 2.71% for SARS-CoV-2. Among the positive cases, SARS-CoV-2 was detected in 37% of SARI cases, compared with 20% for influenza. wo hundred and forty-six SARS-CoV-2 sequences were obtained, with 81% of variants identified, including 59% of OMICRON variants. for influenza, sequencing of the hemagglutinin gene has revealed that all A(H3N2) viruses belong to clade 3c.2a1b, A(H1N1)pdm09 viruses to clade 6B.1A and B viruses to clade V1A.3a.2.

Conclusion: Integrated surveillance of influenza viruses and SARS-CoV-2 through the sentinel influenza surveillance network has been implemented for the period from 2020 to 2022. This demonstrated the flexibility of the system. This surveillance system could play an important role during the post-pandemic phase of the COVID-19

Antibody levels to SARS-CoV-2 based on multi-analyte profiling in Gauteng and the Eastern Cape, South Africa: Six months after the last COVID-19 pandemic wave

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Biography:

Wihelmina Strasheim is a senior medical scientist working in the serology laboratory at the Centre for Respiratory Diseases and Meningitis at the National Institute for Communicable Diseases. She is the laboratory lead and project manager for the SARS-CoV-2 and multipathogen serosurveillance in South Africa (SAMS) study. She is mainly involved in the implementation new multiplex immunoassays. She is also pursuing her PhD part time in antibiotic use and resistance in commercial pig farming.

Background: SARS-CoV-2 seroprevalence in South Africa was >90% after the fourth COVID-19 wave. Monitoring seroprevalence using semi-quantitative assays poses challenges in identifying antibody boosting, waning and distinguishing recent infection or vaccination. We aimed to quantify SARS-CoV-2 antibody levels using multi-analyte profiling and compared levels based on vaccination status.

Methods: We conducted a population-based serosurvey from October to December 2022 in Gauteng and Eastern Cape provinces. Demographic information and dried blood samples were collected. Antibody levels against nucleocapsid (N), spike receptor binding domain (RBD), spike domain 1 (S1) and 2 (S2) proteins were quantified using a bead-based multiplex immunoassay. Antibody levels between vaccinated and unvaccinated individuals were compared using the Wilcoxon rank-sum test.

Results: Overall, 3837 households were visited and 3040 participants [50.9% (1548/3040) Gauteng, 49.1% (1492/3040) Eastern Cape] were enrolled. Participants had a median age of 24 years (interquartile range (IQR):11-50) and 57.7% (1754/3040) were female. Overall, 586 (19.3%) participants had ≥1 previous self-reported SARS-CoV-2 PCR or antigen test, of which 16.7% (98/586) were positive. Of 2196 eligible participants, 870 (39.6%) had received ≥1 dose of COVID-19 vaccine. Among 1257/3040 (41.3%) participants with available results [262 (20.8%) vaccinated and 995 (79.2%) unvaccinated], vaccinated individuals had higher antibody levels against RDB (P<0.001), S1 (P<0.001) and S2 (P=0.0478) [RBD median: 293.3 BAU/ml (IQR:154.1-424.8), S1 median: 427.6 BAU/ml (IQR: 200.1-767.9) and S2 median: 144.4 BAU/ml (IQR:81.7-256.7)] than unvaccinated individuals [RBD median: 127.1 BAU/ml (IQR:34.9-271.1), S1 median: 164.0 BAU/ml (IQR:50.5-376.0) and S2 median: 132.5 BAU/ml (IQR:73.7-211.4)], but not against N (P=0.314) [vaccinated: 15.7 BAU/ml (IQR:4.3-39.8), unvaccinated: 15.7 BAU/ml (IQR:5.9-44.7].

Conclusion: High antibody levels have been maintained in South Africa, consistent with seroprevalence data, despite a reduced number of cases being reported. Multi-analyte testing is useful to detect quantifiable differences in antibody levels and can be used to monitor changes in longitudinal cohorts.

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Preparedness and resilience for emerging threats: development of operational tools and networks for national pandemic preparedness for respiratory pathogens

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Biography:
Hannah Lewis is a senior epidemiologist with over 15 years experience in international health emergency preparedness and response. She currently works at WHO HQ. As part of the Unity Studies team for SARS-CoV-2, she co-ordinated study implementation in the Africa region between 2020-2022 . Previously she worked at the Robert Koch Institute, Germany (2013-2019), WHO Lao PDR Country Office (2008-2012), Statens Serum Institut, Denmark (2006- 2008), Public Health England (2004-2006) and the Department of Health, England (1999-2003). Hannah holds a Master of Public Health from Kings College, University of London (2005) and is an EPIET Alumna (2008).

Background:
National capacity gains made during the COVID-19 pandemic should be sustained and respiratory pathogen pandemic preparedness (RPPP) planning strengthened for future events. The Preparedness and Resilience to Emerging Threats (PRET) initiative is a hazards-based approach to guide future pandemic planning holistically for groups of pathogens by mode of transmission. We describe the technical guidance and operational tools developed by the World Health Organization (WHO) and partners to assist countries in strengthening their national capacities for RPPP planning in-line with PRET Module 1.

Methods:
WHO and partners have built an online resource pack of key technical documents and an accompanying peer learning network to facilitate global sharing of pandemic preparedness resources and good practices. The resource pack includes a RPPP checklist to self-assess national capacities, capabilities and preparedness planning to help identify gaps and priority actions; and a Simulation Exercise package to advocate for, test and improve plans. Resources will be tailored to each region considering the specific context of, and lessons learned in, that Region.

Results:
The PRET Call to Action was issued by WHO on 26 April 2023. The WHO Africa Region conducted a timely workshop in May 2023 to support national implementation of the PRET concepts. Future work includes review and revision of national pandemic preparedness plans; identification of priority actions through application of the RPPP checklist; and simulations to exercise multi-sectoral coordination, triggers for decision making and other priority areas. WHO is working closely with partners and countries to galvanize implementation in a sustainable manner and to develop a roadmap, and a monitoring and evaluation framework, for PRET.

Conclusions:
PRET and its accompanying technical resources facilitate efficiency and coherence in pandemic preparedness. Countries and stakeholders are encouraged to update pandemic plans and strengthen functional capacities for preparedness and response.

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Influenza circulation before and since the pandemic of SARS-CoV-2 in Madagascar

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Biography:
I am Research Fellow and Technical Leader at NIC Madagascar. I'm in charge of developing, monitoring and coordinating research program at NIC laboratory. I aim to study the aetiology of acute respiratory infections, characterize the genetic properties and circulation dynamics of respiratory viruses (RV), and develop diagnostic tools to respond to any new epidemics. I am involved in the development program of human and zoonotic Influenza in collaboration with the Ministry of Health and Ministry of Livestock. I oversee all technical aspects related to RV and participate in local and international research programs. I'm author and co-author of 33 publications.

BACKGROUND
Several countries reported decreased influenza circulation at the beginning of the COVID-19 pandemic. This was attributed to non-pharmaceutical interventions (NPIs) and lockdowns. The present study describes the influenza circulation profile before, and since, the COVID-19 pandemic in Madagascar.

METHODS
Nasopharyngeal (NP) swabs and clinical/demographic data were collected from patients presenting to influenza surveillance sites who met the ILI or SARI case definition, or were suspected of having COVID-19. Samples were tested at the National Influenza Centre by multiplex PCRs. We describe influenza positivity rates comparing results from January 2018 to February 2020 (pre-pandemic period) to those from March 2020 to December 2022 (pandemic period).

RESULTS
During the pre-pandemic period, 30% (738/2495) of collected NP samples were positive for influenza, and influenza circulated year-round with seasonal peaks during the rains (January-March) and austral winters (June-September). During the pandemic period, 9% (729/7867) of samples were positive for influenza. There were five epidemic waves of SARS-CoV-2. During the first two waves (March 2020 to July 2021), influenza was not identified. In August 2021, the number of SARS-CoV-2 cases began to decrease and NPI measures eased. Subsequently, two influenza epidemics occurred from September 2021 to January 2022 (28%; n=327/1168) and from March to May 2022 (20%; n=150/750), overlapping with the third wave of SARS-CoV-2 (December 2021 to February 2022). During the fourth SARS-CoV-2 wave (June-July 2022), influenza circulation was low (7%; n=37/529) whilst a new spike

of influenza cases occurred in November 2022 (43%; n=267/621) after the fifth SARS-CoV-2 wave (October-November 2022).

CONCLUSION
The pattern of influenza circulation in Madagascar changed during the period of COVID-19 and has not yet returned to the steady-state observed pre-COVID-19. The no detection of influenza during the initial COVID-19 period coincided with lockdowns and NPIs suggesting their utility as an influenza morbidity mitigation tool.

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Increase in detection rates for Avian Influenza H5 and H9 subtypes among poultry and wild bird fecal samples in Kenya, 2018-2023

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Biography:
My name is Dr. Romona Ndanyi, a female Kenyan veterinarian working with the Ministry of Agriculture and Livestock Development, Directorate of Veterinary Services (DVS) in Kenya since 1997. I possess a Bachelors' of Veterinary Medicine degree and a Master of Science in in Rural Poultry Production and Health. Currently I am the head the National Veterinary Reference Laboratories (NVRL), Kabete in Nairobi with vast experience in the Pathology and Microbiology laboratories. I am also in charge of coordination of Antimicrobial Resistance laboratory activities and Biorisk management for the Animal Health sector.

Background
Highly pathogenic avian influenza virus (AIV) was first reported in Uganda in early 2017 among domestic and wild birds along the shores of Lake Victoria. We conducted surveillance among poultry in live bird markets (LBMs) and among wild birds at lakes that are roosting sites for migratory birds in Kenya to assess introduction and circulation of AIVs.

Methods
We collected oropharyngeal and cloacal swabs from poultry at 6 LBMs in 2018-2020 and 5 LBMs in 2021-2023. Fecal samples from wild birds were collected from 5 lakes in 2020 and 6 lakes in 2023. Specimens were tested for influenza A virus by real-time reverse transcriptase polymerase chain reaction (rRT-PCR). Viral subtyping was performed on influenza A positive samples by rRT-PCR for H5, H7, and H9. Whole genome sequencing and antigenic characterization of a proportion of positive specimens was performed. A panel of genetically related H9N2 viruses were compared by Hemagglutination Inhibition (HI) assay to six H9N2 Kenya wild type viruses to determine antigenic relatedness through HI fold differences.

Results
Influenza A was detected in 1028/11730 (8.8%) of poultry specimens: 3.9% in 2018-2020 and 17.3% in 2021-2023. Of 451/1028 (43.9%) positive specimens subtyped, 433/451 (96%) were H9. All 34 H9-positive specimens randomly selected for further subtyping were found to be H9N2. The phylogenetic analysis showed they were clustered with minimal genetic variation. Influenza A was detected in 25/9201 (0.3%) wild bird fecal specimens. Two specimens out of 10 selected for

subtyping were successfully subtyped; one was identified as H5N2 virus of the Eurasian lineage following sequencing analysis while the second was subtyped as H11.

Conclusions
Circulation of H9N2 influenza viruses in poultry in LBMs as well as detection of H5N2 in wild birds highlight the potential for AIV establishment in poultry populations and warrants continued surveillance among avian and human populations.

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Influenza surveillance system as a key tool in the management of the COVID-19 epidemic in Burkina Faso

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Biography:

Doctor of veterinary medicine, Ph.D Microbiology and epidemiology, Director of Research at the Institute of research in health sciences and Head of national influenza reference laboratory, President of One Health Association of Burkina Faso

Background: In Burkina Faso, the first cases of COVID-19 epidemic were detected by the national influenza reference laboratory with the support of the influenza surveillance system. Three months later, few data were available to support public health decision making.

Method: From February 5 to April 4, 2020, we collected sociodemographic, medical history and behavioral characteristics of population with recent travel history from high risk countries, contact cases of COVID-19, clinically suspected cases and health care workers by a one-on-one person interview. Nasopharyngeal or oropharyngeal swabs were collected and shipped to the national influenza reference laboratory for molecular diagnosis. Real time RT-PCR assays using the Tib Molbiol protocol and reagents to detect SARS-CoV-2 E and RdRp genes was used. Infection case was defined by the detection of both E and RdRp genes.

Results: Of the 1062 persons examined, 51.2% had history of contact with confirmed cases. Male patients were predominant (62%) with a median age of 43 years (range, 2 - 80 years). Clinically, 71.09%, 57.63%, 37.5% and 1.3% of the study population had cough, fever, shortness of breath and chest pain respectively. By PCR tests, SARS-CoV-2 was detected in 42.4% (450/1,062) of patient and among them, both E and RdRp genes detected in 76.9% (346/450). The dual detection of E and RdRP gene were considered actual COVID-19 cases according to the WHO definition. Isolated detection of the E gene was considered indeterminate and required further testing. By multivariate logistic regression, the patient age ($p = 0.006$) and presence of fever ($p = 0.002$) were the factors positively associated with COVID-19.

Conclusion: PCR assay were effective for COVID-19 diagnostic and the contribution of the Influenza laboratory was critical during the early moments of the pandemic in Burkina Faso.

Relationship Between Influenza and RSV in Children under 15 Years Old and Climatic Factors in the Maputo City, Mozambique (2015-2021)

senhor Paulo Notiço[1]
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Biography:

Paulo Manuel Notiço is a Statistics undergraduate student at Eduardo Mondlane University. Since 2022, he has been a finalist in his course and began his career as a researcher. He worked at the National Health Observatory, in the Climate and Health Platform in Mozambique, providing support in the sentinel surveillance of acute respiratory infections and emerging diseases. Paulo specializes in modeling and triangulating climate data and infectious diseases. His dedication and knowledge have contributed to the understanding and prevention of diseases, aiming to improve the quality of life in communities.

Introduction: Virus-associated acute respiratory infections (ARI) are one of the greatest global public health concerns. While environmental factors are known to be associated with ARI, these associations have not been systematically evaluated in Mozambique. This study aimed to investigate the relationship between ARI and climatic factors in the city of Maputo between 2015 and 2021.

Methods: We analyzed the weekly counts of ARIs, respiratory syncytial virus (RSV) and influenza obtained from ARI sentinel surveillance to assess associations with climatic variables, including maximum and minimum temperature, relative humidity, total precipitation, and wind speed obtained from National Institute of Meteorology, Mozambique. The generalized additive model for location, scale and shape was employed, including smoothed climate variables with significant lagged effects.

Results: The mean cases of ARI, influenza, and RSV were 1.470, 44, and 60 cases, respectively. The incidence of ARI was positively associated with total precipitation (p-value<0.001), and negatively associated with relative humidity (p-value=0.029), suggesting a seasonal pattern peaking in the summer. There was a negative association between influenza incidence and the minimum temperature (p-value=0.0287), and a positive relation between incidence and precipitation (p-value<0.001), and wind speed (p-value=0.0286) suggested higher incidence in summer. RSV was positively associated with wind speed (p-value<0.001), precipitation (p-value=0.00228), and maximum (p-value=0.0004), and minimum temperatures (p-value<0.001), with peak incidence in summer.

Conclusions: Climate conditions were associated with the occurrence of viral acute respiratory infections. Timing of the adoption of preventive measures should coincide with the onset of these conditions for ARI as a whole, and for pathogen-specific ARI.

Keywords: Acute respiratory infections; Children; Climatic factors; GAMLSS.

Impact of malnutrition on clinical outcomes of patients hospitalized with respiratory illnesses in Kakuma, Kenya

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Biography:

Joel Machuki is a Research Program Manager for the Henry Jackson Foundation of Medical Research International where he provides support to the CDC funded program titled, Surveillance and Response to Avian and Pandemic Influenza and Non-Influenza Respiratory Pathogens in Kenya. He holds a master's in public health in Epidemiology and population health from Maseno University and a Bachelor of Science in Nursing from University of Eastern Africa, Baraton. He has more than 8 years' experience in research and has authored 1 publication.

Background

A sizable fraction of patients in hospitals suffer from malnutrition. The risk of negative clinical outcomes, such as lengthier hospital admissions and mortality, is higher among hospitalized children under the age of five who are malnourished. Uncertainty exists regarding the impact of malnutrition on clinical outcomes in individuals with respiratory illnesses who require hospitalization. This study aimed to investigate the prevalence of and patient outcomes among malnourished children hospitalized with respiratory illness at Kakuma refugee Camp.

Methods

We utilized Severe acute respiratory Illness (SARI) surveillance data from Kakuma refugee camp in Kenya. The target population was under five years old patients hospitalized with respiratory illness between January 2019 and December 2022. Malnutrition cases were identified through clinical assessment using measuring mid upper arm circumference (MUAC). Respiratory illness was defined as acute illness in the last 10 days with fever (measured (≥38°C) or history of fever), cough and requiring hospitalization. Measures for severity were duration of hospitalization and mortality.

Results

The study established that malnutrition was prevalent in 1101 out of 2981 (36.9%) cases with respiratory illness. Half of children with malnutrition were under one year (51.3%). Additionally, majority 701/1101 (63.6%) of the malnourished patients were seen in the years 2021 and 2022. Malnourished cases were likely to stay longer (7 days or more) in the hospital (23.3% vs 12.9%; $p<0.001$) or die during the admission (2.5% vs 1.2%; $p=0.005$).

Conclusions

The risk of mortality and longer hospital stays in hospitalized patients with respiratory illness is significantly higher in patients with malnutrition.

Keywords: Malnutrition; Clinical outcomes; Respiratory illness

Seasonal influenza vaccine effectiveness in South Africa pre- and post-COVID-19 pandemic, 2017-2019, 2022

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Biography:

Nicola graduated from the Cape Peninsula University of Technology with a Bachelor of Health Science degree in Medical Laboratory Science. She then went on to earn a Master of Science degree in Epidemiology specializing in Biostatistics and Epidemiology from the University of the Witwatersrand. She is currently an Epidemiologist and Biostatistician with the Center for Respiratory Diseases and Meningitis at the National Institute for Communicable Diseases.

Background

South Africa introduced a national influenza vaccination campaign in 2010, however influenza remains a significant cause of morbidity and mortality. Influenza vaccine effectiveness (VE) estimates from 2005–2015 ranged from 46–87% during periods of good strain match. However, during periods of A(H3N2) strain genetic drift, VE estimates were significantly lower (-14–38%). We aimed to assess influenza VE against laboratory-confirmed influenza among outpatients aged ≥6 months seeking care for influenza-like-illness (ILI) to guide the GIVE report and vaccine composition selections.

Methods

We conducted a test-negative case-control study to assess annual influenza VE at sentinel private general practices in eight South African provinces during 2017–2019 and 2022; 2020 and 2021 were excluded because of no or atypical influenza seasons with localised outbreaks. Dominant strains are those more prevalent among positive cases. We created multivariable logistic regression, adjusting for season, to estimate VE against laboratory-confirmed influenza in all ages, stratified by subtype/lineage.

Results

Vaccine coverage among controls was 7%, 9%, 10% and 12% in 2017 (n=1142), 2018 (n=1231), 2019 (n=974), and 2022 (n=807), respectively. The dominant subtype was A(H3N2) in 2017 at 71% (467/654,) and 2019 at 94% (654/698), and A(H1N1)pdm09 in 2018 at 56% (357/640) and 2022 at 37% (127/339). VE against A(H3N2) for all ages was 19% (95% confidence interval (CI), -42%–54%) and 44% (95% CI, 6%–67%) in 2017 and 2019, respectively. VE against A(H1N1)pdm09 for all ages was 55% (95% CI, 17%–76%) and 49% (95% CI, -15%–78%) in 2018 and 2022 respectively.

Conclusion

Lower VE in 2017 and 2022 may be attributed to strain mismatch. Significant VE in subsequent years could have prevented a significant number of severe cases. Campaigns to improve influenza vaccine coverage may significantly reduce influenza-associated morbidity and mortality and may provide more robust VE estimates.

A qualitative assessment of influenza vaccine uptake among children and its impact on the childhood immunisation program in Kenya

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Biography:
Nzisa Liku is a medical doctor with training and experience in public health programs and research design for > 9 years. She holds a Bachelor's degree in Medicine and Surgery from University of Nairobi, Kenya and a Master's degree in Public Health from Edinburgh University, Scotland.

In her current position as a Senior Public Health Advisor in the Influenza Division at CDC, she coordinates the implementation of an influenza sentinel surveillance program and influenza vaccination activities. Previously, she led teams to design, implement and monitor projects in mortality surveillance, health information systems and outbreak management.

Background: Influenza is a significant contributor to acute respiratory infections (ARI), and children <5 years are at increased risk of severe influenza disease. In Kenya, while the highest rates of influenza-associated hospitalization are observed among children <2 years of age, the influenza vaccine is not included in the Kenya Expanded Programme of Immunization (KEPI). To inform roll-out of a national influenza vaccination program, we implemented an influenza vaccine demonstration project in Nakuru and Mombasa counties in Kenya from 2019 to 2021, to establish reasons for uptake and refusal of the vaccine among caregivers of children aged 6-23 months and the impact of influenza vaccination on the wider immunization program.

Methods: Using semi-structured questionnaires, we conducted eight focus group discussions among caregivers recruited through community health volunteers, and twelve key informant interviews among healthcare workers at demonstration facilities. We used thematic analysis to code emergent themes per the WHO vaccine hesitancy matrix.

Results: Community members brought their children for influenza vaccination and healthcare workers promoted the vaccine to caregivers. Despite the use of various channels of communication such as posters and community health volunteers, vaccine hesitancy was driven by perceptions of inadequate sensitization and low disease severity among caregiving community members. Contextual factors like the COVID-19 pandemic both promoted and reduced uptake, healthcare workers were a trusted source of information on vaccines, and concerns were raised among parents regarding the number of vaccines recommended for children. Healthcare workers reported identifying and vaccinating more routine vaccine defaulters during the demonstration project period.

Conclusion: The influenza vaccine was well received by both healthcare workers and community members. Vaccine uptake was affected by issues such as misconceptions about the vaccine and the COVID-19 pandemic, perceptions of low disease severity, and vaccine overload. The demonstration project strengthened the immunization program by facilitating detection of defaulters.

Implementing seasonal influenza vaccination in the era of COVID-19, in South Africa (2011-2022)

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Biography:

Wayne Ramkrishna is the Deputy Director for Zoonotic Diseases in the National Department of Health; he played a key role in establishing the Zoonotic Diseases Unit as well as the One Health Forum of South Africa. He was actively involved in the country's epidemic preparedness and response to the influenza pandemic, Ebola outbreak, Zika virus, MERS-CoV, rabies and COVID-19. He also played a lead role in developing several national policies and guidelines including the National Pandemic Preparedness Plan, National Influenza Policy and the National Epidemic Preparedness and Response Guidelines. He is the IHR National Focal Point for Zoonotic Diseases.

Background

Seasonal influenza causes substantial morbidity and mortality in South Africa resulting in an estimated 40,000 hospitalizations and 11,000 deaths annually. The Department of Health conducts annual national influenza vaccination campaigns since 2010, targeting people at increased risk for severe influenza illness and death (target groups). The influenza vaccination programme faced unique challenges during the COVID-19 period. The objective of this report is to describe the changes in the national influenza vaccination programme following the emergence of COVID-19.

Methods

During 2011-2019, trivalent inactivated influenza vaccine (TIV) was used in the South African public health sector; from 2020, a combination of TIV and quadrivalent inactivated influenza vaccine (QIV) were used.

Influenza vaccines were procured by provinces and distributed to public health facilities country-wide. Vaccinations were recorded on tally sheets.

Results

Before COVID-19 on average 912 575 (range: 800 000-1 040 000) vaccines were procured and 824 292 (range: 706 374-944 150) were utilised annually. During COVID-19, in 2020, 1 203 660 were procured and 1 008 311 (84%) utilised; in 2021, 871 910 were procured and 612 848 (70%) utilised and in 2022, 688 838 procured and 539 533 (78%) utilised. Health care workers (HCWs) who were not previously a target group were added during the COVID-19 pandemic to protect the health workforce from influenza.

Conclusion

In 2020, uptake of influenza vaccines increased by 64 161 (6.8%) compared to 2019 (944 150). This was mainly due to the Department of Health procuring and distributing additional vaccines to prevent influenza, protect HCWs and conserve medical resources for COVID-19 patients. HCWs contributed to 17.6% (177 718) of the vaccinations.

In 2021 and 2022, both procurement and uptake of influenza vaccines declined compared to 2019, mainly due to the concurrent COVID-19 vaccinations which took precedence over influenza.

Deciphering the circulation dynamics of RSV in Madagascar over the past decade

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Biography:

I am a PhD student in the Department of fundamental and applied Biochemistry at the University of Antananarivo, Madagascar. Also, I am working as a research engineer at the NIC, Virology unit of Institute Pasteur of Madagascar.

I am mainly in charge of NGS sequencing of RSV with ILLUMINA technology and phylogenetic analysis. As a PhD student, I'm working on the seasonality mechanism and phylodynamic pattern of respiratory syncytial virus circulated in Madagascar.

BACKGROUND

RSV is a leading cause of acute respiratory infections (ARI) in children under 5. In Madagascar, where it is estimated to account for 11299 hospitalizations per year, RSV circulation is seasonal, occurring primarily during the first half of the year. Here, we aimed to understand climatic factors driving the RSV circulation dynamics through two approaches.

METHODS

Between 2011 and 2022, a total of 312 RSV G gene sequences were generated from RSV positive samples collected from our ARI surveillance. Initially, they were obtained by Sanger sequencing, but from 2021 they were generated by Next Generation Sequencing. Sequences from countries with routine commercial flights and shipping routes to Madagascar were retrieved to conduct phylodynamic analyses using Bayesian Evolutionary Analysis Sampling Trees. In addition, Generalized Additive Models and Generalized Linear Mixed Model models were used to study the role of meteorological parameters on RSV prevalence.

RESULTS

A complex local circulation dynamic of RSV was observed during the investigation period. Strains arose either from new introductions or from local evolution of formerly circulating strains. For RSV type A, a circulation pattern characterized by local evolution and multiple introduction events during the same epidemic was observed while for RSV type B multiple introductions occurred during one epidemic. Malagasy strains originated from France, Spain and China. The multivariate analysis of meteorological parameters showed that an increase in rainfalls at 80-100 mm significantly accelerated RSV transmission ($p<2e-16$) triggering an epidemic six weeks later. Similarly, a temperature between 18°C-20°C accelerated viral transmission ($p<2e-16$) leading to a peak three weeks later.

CONCLUSIONS

These findings may be helpful for public health system planning and educational alerts to clinicians for anticipating the seasonal occurrence of RSV epidemics and to expedite appropriate patient management. These results are keys for managing RSV epidemics and to adapt future vaccination strategies.

Timing of seasonal influenza epidemics for 25 countries in Africa during 2010-2019: A retrospective analysis

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Biography:

Perrine Marcenac is an epidemiologist in the Global Influenza Branch of the Influenza Division at US CDC where her work focuses primarily on vaccine effectiveness studies, randomized controlled trials, and global influenza data analysis and modeling. She joined US CDC in 2019 as an Epidemic Intelligence Service Fellow. She has a PhD in Biology from Harvard University and completed a post-doctoral fellowship at the Harvard T. H. Chan School of Public Health.

Background:Using country-specific surveillance data to describe influenza epidemic activity could inform decisions on the timing of influenza vaccination. We analysed surveillance data from African countries to characterize the timing of seasonal influenza epidemics to inform national vaccination strategies.

Methods: We used publicly available sentinel data from African countries reporting to the WHO Global Influenza Surveillance and Response FluNet platform that had data collected during 2010–19. We calculated a 3-week moving proportion of samples positive for influenza virus and assessed epidemic timing using an aggregate average method. The start and end of each epidemic were defined as the first week when the proportion of positive samples exceeded or went below the annual mean, respectively, for at least 3 consecutive weeks. We categorized countries into five epidemic patterns: northern hemisphere (NH), with epidemics occurring in October–March; southern hemisphere (SH), with epidemics occurring in April–September; primarily NH with some epidemic activity in SH months; primarily SH with some epidemic activity in NH months; and no clear pattern.

Findings: Of the 34 countries reporting data to FluNet, 25 had at least 3 years of data, representing 46% of the countries in Africa and 89% of Africa's population. Study countries reported RT-PCR respiratory virus results for a total of 503,609 specimens (median 12971 [IQR 9607-20960] per country-year), of which 74,001(15%; median 2078 [IQR 1087–3008] per country-year) were positive for influenza viruses. 248 epidemics occurred across 236 country-years of data (median 10). Six(24%) countries had a NH pattern. Eight(32%) had a primarily NH pattern with some SH epidemics. Three(12%) had a primarily SH pattern with some NH epidemics. Three(12%) had a SH pattern. Five(20%) had no clear pattern.

Interpretation: Most countries had identifiable influenza epidemic periods that could be used to inform authorities of non-seasonal and seasonal influenza activity, guide vaccine timing, and promote timely interventions.

Evaluation of the impact of influenza, SARS-CoV-2 and RSV on mortality in Antananarivo, Madagascar, 2016–2023

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Biography:

Dr Joelinotahina Verohasina is a young medical doctor. His main duty is to coordinates several surveillance activities in Madagascar, including monitoring mortality due to respiratory infections, and surveillance of severe acute respiratory infections. his field of activity mainly concerns respiratory viruses such as Influenza and other respiratory viruses (respiratory syncytial virus, sars cov-2, rhinovirus). He has been responsible for coordinating these surveillance systems since 2016.

Background

Influenza, SARS-CoV-2 and RSV are respiratory viruses with the similar mode of transmission. We assessed correlations between pathogen-specific influenza-like illness (ILI) and severe acute respiratory infection (SARI) consultations and ARI-associated mortality in Antananarivo, Madagascar, before and since the COVID-19 pandemic.

Methods

We used data from 2016-2023 from the two health facilities conducting ILI surveillance and from a public hospital conducting SARI surveillance in Antananarivo. In parallel, mortality surveillance data, including verbal autopsy-determined cause of death (ICD-10), were collected. We calculated the correlation between ILI and SARI surveillance signals and ARI-associated mortality from our mortality surveillance system.

Results

From January 2016 to April 2023, we recorded 76,958 deaths, of which 7.1% were attributed to ARI (J0 to J22 according to ICD-10). Regarding patients <5 years old (4498 deaths, from January 2016 to December 2019), there was a strong positive Pearson correlation between the number of reported deaths due to ARI and the number of Influenza-associated SARI (r=0.72, p=0.0001) while the correlation was lesser between the number of deaths (n=3344) and the number of RSV-associated SARI for patients <2 years old (r=0.40, p=0.001). From 2020 to April 2023, a significant correlation was observed between the number of deaths for patients <5 years related to ARI and influenza at the end of 2022 (r=0.39, p=0.0008) as with the number of deaths related to ARI and SARS-CoV-2-positive SARI cases (r= 0.54, p=0.000001) among people aged over 50.

Conclusion

Prior to the COVID-19 pandemic there was a strong correlation between ARI-attributable mortality and influenza-associated SARI. The correlation was less strong for RSV. Since the COVID-19 pandemic, the correlation between ARI-attributable mortality and influenza decreased, but there was a moderate correlation with SARS-CoV-2 SARI. These findings suggest that ILI and SARI data surveillance may serve as baseline for ARI-attributable mortality among the Malagasy population.

Severe Respiratory Illness and clinical outcome of patients with sickle cell disease hospitalized in two Western Kenya Referral hospitals.

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Biography:
Peter Kinuthia is a Program Coordinator working with Henry Jackson Foundation Medical Research International where he coordinates Influenza surveillance activities in the MOH /CDC funded Programs on Influenza and Non-Influenza Respiratory Pathogens. He hold a Master of Organizational Development and Management from United States International University -Africa and a Bachelor of Health Systems Management from Kenya Methodist University, Nairobi. He has more than 15 years experience in Influenza surveillance. Authored 5 publications.

Background
Patients with sickle cell disease are at a greater risk of acute respiratory infection. There is limited data on the clinical outcomes of patients admitted with sickle cell illness requiring hospitalization due to respiratory illness. This study compared clinical outcomes among sickle cell disease (SCD) and non-SCD patients admitted with respiratory illness at two referral hospitals in western Kenya.

Methods
We utilized hospital-based surveillance data from the Siaya and Kakamega County Referral and Teaching Hospitals (CRTH). The targeted population were patients of all ages admitted with respiratory illness (defined as: cough or difficulty in breathing in these hospitals between January 2019 and December 2022. Sickle cell disease status of the patients were determined through medical record reviews. Inpatient follow-up was conducted to determine the outcome of the admission.

Results
A total of 1925 patients were hospitalized, majority of the patients 1564 (81.3%) were from Siaya CRTH. Majority 1425 (74%) of the patients were aged < 5 years and 66 (3.4%) had SCD. The proportion of patients with SCD was higher in Kakamega compared to Siaya CRTH (6.4% [23/361] vs. 2.7% [43/1564], p<0.01). Most of the hospitalizations of SCD patients 53 (80.3%) were identified in 2019 and 2020. Hospitalized SCD patients were fairly older compared to non-SCD patients (median [IQR] age 4.3 [2.8-5.5] vs. 2.0 [0.8-5.1], p<0.001). There were more SCD patients requiring mechanical ventilation (3% vs. 0.3%; p = 0.03) and intensive care (54.6% vs. 34.6%; p< 0.01) than non-SCD patients. There was no difference in the duration of hospitalization and mortality between the SCD and non-SCD patients.

Conclusions
SCD patients have more severe respiratory illness than non-SCD patients.

Keywords: Sickle Cell Disease, Clinical outcomes, Severe Respiratory Illness

Sentinel site surveillance for influenza and other respiratory viruses in Uganda: August 2022 – February 2023

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Biography:

Mr. John Kayiwa is a biomedical scientist with over 15 years of experience in research. John is affiliated with UVRI and workes on various projects including Influenza surveillance, arbovirus surveillance, and viral hemorrhagic fever outbreaks of Ebola Bundibugyo and Marburg in 2007. John also works with Colorado State University scientists on a program investigating the ecology, epidemiology, and surveillance for emerging viral pathogens of Uganda bats. John also works with University of California, Davis for the Epicenter for Emerging Infectious Diseases Intelligence program investigating the epidemiology of coronaviruses, arboviruses and filoviruses which include emerging viruses currently threatening global security.

There is limited surveillance and laboratory capacity for non-influenza respiratory viruses in Uganda. We leveraged the influenza sentinel surveillance program of Uganda to detect other respiratory viruses among patients presenting with acute respiratory infection. Sixteen hospital-based sentinel sites representing different geographic areas of Uganda enrolled patients with influenza-like illness (ILI) and severe acute respiratory infection (SARI) between August 2022 – February 2023. All the collected nasal and throat specimens in viral transport medium were tested for 21 respiratory pathogens using the FTD21 kit by reverse transcription polymerase chain reaction (RT-PCR). We tested 687 including 471 ILI and 216 SARI cases during the study period.. Among ARI cases RV (14.7%) were the most frequently detected viruses followed by RSV (8.2%), HADV (6.7%), EV (4.2%), FluA (3.6%), HCOV 229E (3.3%), FluB (2.5%), HBOV (1.9%), HPIV4 (1.5%), HCOV NL63 (1.3%), HCOV 043 (1.2%), HMPV (1.0%), HPIV3 (0.9%), HCOV HKU (0.6%), HPIV2 (0.6%) and HPIV1 (0.2%). Our study demonstrated the feasibility of expanding influenza surveillance systems for surveillance of other respiratory viruses in Uganda.

Viral and bacterial etiologies of acute respiratory infections in suspected cases in the Central African Republic

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Biography:
I started my scientific career at the Institut Pasteur de Bangui (IPB) as a trainee as part of my master's degree in biology. I then enrolled for a thesis at the doctoral school of tropical infectiology in Franceville, Gabon, where I worked on "Viral and bacterial etiologies of acute respiratory infections in suspected cases in the Central African Republic from 2015 to 2018: Frequency of detection, risk factors and molecular characterisation of the viruses identified".

I am currently responsible for surveillance of influenza and other respiratory pathogens at the IPB.

Background: Acute respiratory infections are one of the main causes of admission and mortality in children under five in developing countries. Limited data from Africa suggest the circulation of respiratory viruses. In the Central African Republic, the aetiologies of respiratory infections in children under five are poorly known and poorly documented.
Objectives: to determine the aetiologies of acute respiratory infections, characterise the main respiratory viruses and assess their clinical impact.

Methods: collect samples meeting the WHO definition of suspected influenza cases. The samples were then analysed using RT-PCR and statistical tests. Finally, to carry out phylogeny on the sequences of the genes of interest.

Results: From January 2015 to December 2018, 3903 nasopharyngeal samples were recorded, including 820 collected at the paediatric complex. At least one virus was detected in 999/3903 (25.6%) samples, distributed as follows: Human respiratory syncytial virus (hRSV), 312/3903 (8%); Rhinovirus, 296/3903 (7.6%); Influenza A, 219/3903 (5.6%); Influenza B, 116/3903 (3%). During the study period, hVRS 131/820 (16%) circulated predominantly in children hospitalised in intensive care, followed by Rhinovirus 68/820 (8.3%) and Influenzavirus 61/820 (7.4%). The circulation of hVRS and Influenzaviruses (A/H1N1pdm09 80/221 (36.2%); A/H3N2 139/221 (63%); B/Victoria 66/116 (56.9%) and B/Yamagata 22/116 (19%)) is increased during the rainy season, while that of Rhinovirus is inversely seasonal. An association between the individual presence of 4 bacteria and severe clinical signs was observed. Phylogenetic analyses showed that several distinct genetic groups of viruses are involved in these infections.

Conclusion: The aetiologies of respiratory infection in CAR are viral (25.6%) and 47.4% are bacterial. Several viral variants and a genetic diversity of viruses have been found in CAR.
Key words: acute respiratory infections, aetiologies, genetic diversity, viruses, bacteria, children under 5, CAR.

Risk factors for severe COVID-19 among children and adolescents enrolled in acute respiratory infection sentinel surveillance in South Africa, 2020-2022

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Biography:

Kate Jensen, with a critical care nursing background and based in Cape Town, is currently employed as a project manager for all GERMS-SA surveillance projects under the Division of Public Health, Surveillance and Response for the National Institute of Communicable Diseases. She is also in the final year of completing her Masters in Public Health specialising in epidemiology and biostats through the University of Cape Town.

Background:
Identifying children at risk for severe disease from Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) may guide future morbidity mitigation interventions. We evaluated risk factors for hospitalisation for respiratory coronavirus disease 2019 (COVID-19) among patients aged ≤18 years.

Methods:
From April 2020 through March 2022, all patients were systematically enrolled at four out-patient influenza-like illness (ILI) and 10 in-patient severe respiratory infection (SRI) surveillance sites and tested for SARS-CoV-2 infection using polymerase chain reaction. We assessed factors associated with SARS-CoV-2 SRI hospitalisation. Proportions along with univariate and multivariable random effects logistic regression to determine odds ratios were used to compare characteristics of in-patient versus out-patient disease. Variables for models were chosen a priori according to a directed acyclic graph.

Results:
Of 6055 participants aged ≤18 years, 5791 (96%) were tested for SARS-CoV-2. 92/1145 (8%) of the patients with ILI and 225/4646 (5%) of the patients with SRI tested SARS-CoV-2 positive. Factors associated with SARS-CoV-2 SRI hospitalisation were age <6 months [adjusted odds ratio (aOR) 8.0, 95% confidence interval (CI) 2.7-24.0] compared to 1-4 years; underlying condition other than HIV [aOR 5.8, 95% CI 2.3-14.5]; laboratory confirmed Delta [aOR 2.8, 95% CI 1.1-7.3] or Omicron variant [aOR 4.9, 95% CI 1.7-14.1] compared to ancestral SARS-CoV-2; or respiratory syncytial virus (RSV) co-infection [aOR 6.2, 95% CI 1.0-38.2]. The proportion of HIV-exposed uninfected children with ILI [0/92, 0%] was low compared to those with SRI [18/159, 11%] suggesting an association requiring further investigation.

Conclusion:
Our findings confirm previous research that identified age <6 months or having an underlying condition as risk factors for SARS-CoV-2 SRI. RSV is likely the primary infection resulting in hospitalisation for those co-infected, and further studies are needed to explore this relationship. Sentinel surveillance programmes are useful to monitor the epidemiology of COVID-19 in children and adolescents.

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Characterizing seasonal influenza patterns in the Democratic Republic of the Congo

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Biography:
My name is Muhemedi Saleh. I am a scientific staff at Kinshasa School of Public Health in DR Cogo. My research area is acute respiratories infection and I have already published five articles on Influenza. In addition, I have more than 10 years of experience on Influenza surveillance in DRCongo.

Background: Since 2007, the Democratic Republic of Congo (DR Congo) has implemented a seasonal influenza sentinel surveillance system across 11 sites with sample testing at a national influenza reference laboratory in Kinshasa. Due to logistical difficulties, the number of sites was gradually reduced to four in 2019. Here, we describe the characteristics of each influenza season, including the beginning, end, intensity, and the different alert thresholds met.

Methods: In this cross-sectional study, we used the PISA indicators to assess influenza seasonality in DRC. We accessed the WHO web tool (https://worldhealthorg.shinyapps.io/averagecurves/), to generate weekly percentages of positive ILI and SARI cases to produce average curves from 2010 to 2022 and compare them to the epidemic curve of the 2021-2022 influenza season. We determined thresholds of average and epidemic curves, including epidemic, moderate, high, and extraordinary thresholds.

Results: A total of 21 influenza waves were identified between 2010 and 2022. From the ILI data, the average curve showed two waves per year: the first ran from the 40th to 15th week with a peak in the 52nd week, and the second wave extended from the 10th to the 40th with a peak in the 19th week. For SARI data, two waves were also observed in the same period of ILI data, with peaks in the 52nd and during the 19th week. Overall, the average intensity of the waves was moderate.

Conclusion: The use of PISA indicators to assess the severity of seasonal epidemics and predict the influenza season has been a valuable tool to better prepare for the upcoming influenza pandemic in DR Congo.

Keywords: Influenza, Season, DRC

Epidemiology and genetic characterization of respiratory syncytial virus in children with acute respiratory infections: findings from the influenza sentinel surveillance network in Central African Republic, 2015 to 2018

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[1]Institut Pasteur De Bangui

Biography:
I started my scientific career at the Institut Pasteur de Bangui (IPB) as a trainee as part of my master's degree in biology. I then enrolled for a thesis at the doctoral school of tropical infectiology in Franceville, Gabon, where I worked on "Viral and bacterial etiologies of acute respiratory infections in suspected cases in the Central African Republic from 2015 to 2018: Frequency of detection, risk factors and molecular characterisation of the viruses identified".

I am currently responsible for surveillance of influenza and other respiratory pathogens at the IPB.

Background and aims: Respiratory syncytial virus (RSV) is one of the main viral pathogens causing acute respiratory infections in children under 5 years of age, but has seldom been studied in Central African Republic (CAF). Taking advantage of the national influenza surveillance network in CAF, this study aimed at providing the first insights into RSV prevalence and seasonality over 4 years of surveillance and the clinical manifestations of RSV in CAF.

Methods: A total of 3903 children under 5 years matching the influenza-like illness (ILI, 68.5%) or severe acute respiratory infection (SARI, 31.5%) case definitions were recruited from January 2015 to December 2018. The presence of RSV viral RNA in nasopharyngeal samples was assessed by RT-PCR, followed by RSV-A and –B typing and Sanger sequencing on a subset of samples. Phylogenetic analyses were carried on partial G protein sequences. Associations between RSV and demographic or clinical manifestations were investigated by statistical analyses.

Results: RSV prevalence was significantly higher in infants < 6 months (13.4%), in hospitalized children (13.3% vs 5.5%) and in male patients (9.5% vs 6.4%). An overall prevalence of RSV of 8.0% in the period of 2015-2018 was shown, with significant annual (6.4%-10.6%) and seasonal (12.7% in rainy season vs 3.0% in dry season) fluctuations. While RSV seasons in 2015, 2016 and 2018 were relatively similar, 2017 showed deviations from the overall patterns with significantly higher RSV circulation and an outbreak peak 3-5 months earlier. Concomitant circulation of RSV-A and RSV-B with an alternating predominance of RSV-A and RSV-B strains and temporal RSV-A genotype replacement from NA1 to ON1 were observed.

Conclusion: This study represents the first in-depth epidemiological analysis of RSV in CAF and provides first insights into RSV genetic diversity and seasonality in the country.

Keywords: Central African Republic, children, epidemiology, genotype, respiratory syncytial virus, seasonality

Factors associated with Severe Respiratory Illness (SRI) and mortality in hospitalised individuals aged 5 - 19 years in South Africa, 2009 - 2019

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Biography:

Rixongile is a dedicated scientist currently enrolled at the South African Field Epidemiology Training Programme at the National Institute for Communicable Diseases. She is currently completing her training in field epidemiology at the Centre for Respiratory Diseases and Meningitis. Rixongile is also pursuing her master's degree in Epidemiology and Biostatistics from the University of Pretoria, further honing her analytical skills. Her passion for epidemiology and her commitment to improving public health in South Africa make her a valuable asset to the SAFETP and a promising future leader in the field of infectious disease control.

Severe Respiratory Illness (SRI) is a major cause of hospital admissions and deaths worldwide. SRI in older children and adolescents is not well described in South Africa. We describe demographic characteristics, clinical presentation and factors associated with mortality among individuals aged 5-19 years hospitalised with SRI in South Africa, 2009-2019.

We conducted a cross-sectional secondary data analysis of individuals 5-19 years admitted with SRI and enrolled in pneumonia surveillance programme at ten sentinel hospitals in five provinces, from February 2009 through December 2019. Demographic and clinical data were collected. Nasopharyngeal swabs were collected and tested for influenza and respiratory syncytial virus (RSV) from 2009-2019, other respiratory viruses including rhinovirus, adenovirus and enterovirus were tested from 2009 to 2016 by real-time reverse transcription polymerase chain reaction. Patients were followed up for in-hospital outcomes. Factors associated with mortality were assessed using multivariable logistic regression.

From 2009 through 2019, 1511 individuals aged 5-19 years were enrolled and 52% (783/1505) were male. The median age was 8 years (interquartile range: 6-14 years). HIV status was available for 1248, of which 44% (547/1248) were living with HIV (LWH) and 55% (246/444) were on antiretroviral therapy. From 2009-2016, predominant pathogens identified were rhinovirus (28%, 330/1192), and adenovirus (10%, 111/1118). Influenza and RSV contributed 9% (111/1246) and 4% (44/1230) respectively. From 2009-2019, influenza was detected in 9% (128/1491) and RSV in 3% (51/1475). The most common underlying condition was asthma (5%, 80/1503). Twenty-eight percent (419/1495) required oxygen therapy, <1% (4/1493) required mechanical ventilation and <1% (4/1493) were admitted to intensive care unit. The in-hospital case fatality ratio was 2.4% (36/1496). On

multivariable analysis, adjusting for age and mechanical ventilation, LWH was significantly associated with mortality (adjusted odds ratio, 5.5; 95% confidence interval, 2.0 – 15.0).

Older children and adolescents LWH were at increased risk of SRI-related mortality.

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Red cells and platelets levels are not affected by SARS-CoV-2 infection severity: an observational study of a Mozambican population

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Biography:

Degree in Biological Sciences guidance on Health, Eduardo Mondlane University, Mozambique

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May 2011- Feb 2013: Professional volunteer internship at the Microbiology Laboratory, Maputo Central Hospital- Mozambique.Since 2013 supervisor of safety laboratory of the Polana Caniço Health research and Training Center (CISPOC). 2013-2017: involved on the study of Etiology of Acute syndrome fever in among febrile adult patients admitted at Polana Caniço Hospital, Maputo- Mozambique

Involved in HIV and Tuberculosis research over past 8 years. Since 2020 have been working with medicinal plants, for therapeutic purposes (immunological studies)

Key words: COVID-19, severity, Hematology, Biochemistry

Background: Alterations on haematological and biochemical parameters, have been reported and study as COVID-19 biomarkers of disease severity. However, little is known about these changes on African context. In this study we evaluated the clinical, haematological, and biochemical parameters of SARS-CoV-2 RT-PCR positive Mozambican individuals with different clinical presentations.

Methods: In a cross sectional study carried out from February 2021 to January 2022, individuals aged above 18 years were recruited on COVID-19 surveillance units and isolation centers in Maputo. A pre-structured questionnaire were administered to collect clinical information while, blood and nasopharyngeal samples were collected to perform SARS-CoV-2 RT-PCR and cell blood count and biochemistry. Descriptive statistics were used to present data and Kruskal Wallis to access difference between groups medians. Data was analyzed in SPSS version 20 and Prisma version 9 with an α of 0.05.

Results: 85 individuals stratified in negative (n=22), asymptomatic (n=21), mild (n=16), moderate (n=5) and severe (n=21). Hypertension and diabetes were common comorbidities in moderate and severe compared with other groups (p=0.033). The levels of the hematological parameters WBC (p=0.002) and neutrophils (p=0.000) increased along with an increase in case severity while lymphocyte were decreasing (p=0.000). No differences were found between groups levels of red blood cells, platelets. Serum levels of metabolic parameters such as glucose (p=0.000) and urea (p=0.006) were more than 1.2 times increased on severe cases when compared to other groups. Liver function proteins such as C-reactive protein (p=0.000) were 82 times higher on severe cases when compared to other groups.

Conclusions: Our study found significant changes on several haematological and biochemical parameters and associate those with COVID-19 severity. Is to note the unchanged on red and platets series parameters suggesting that may be peculiarities in the manifestation of COVID-19 in the Mozambican context.

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RESPIRATORY PATHOGENS IN PATIENTS DIAGNOSED WITH SEVERE ACUTE RESPIRATORY ILLNESS — ZAMBIA 2022

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[1]National Influenza Centre-Ministry of Health, [2]U.S Centres for Disease Control and Prevention

Biography:

Miniva Mwanza is a Laboratory scientist with over 5 years experience in Molecular Biology currently based at the Zambia National influenza Centre serving as the Laboratory technical in charge. She holds a bachelor of Science degree in Microbiology and is currently pursuing a Masters in One Health Laboratory Diagnostics Science. Her key research areas include but not limited to bioinformatic and predictive virology of emerging and reemerging pathogens of public Health interest.

INTRODUCTION

Globally, respiratory infections are a leading cause of mortality. In Zambia, influenza and SARS-CoV-2 (SCV2) seasonality has not previously been described, however year-round cases of respiratory illness are observed with epidemics common during the warm-wet (January-May) and hot-dry (August-November) seasons. We conducted multi-pathogen testing throughout the year to describe circulating pathogens in Zambia.

METHODS

Samples from patients meeting the current WHO severe acute respiratory infection (SARI) case definition were tested for influenza and SCV2 using CDC's influenza/ SCV2 multiplex polymerase chain reaction (PCR) assay at the Zambia National Influenza Centre laboratory. Test-negative samples were then tested by Fast-track diagnostics multiplex real-time PCR (FTD-33).

RESULTS

From January-December, 2022, 2284 samples were tested, and 133 (6%) and 322 (15%) were positive for influenza and SCV2, respectively. FTD-33 testing was conducted on 1440 of the test-negative samples. Of these, 840 (58%) were positive; 442 (53%) had 1 pathogen detect and 398 (47%) had ≥2 pathogens detected. For those with ≥2 pathogens, 78 (20%), 114 (29%), and 206 (52%) were positive for viral pathogens only, bacterial pathogens only, and both, respectively.The most frequent pathogens detected in the samples were Streptococcus pneumoniae [347 (16%)], Klebsiella pneumoniae [237 (11%)], Moraxella cataharrlis [228 (10%)], Hemophilus influenzae [220 (10%)], Rhinovirus [211 (10%)], RSV [211 (10%)], Adenovirus [179 (8%)] and Staphylococcus aureus [164 (7%)]; S. pneumoniae, H. influenzae and RSV may be vaccine preventable.

CONCLUSION

Most SARI patients were influenza and SCV2 test-negative. Multi-pathogen testing of test-negative samples identified a large number of pathogens, providing important information about common causes of respiratory infections in Zambia. Result interpretation is complicated by the frequent detection of ≥2 pathogens. A few of the common pathogens detected are vaccine-preventable, suggesting opportunities for public health action. Further testing may elucidate epidemiological characteristics, disease-specific associations, and preventive and treatment measures for SARI in Zambia.

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INFLUENZA SENTINEL SURVEILLANCE AS A TOOL FOR DETECTING VIRAL RESPIRATORY OUTBREAKS

Ms Namitondo Agness Mushabati[1], Mr Edward Chentulo[1], Ms Miniva Mwanza[1], Mr Reuben Mwanza[1], Ms Chilala Jere[1], Mr Paul Simusika[1], Dr. Daniel Owusu[2], Dr Jonas Z. Hines[2], Dr. Aaron M. Samuels[2], Dr. Mwaka Monze[1]

[1]National Influenza center- Ministry of Health, [2]U.S. Centers for Disease Control and Prevention

Biography:

Namitondo Agness Mushabati received a bachelor's degree in Biomedical Sciences from the University of Zambia (UNZA) in 2020. She is currently pursuing a Masters of Science degree in Infectious diseases and zoonosis with UNZA. Her research interest include; health related research, particularly molecular epidemiology and bioinformatics. She is currently working as a laboratory scientist under the influenza sentinel surveillance program in Zambia.

INTRODUCTION

During April 2021 and April 2023, three discrete occurrences of significant increases in patients meeting the influenza like illness (ILI) and severe acute respiratory illness (SARI) case definitions were reported to the Zambia National Public Health Institute (ZNPHI), resulting in follow-up investigations. The existing routine influenza surveillance system was leveraged to establish the cause of these events demonstrating its utility in respiratory disease outbreak investigations.

METHODS

In response to these reports from Lusaka, Zimba, and Chipata, additional individuals meeting the ILI or SARI case definition were enrolled for naso- and oro-pharyngeal sample collection and collection of data on patient demographics, clinical history, disease course and vaccination history. Specimens from these individuals were sent to the National Influenza Center (NIC) for an expanded testing array, the fast-track diagnostics-33 (FTD-33), to test for 33 pathogens. This test was used as a first-line instead of the influenza/ SARS COV2 multiplex routinely used in the surveillance program to expedite screening for multiple pathogens.

RESULTS

During April 2021 and April 2023, three distinct outbreaks were investigated and 133 samples were analysed from Lusaka (88), Chipata (11) and Zimba (34). Of the total samples tested, 72 (54%) were positive for influenza [32 (24%) A/H1N1, 40 (30%) A/H3N2], 11 (8%) were positive for RSV and 2 (1.5 %) for SARS-CoV-2.

CONCLUSION

The NIC confirmed the outbreaks to be predominantly driven by influenza A viruses and shared the data with the ZNPHI and other stakeholders. This data will be useful as the country weighs the need for influenza vaccination. The RSV outbreak spurred on plans to collect RSV burden of disease estimates to guide possible RSV vaccine introduction. Overall, these experiences demonstrated the value of leveraging the ILI/SARI surveillance system for enhanced testing to confirm outbreaks and causal pathogens.

Creating a clinical decision-making algorithm to build capacity for COVID-19 case management within the community

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Biography:

Mozambican junior researcher since late 2017 with a bachelor's degree in Veterinary Medicine from one of the most prestigious Universities in the country. My current work field involves event, laboratory and community-based surveillance of zoonotic pathogens (vector, air and food-borne). Currently part of research studies that address epidemiology and characteristics of SARS-CoV-2 in children, the evaluation of a digital platform for early detection of COVID-19 cases within the community and also the transmission of, the impact of co-morbidities on, and immunity against SARS-CoV-2. I was also part of the first team of laboratory response to the COVID-19 pandemic in Mozambique

Background: Recording and reporting diseases within the community is a high burden. Early detection has been considered crucial in a country such as Mozambique due to its low capacity for risk management of emerging diseases. Using mobile devices to capture disease events in the community is a tool developed to enhance timely reporting and prompt response, particularly of those cases that do not report to the health facilities, preventing the health surveillance system from including this information in their databases for future decision-making purposes. Nevertheless, with the help of a mathematically developed algorithm, these same captured events can establish an efficient report flow and promote early detection, by predicting likely disease conditions based on the signs and symptoms reported, thus reducing the spread of diseases and enhancing the local capacity for case management.

Objective: Reduce the gap in the health systems database regarding emerging disease cases in remote areas using digital disease surveillance systems as predictive information and communication technologies.

Methodology: Signs and symptoms collected from the community-based surveillance conducted for the evaluation of COVID-19 case capture using a digital platform between May and October 2021 were analyzed and compared to the clinical manifestation of COVID-19-positive patients from the existing laboratory-based surveillance to determine the accuracy of the digital tool developed. This tool will create an algorithm using a logistic regression model to obtain the probability of occurrence and the influence of each independent variable on the event studied.

Results: The community-based surveillance (1801 cases), through the Afyadata tool, captured 425 more cases than the laboratory-based surveillance (1376 cases) currently established and, based on the set of signs and symptoms reported by the former, the tool was able to accurately identify 95.71% (CI:95.05%; 96.31%) COVID-19 cases. The algorithm will rapidly and efficiently identify probable respiratory infections based on captured symptoms.

Leveraging influenza surveillance to detect other respiratory viruses of public health relevance: analysis of surveillance data, Ghana: October, 2022 - February, 2023

Miss Cecilia Takyi[1], Mr. Yaw Awuku-Larbi[1], Mrs. Gifty Mawuli Sarpong[1], Dr. Ivy Asantewaa Asante[1], Dr. Mildred Adusei-Poku[1,2], Dr. Nana Afia Asante Ntim[1], Mr Jonathan Klutse[1,2], Mr Joseph Ahia Quarcoo[1], Mr Stephen Ofori Nyarko[1], Ms Linda Boatemaa[1], Miss Vanessa Magnusen[1], Miss Jennifer Wutsika[1], Miss Esinam Amenuvor[1], Mr Samuel Ago[1], Ms Juliet Wordui[1], Miss Loretta Kwasah[1], Miss Roberta Tackie[1], Miss Ama Nyansema Sekyi-Yorke[1], Mr Joseph Anum Nyarko[1], Dr Franklin Asiedu Bekoe[3], Mr. Obed Bangdome Ofori[4], Dr. Naiki Attram[5], Dr. Shirley Nimo-Paintsil[5], Dr. Sanders Terrel[5], Prof. William Kwabena Ampofo[1], Dr Ndahwouh Talla Nzussouo[6], Dr. Daniel Owusu[6], Dr. Charles Myrna[6], Dr. Dennis Odai Laryea[4]

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Biography:

Cecilia Takyi is a young researcher with an interest in researching into vaccine manufacturing for viral respiratory pathogens. Cecilia has a background in Biological Science where she developed skills in problem-solving and scientific writing. Working in the virology lab, she has built expertise in molecular identification and characterization of viral respiratory pathogens. She also loves reading, listening to music, and taking care of animals.

Background: Lessons learnt from the COVID-19 pandemic highlight the need to extend influenza surveillance to detect other respiratory viruses to better prepare for pandemics. We describe the epidemiology of selected respiratory viruses in Ghana, leveraging a sentinel surveillance platform established for influenza.

Method: We collected and analysed epidemiologic and laboratory data from outpatients and in-patients of all ages attending any of 36 sentinel sites and met the WHO case definition for influenza-like illness (ILI) and severe acute respiratory illness (SARI). We analysed specimen using singleplex RT-PCR for detecting respiratory viruses: influenza, SARS-CoV-2, Adenovirus (AdV), seasonal coronavirus (HKU1, OC43, 229E, NL63), human metapneumovirus (hMPV), parainfluenza virus (PIV-1, 2, 3), and respiratory syncytial virus (RSV).

Results: From October 2022 through February, 2023, at least one respiratory virus was detected in 1024 (43.6%) of 2053 specimens. Influenza viruses were commonly detected (360, 15.3%), followed by SARS-CoV-2 (179, 7.6%,), AdV (174, 7.4%,), OC43 (110, 4.7%,), and RSV (82, 3.5%,). Of the 2053 specimen collected, 504 (24.5%) were from children aged <15 years, 1070 (52.1%) were from individuals aged ≥15 years and 479 had age unknown. Among children aged <15 years, influenza (110, 21.8%,), AdV (51, 10.1%,) and RSV (34, 6.4%,) were most prevalent. For individuals aged >15 years, influenza (182, 17%,), SARS-CoV-2 (100, 9.3%,), AdV (63, 5.9%, and OC43 (41, 3.8%,) were commonly detected. Detection rate for any pathogen was higher in ILI than in SARI patients (47.4% vs 35.1%, p-value<0.001). Co-infections were found in 3% (31/1024) positive specimens with RSV and AdV being most prevalent co-infection (29%, 9/31).

Conclusion: The expansion of influenza sentinel surveillance to include other respiratory viruses provides an opportunity to gather information and monitor the activity of these viruses. This is essential to guide clinical management, preventative, and control measures, to better prepare for epidemics or potential pandemics.

Identification and Characterization of SARS-COV-2 among Healthcare Workers in selected Health Facilities in Ghana

Mrs Vanessa Magnusen[1,2], Dr Yaw Bediako[2], Dr Ivy Asante[1], Dr Peter Quashie[2], Ms Linda Boatemaa[1], Ms Aisha Massud Mohammed[2]
[1]Noguchi Memorial Institute Of Medical Research, [2]West African Centre for Cell Biology of Infectious Pathogens, University of Ghana

Biography:

I am a new researcher in the field of Virology. With an MPhil degree in hand, my expertise lies in unravelling the intricate mechanisms of viral infections. For the past four years, I have been an invaluable asset at the renowned Noguchi Memorial Institute for Medical Research's Virology Department, where my contributions as a dedicated research assistant have significantly aided our surveillance of animal and human influenza. My research so far has focused on deciphering the host-virus interactions. My extensive laboratory experience make me an ideal candidate to present my research findings at this prestigious scientific conference.

Background: Sever Acute Respiratory Syndrome coronavirus 2 (SARS-CoV-2), remains a respiratory virus of international concern, causing over 604 million deaths globally. As of 30th May 2023, Ghana confirmed over 168,000 cases and 1400 deaths. Healthcare workers (HCWs) are at the forefront of the fight against COVID-19 and are thus at an increased risk of being exposed to SARS-CoV-2. HCWs could therefore potentially play a vital role in hospital transmissions of the virus from patient to healthcare worker as well as among themselves.

Methods: This study aimed to identify and characterize SARS-CoV-2 among healthcare workers in two major hospitals in Ghana. Oropharyngeal swabs were collected from 204 healthcare workers between 0ctober to December 2020 from the Greater Accra Regional Hospital and Cape Coast Teaching Hospital. Samples underwent RNA extraction, RT-qPCR and sequencing.

Results: The overall SARS-CoV-2 positivity among healthworkers was 2.5% (5/204). The gender distribution analysis of samples collected showed significantly more females (60.78%) than males (39.22%). Participants were sampled from five departments: Covid ICU (10%), Paediatrics (31%), Neonatal intensive care unit (18%), Accident and emergency (25%) and General medicine (16%). Weekly positivity showed that 40% (2) of positive samples were obtained during week 2, 40% (2) during week 3 and 20% (1) during week 6. 1 out of 5 positive samples was IgG positive at baseline showing reinfection.

Conclusion: Results suggests continuous monitoring of SARS-CoV-2 among HCW's.

MOLECULAR AND EVOLUTIONARY CHARACTERIZATION OF RESPIRATORY SYNCYTIAL VIRUS IN MOZAMBIQUE, MAPUTO, 2015-2020

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Biography:

I have a degree in biology and a master's degree in Tropical medicine. I work at Instituto Nacional de Saúde in Mozambique. I have been working with respiratory viruses (RSV and SARS-CoV-2) and sequencing for HIV and SARS-CoV-2.

Introduction: Respiratory-syncytial-virus (RSV) is the main cause of lower respiratory tract infections and hospitalization in children aged <5 years. This study intended to determine the genotypes and the phylogeographic characteristics of RSV circulating in Maputo, between 2015 and 2020.

Methodology: Between 2015 and 2020, 1877 children under-two-years old with mild influenza-like illness (ILI) and severe acute respiratory infection (SARI) were enrolled in acute respiratory infection surveillance. Nasopharyngeal swabs were collected and tested for RSV using real-time RT-PCR and were sequenced through Illumina platforms. Children who met the WHO case definition with the shortest duration of symptoms were included for testing, and for genotyping, samples with Ct below 30 were included. Bioinformatics analyses were performed. Global and regional RSV sequences obtained from GISAID, NCBI. PhyML, BEAST 1.10 and FigTree 1.4.4, were used for bioinformatics analyses and visualization.

Results: RSV was detected in 21.5% (403/1877), of which 23.7% (391/1650) were SARI. RSV-A and RSV-B co-circulated throughout the study period with alternating predominance each year. Phylogenetic analyses done for 33% (133/403) of specimens revealed the circulation of genotype GA2, lineages GA2.3.3, GA2.3.5, and GA2.3.6b for RSV-A and genotype GB5, lineages GB5.0.2, GB5.0.3, GB5.0.4a and GB5.0.5a for RSV-B. In 2017 and 2018 the RSV-A sequences were similar to sequences from Kenya, Australia, and Argentina and the RSV-B sequences to those from Australia, Côte d'Ivoire, and England. The association of Mozambican RSV sequences with lineages circulating in multiple localities is suggestive of the complex transmission dynamics of this virus. The circulation pattern of RSV-A and RSV-B in Mozambique can potentially be characterized as co-circulation of multiple lineages resulting from independent introductions.

Conclusions: Were detected high positivity of RSV in SARI children (23.6%), there was co-circulation of RSV-A and RSV-B and their respective lineages, and the Mozambican RSV sequences were similar to many from other countries.

COMPARATIVE EVALUATION OF THE CDC MULTIPLEX KIT AND THE FTD 33 MULTIPLEX KIT FOR THE DETECTION OF INFLUENZA A AND B VIRUSES

Ms Banda Taonga[1], Ms Miniva Mwanza[1], Ms Agness Mushabati[1], Ms Chilala Jere[1], Mr Reuben Mwanza[1], Ms Leah Mukwasa[1], Mr Edward Chentulo[1], Mr Paul Simusika[1], Mr Daniel Owusu[2], Mr Sam Yingst[2], Dr Jonas Z. Hines[2], Dr. Aaron M Samuels[2], Dr Mwaka Monze[1]

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Biography:

Taonga Banda is currently Laboratory Scientist at the National Influenza Centre in Zambia, based at the Tropical Disease Research Centre. In 2021 She obtained her Bachelors degree in Biology with a major in Microbiology from The Copperbelt University. She has over the years been involved in various works and research such as Whole genome sequencing, surveillance testing for influenza and sar-cov-2 and malaria research. she has showcased her interest and strength in molecular biology which has been remarkable especially during the first trials of Covid-19 whole Genome Sequencing at Tropical Disease Research Centre. Taonga young lady eager to learn more.

INTRODUCTION

Since 2010, Zambia's National Influenza Centre (NIC) has been performing influenza surveillance in patients with severe acute respiratory illness. Confirmation of viral infection was performed using real time reverse transcriptase polymerase chain reaction (RT-PCR). We used the CDC Influenza/SARS-CoV-2 Multiplex Assay and Fast Track Diagnostics (FTD) -33 Respiratory pathogen to screen SARI samples for influenza A and B.

METHODS

Between January 2021 and December 2022, nasopharyngeal and oropharyngeal swabs from SARI cases were examined using the FTD-33 Kit and the CDC Influenza/SARS CoV 2 multiplex tests. The CDC Influenza/SARS CoV 2 rT-PCR panel was used as the reference test to assess the sensitivity of the FTD-33 Kit for detecting influenza A and B by comparing the positivity rate and cycle thresholds values (CT). Influenza A and B were the only viruses shared by both kits, hence only tested.

RESULTS

Between January 2021 and December 2022, 787 samples were tested from children who met the SARI case definition using the CDC influenza/SARS CoV2 and the FTD 33 assays. 46 (5.8%) were positive for influenza; influenza A 13 (1.7%), and influenza B 33 (4.2%) on the CDC multiplex whilst 39 (4.96%) were positive for influenza; influenza A 14 (1.78%) and influenza B 25 (3.18%) on FTD 33 assay. The kappa statistic measured an almost perfect agreement of 0.9 and the sensitivity of the FTD 33 was 84.7%. There were 8 (1%) discordant results between the two kits, with concordant results having relatively low cycle threshold values (18-34), whereas discordant results had high CT values (35-40) on the reference test.

CONCLUSION

The influenza A and B results were comparable between the two assays, with sensitivity of more than 80% indicating that the FTD 33 can reliably detect influenza.

KEY WORDS

Influenza/SARS CoV 2 assay, FTD 33 assay, Discordant, Influenza, CT values

The burden of influenza among Kenyan pregnant and postpartum women and their infants, 2015–2020

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Biography:

Nancy has 17 years of experience of leading epidemiologic research and public health in the field of infectious disease research and prevention, especially related to respiratory diseases and maternal-child health. She combines a basic science background (Biology and Chemistry), with advanced training in Applied Epidemiology and Biostatistics, Project Management and doctorate training in Project Monitoring and Evaluation. For 10 years, she managed and continues to support the national sentinel surveillance system for influenza and other respiratory pathogens. She has designed, managed, and continue to provide technical oversight to maternal and child health research and surveillance programs in western Kenya.

Background

In tropical Africa, data about influenza-associated illness burden are needed to assess potential benefits of influenza vaccination among pregnant women. We estimated the incidence of influenza among pregnant women and their infants in Siaya County, Kenya.

Methods

We enrolled women at <31 weeks of gestation and conducted weekly follow up until 6 months postpartum to identify acute respiratory illnesses (ARIs). We defined ARI among mothers as reported cough, rhinorrhoea or sore throat and among infants as maternal-reported cough, difficulty breathing, rhinorrhoea or clinician diagnosis of respiratory illness. We collected nasal/nasopharyngeal and oropharyngeal swabs from mothers/infants with ARI and tested for influenza A and B using molecular assays. We calculated antenatal incidence of laboratory-confirmed influenza among mothers and postnatal incidence among mothers and infants.

Results

During June 2015 to May 2020, we analysed data from 3,026 pregnant women at a median gestational age of 16 weeks (interquartile range [IQR], 13, 18) and followed 2,550 infants. Incidence of laboratory-confirmed influenza during pregnancy (10.3 episodes per 1,000 person-months [95% confidence interval {CI} 8.6–11.8]) was two-fold higher than in the postpartum period (4.0 [95% CI 2.6–5.5]; p< 0.01). Incidence was significantly higher among human immunodeficiency virus (HIV)-infected pregnant women (15.6 [95% CI 11.0–20.6] vs. 9.1 [95% CI 7.5–10.8]; p< 0.01). Incidence among young infants was 4.4 (95% CI 3.0–5.9) and similar among HIV-exposed and HIV-unexposed infants.

Conclusion

Our findings suggest a substantial burden of influenza illnesses during pregnancy, with a higher burden among HIV-infected mothers. Kenyan authorities should consider the value of vaccinating pregnant women, especially if HIV-infected.

Combined virological surveillance of SARS-CoV-2 and Influenza in Ghana, 2021-2022

Miss Jennifer Wutsika[1], Mr. Yaw Awuku-Larbi[1], Mrs Gifty Mawuli Sarpong[1], Dr. Ivy Asantewaa Asante[1], Mr. Jonathan Klutse[1,2], Dr. Mildred Adusei-Poku[1,2], Dr. Nana Afia Asante Ntim[1], Mr. Joseph Ahia Quarcoo[1], Mr. Stephen Ofori Nyarko[1], Mr. Richard Asomadu Obeng[1], Miss Linda Boatemaa[1], Miss Vanessa Magnusen[1], Mr Samuel Ago[1], Miss Esinam Amenuvor[1], Miss Juliet Wordui[1], Miss Roberta Tackie[1], Miss Lorreta Kwasah[1], Miss Ama Nyansema Sekyi-Yorke[1], Miss Cecilia Takyi[1], Miss Ivanda Adwoa Twumwaah Gyapon[1], Mr. Joseph Anum Nyarko[1], Mr. Innocent Doku[1], Miss Isabella Asamoah[1], Dr. Franklin Asiedu Bekoe[3], Mr. Obed Bangdome Ofori[4], Dr. Naiki Attram[5], Dr. Shirley Nimo-Painstil[5], Dr. Sanders Terrel[5], Prof. William Kwabena Ampofo[1], Dr. Ndahwouh Talla Nzussouo[6], Dr. Daniel Owusu[6], Dr. Charles Myrna[6], Dr. Dennis Odai Laryea[4]

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Biography:

Jennifer Wutsika is a dedicated research assistant at Africa's prestigious Noguchi Memorial Institute for Medical Research. With a passion for biomedical research, she actively contributes to the surveillance of influenza and other respiratory viruses in Ghana. Jennifer's interest lies in studying influenza virus-host interactions, investigating host adaptation and pathogenesis. Her ultimate goal is to contribute greatly to infectious disease research and vaccine development. Apart from her scientific pursuits, Jennifer finds solace in the enchanting melodies of music and the captivating world of literature. She embodies the belief that anything worth doing is worth doing well.

Background: As a result of lessons learnt from the COVID-19 pandemic, the WHO Global Influenza Surveillance and Response System (GISRS) recommends the integration of SARS-CoV-2 into influenza sentinel surveillance systems worldwide. In line with this, the Ghana National Influenza Center (Ghana-NIC) initiated the combined detection of SARS-CoV-2 and influenza infections from November, 2020. Here, we report on co-circulation of influenza and SARS-CoV-2 viruses in Ghana during 2021-2022.

Methods: Patients with influenza-like illness (ILI) (temperature $\geq 38^0$C/reported fever and cough, onset ≤10 days) or severe acute respiratory illness (SARI) (admitted patients with temperature $\geq 38^0$C/reported fever and cough, onset ≤10 days) from 36 influenza sentinel sites between January 2021 through December 2022 provided respiratory samples. We tested the samples at the Ghana-NIC for detecting influenza/SARS-CoV-2 viruses using RT-PCR with multiplex primers/probes and assays provided by the United States Centres for Disease Control and Prevention (US-CDC) International Reagent Resource (IRR). We calculated proportions of influenza and SARS-CoV-2 infections among patients with respiratory illness.

Results: Over the reporting period, a total of 12,422 samples were collected and processed; 10,190 ILI and 2,232 SARI cases. Influenza and SARS-CoV-2 were detected in 6.3% (1,969/12,422) and 16.6% (2,069/12,422) of all samples processed, respectively. Most influenza-positive cases were recorded in males, while females accounted for most SARS-CoV-2-positive cases. Patients aged 5 to 14 and 15 to 24 years each had the highest influenza virus detection rates of 21.4%, while those aged 45 to 64 had the highest SAR-CoV-2 detection rate of 22.5%. Coinfections were detected in 32 (0.26%) patients within the two-year period.

Conclusion: The detection of dual influenza and SARS-CoV-2 infections indicates the value of simultaneous investigation of multiple pathogens. These findings show the effectiveness of integrating surveillance for respiratory illness for enhanced and targeted public health interventions, such as case detection, management, and immunization.

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Seasonal Influenza Vaccination in Kenya: What Determines Healthcare Workers’ Willingness to Accept and Recommend Vaccination?

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Biography:

Nancy has 17 years of experience of leading epidemiologic research and public health in the field of infectious disease research and prevention, especially related to respiratory diseases and maternal-child health. She combines a basic science background (Biology and Chemistry), with advanced training in Applied Epidemiology and Biostatistics, Project Management and doctorate training in Project Monitoring and Evaluation. For 10 years, she managed and continues to support the national sentinel surveillance system for influenza and other respiratory pathogens. She has designed, managed, and continue to provide technical oversight to maternal and child health research and surveillance programs in western Kenya.

Background

Data about healthcare workers’ (HCW) willingness to accept or recommend seasonal influenza vaccination in countries without influenza vaccination programs are limited.

Methods

We conducted a cross-sectional survey in 7 of the 47 counties in Kenya to examine knowledge, and perceptions of HCWs towards seasonal influenza disease and vaccination. We targeted to enroll all HCWs who deliver clinical services directly/peripherally to patients from 5 health facilities in each county. We used chi square tests and logistic regression models to identify variables associated with HCW’s willingness to accept or recommend seasonal influenza vaccination.

Results

From May-June 2018, we enrolled 2,035 HCWs, representing 49% of the targeted respondents, from 35 facilities. Most of the HCWs (82.1%) were from public health facilities. Among HCWs who had heard of seasonal influenza, 87.3% (1,420/1,627) believed that it could cause severe illness. Most HCWs (1,076/1,209, 89.0%) were willing to receive the seasonal influenza vaccine if it was recommended for them and provided for free, and 91.4% (1,441/1,576,) would vaccinate their patients or recommend vaccination if the vaccine was available. Only 17.6% (213/1212) had ever received the vaccine. HCWs who believed that influenza could cause severe illness (adjusted odds ratio [aOR] 2.2; 95% CI 1.3-3.5) and that people around them were better protected if they were vaccinated (aOR 3.1; 95% CI 2.0-4.6) were more willing to get vaccinated. Willingness to recommend vaccination to patients was higher among HCWs who had seen patients with influenza (aOR 1.7; 95% CI 1.2-2.5), believed it could cause severe illness (aOR 2.0; 95% CI 1.3-3.2) and that people around them are better protected if the HCW is vaccinated (aOR 3.6; 95% CI 2.3-5.7).

Conclusion

Our findings suggest favorable attitudes among HCWs towards seasonal influenza vaccination, many of whom are motivated by the desire to protect others around them.

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EVIDENCE OF WHOOPING COUGH DUE TO Bordetella pertussis AND COINFECTION OTHER RESPIRATORY PATHOGENS

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[1]National Public Health Laboratory

Biography:

Ms.Venusia Zang Obame, Master Science in Genome Cell Development and Evolution specialty genetic, molecular biology of microorganisms from University of Paris 11, France. I am currently working at the Gabonese National Public Health laboratory where I am the Influenza viruses sentinel surveillance coordinator. I performed the launch of Influenza viruses sentinel surveillance activities, the management of external quality assessment for HIV-early infant diagnosis and viral load from public health agency of canada.

EVIDENCE OF WHOOPING COUGH DUE TO Bordetella pertussis AND COINFECTION OTHER RESPIRATORY PATHOGENS

Background

Whooping cough is a serious and potentially fatal disease, particularly in newborns. Mortality is higher in developing countries, especially where vaccination coverage is low. There is no surveillance system in Gabon, which makes diagnosis difficult. Following the introduction of the prospective respiratory pathogens surveillance, established in three hospitals in Libreville, we described the cases of three burden childhood of 58 days who died from confirmed cases of whooping cough due to Bordetella pertussis.

Methods

We recruited three hospitalized newborns named B1, B2 and B3 according to the order of emergence from the womb. Samples were collected using nasopharyngeal swabs or nasopharyngeal aspirates, we extracted RNA/DNA by using QIAamp Viral RNA Mini Kit and the detection was done is two steps. Influenza A and B viruses, Sars-Cov-2 and RNase P Internal Control were first tested with Influenza FluSC2 Multiplex kit from CDC, Atlanta, USA. Samples tested negatives, were then analysed for other respiratory pathogens by real-time RT-PCR using Fast Track Diagnostic (FTD) Respiratory pathogens 33 kit. This multiplex Real-time RT-PCR can identify thirty-three respiratory pathogens in a single reaction mixture.

Results

From the triplet's baby, two died from sever acute respiratory infection (SARI). Bordetella pertussis was found in co-infection for B2 with klepsellia pneumoniae and B1 with Haemophilus influenza, Pneumocystis jirovecci, Human Rhinovirus and Streptococcus pneumoniae.

Conclusion

This reported case must help our public health system to explore new vaccination strategies in Gabon, against morbidity and mortality with Bordetella pertussis in newborn under 2 months of age, those who are too young to receive the first dose of DTP vaccine. There is a need to continue to immunize children and adults (as a reservoir) and in particular pregnant women.

Keywords

Whooping cough, Bordetella pertussis, Gabon

Early Warning Systems for Respiratory Disease Outbreaks: Lessons Learned from Nakuru County, Kenya, 2021

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Biography:

Healthcare epidemiologist (Infection Control and AMR), at Division of Global health Protection (DGHP), Centers for Disease Control and Prevention (CDC)-Kenya.A clinician with over 25 years of clinical experience, training healthcare personnel and public health. Currently, leading, SARI surveillance, IPC /AMR program, Division Global health protection (DGHP), CDC-Kenya. Special interest epidemiology/drivers of HAIs. Founder/leader of infection prevention Network Kenya (IPNET-K) and Vice-Chair of global Antibiotic resistance program (GARP). Former board member of Infection Control African Network (ICAN), and the international federation of infection control (IFIC), an International Ambassador for SHEA and served as a member of external affairs committee.

Background: Clusters of acute respiratory illness (ARI) are challenging to investigate in many settings due to non-specific clinical presentations, challenges in specimen collection/testing, variability in health-seeking behaviors, and systemic resource limitations. Event-based surveillance (EBS), defined as the “organized collection, monitoring, assessment, and interpretation of mainly unstructured ad hoc information regarding health events or risks, can allow for the early detection and real-time reporting of public health events. September 2019, community EBS (CEBS) system was initiated in Kenya and expanded to include COVID-19-related reporting in May 2020. We highlight the contributions of CEBS in cluster detection to public health investigation.

Methods: March 2, 2021, a community health volunteer participating in CEBS reported a cluster of three (3) ARI cases. Signal was triaged and verified as an event by the assigned community health assistant (CHA), who reported it to the sub-county health team (SCHT). The SCHT initiated investigations on March 4, 2021, which established cases of acute respiratory illness (ARI) had been seen at the local health facility from mid-February 2021 but not reported before the cluster signal was detected by the CHV.

Results: Investigation identified 176 ARI cases in Gilgil dating from February 14–March 28, 2021. Ninety -one (51.7%) were among children <5 years; n=46 (26.1%), were hospitalized. Cases were distributed among residents of 24 villages within two wards (the lowest administrative division) of Gilgil. SARS-CoV-2 was detected in specimens from 34/79 (43.0%) patients. Contacts (n=188) were traced and placed on home-based isolation and care (HBIC).
ISS data from the NCRH showed a peak in SARI cases during late March 2021. Of 132 SARI cases reported from February 14–March 31, 7 (5.3%) were among residents of Gilgil; the remainder (94.7%) were from other sub-counties of Nakuru County.

Conclusions: CEBS has ability to leverage community connections allowing early warning and control of potential public health threats.

Incidence of SARS-CoV-2 and Influenza Viruses among Pregnant and Postpartum Women and their Infants, Siaya County, Kenya 2020–2021

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Biography:

Nancy has 17 years of experience of leading epidemiologic research and public health in the field of infectious disease research and prevention, especially related to respiratory diseases and maternal-child health. She combines a basic science background (Biology and Chemistry), with advanced training in Applied Epidemiology and Biostatistics, Project Management and doctorate training in Project Monitoring and Evaluation. For 10 years, she managed and continues to support the national sentinel surveillance system for influenza and other respiratory pathogens. She has designed, managed, and continue to provide technical oversight to maternal and child health research and surveillance programs in western Kenya.

Background

Little is known about the incidence of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) among pregnant women in Sub-Saharan Africa. We quantify the incidence of symptomatic laboratory-confirmed SARS-CoV-2 and influenza infections among pregnant and postpartum women and their infants in one county in western Kenya to assess the value of prioritizing vaccination for this population.

Methods

We enrolled pregnant women seeking prenatal care at Siaya County Referral and Bondo Sub-County hospitals and called or visited them at home once a week until six months postpartum to identify respiratory illness. We similarly followed their infants for six months. Staff obtained nasopharyngeal and oropharyngeal (NP/OP) swabs within 10 days of illness onset from patients presenting with COVID-like illness (CLI) and Acute Respiratory Illness (ARI) and tested these by real-time reverse transcription polymerase chain reaction for SARS-CoV-2 and influenza A and B viruses at the Kenya Medical Research Laboratory in Kisumu.

Results

During May 2020–August 2021, we enrolled 1,329 pregnant (<31 weeks of gestation) women. Overall, 342/1192 (29%) pregnant women, 206/1,015 (20%) postpartum women, and 415/1,015 (41%) infants developed at least one CLI episode. Among CLI episodes that had a swab collected, 37/354 (10%) pregnant women, 26/218 (12%) postpartum women, and 14/407 (3%) infants tested positive for SARS-CoV-2. The incidence rate (per 1000 person-months) of SARS-CoV-2 increased from 4.8 May-December 2020 to 9.3 January-August 2021 among pregnant women; 2.4 to 6.4 among postpartum women; and 1.2 to 3.4 among infants. We did not detect any influenza in 2020; the incidence rate of influenza during January-August 2021 was 2.8, 0.4 and 1.6 among pregnant women, postpartum women, and infants, respectively.

Conclusions

The incidence of SARS-CoV-2 in pregnant and postpartum women and their infants increased during the study period. These findings highlight the need to prioritize COVID-19 vaccination for pregnant and postpartum women.

The Global Influenza Hospital Surveillance Network (GIHSN): Data Sharing for Action

Prof Marta Nunes[1], on behalf of GIHSN collaborators on behalf of GIHSN collaborators on behalf of GIHSN collaborators[1]
[1]Center of Excellence in Respiratory Pathogens

Biography:

She has expertise in hospital-based surveillance, influenza vaccination, pertussis vaccination and in quantifying the full public health value of vaccines, including implementation issues.

The Global Influenza Hospital Surveillance Network (GIHSN) operating under a multi-stakeholder public-private partnership governance started in 2012 as a network of 21 hospitals. While initially collecting information mainly from influenza patients, it progressed to include other respiratory viruses (ORV).

The GIHSN sites actively enrol year-round hospitalized patients with respiratory illnesses. Using standard protocols, demographic and clinical information are recorded, respiratory specimens are collected and tested for influenza and ORV by RT-PCR. The network objectives are to describe the epidemiology of viral-associated hospitalizations and to better understand viral circulation, related severity, and risk factors. In recent years, it has evolved to include linking epidemiologic and clinical information with viral whole genome sequencing (WGS) data to explore the association of viral genotypes and severity or vaccine-breakthrough cases and support vaccine strain selection. The WGS data is uploaded to GISAID and shared with WHO.

The GIHSN expanded to include more than 100 sites among 20 countries from both hemispheres and inter-tropical areas. Overall, since the start of the network, 143200 patients have been enrolled, including 24488 influenza cases and 42342 patients with ORV. The annual positivity rate for influenza ranged from 29% in 2019 to 2% in 2020. At least one scientific manuscript has been published per year describing different aspects of each season. Nonetheless the data and/or samples gathered through the GIHSN can be leveraged either by GIHSN sites or other not-for-profit institutions for additional projects to better understand the burden of viral respiratory illnesses and identify new pathogens.

Resilient surveillance systems like the GIHSN are important to understand the circulation and burden of different respiratory viruses to guide public health decision making, research and development initiatives. Emerging infectious diseases represent ongoing threats and the GIHSN illustrates the feasibility and pertinence of public and private sector collaborating to optimize global efforts.

Prevalence and risk factors among Covid-19 travelers in Post-pandemic era

Miss Lombe Kampamba[1], Ms Taonga Banda[1], Mr Dickson Kasombwe[1], Mr Andrew Chongwe[1], Mr Sydney Mwanza[1], DR Justin Chileshe[1], Dr. Gershom Chongwe[1]
[1]Tropical Diseases Research Centre (TDRC)

Biography:

Lombe Kampamba is a Staff Development who has been working at Tropical Diseases Research Centre (TDRC) for the last three years. She received her Bachelors Degree from the University of Limpopo and is currently pursuing her Master of Public Health at the University of Lusaka. As a new researcher, I am eager to gain more confidence in my research capabilities as well as my research write up as I would like publish research to inform policy and win grant awards for TDRC.

Background

Travelers from China were the main source of the COVID-19 disease's importation to other nations. While travel bans were introduced, many developing countries did not enforce them in order to help sustain their economics. Mitigation measures were implemented to facilitate the elimination and reduction of COVID-19 while borders continued to allow trade and travel. The objective of the study is to evaluate COVID-19 prevalence and risk factors among travelers from the Copperbelt in Zambia. Information on the contribution of travelers to the prevalence of COVID-19 is key to identify measures that would reduce secondary infections, various Covid-19 strains and future pandemics

Methods

In this retrospective study, individuals travelling out of the country who got tested from Tropical Diseases Research Centre (TDRC) in Ndola, with positive PCR results for Covid-19 infection were included. The prevalence of Covid-19 and risk factors such as age, sex and district among were estimated in post pandemic era.

Results

1984 of 3313 were included in study, the mean age was 39.2, with 78.3% being male. Covid-19 prevalence was 1.8% with most cases coming from Ndola district (1.11%). However the proportion with the highest number of travelers was Kitwe 37.7%. There were higher odds of Covid-19 cases in the more urban districts such as Kitwe and Ndola in comparison to Mpongwe and Masaiti districts which are less developed ($p \leq 0.05$). Higher odds of Covid-19 among older travelers in comparison to younger age categories ($p > 0.05$). They were higher odds covid-19 cases in males than in females ($p >= 0.05$)

Conclusion

Despite the low positive rate of Covid-19 tested among travelers in post Covid-19 era due to mitigation measures implemented, there is still need to ensure measures such as regular review of illness trends, vaccinations and Covid-19 test via PCR are available for travelers in post pandemic era.

RISK FACTORS FOR SEVERE OUTCOMES FROM INFLUENZA AND RSV INFECTIONS IN MAPUTO, MOZAMBIQUE

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[1]Repartição do Observatório Nacional de Saúde, Instituto Nacional de Saúde, [2]Repartição de Virologia, Instituto Nacional de Saúde, [3]Repartição de Vigilância, Instituto Nacional de Saúde, [4]Center for Disease Control and Prevention

Biography:

Graduated in Applied Biology from Eduardo Mondlane University in 2022. Currently, intern at the National Institute of Health, in the Surveillance of Acute Respiratory Infections.

Introduction: Knowledge of risk factors for severe disease is important for patient management; however, risk factors for severe outcomes associated with influenza and respiratory syncytial virus (RSV) illnesses in Mozambique have not yet been assessed.

Methods: We analyzed influenza-like illness (ILI) and severe acute respiratory infection (SARI) sentinel surveillance data collected from 2015–2023 in Maputo, Mozambique to identify factors associated with influenza- and RSV-associated hospitalizations. We report crude and adjusted odds ratios (aOR) and 95% confidence intervals obtained from logistic regression.

Results: ILI and SARI sentinel surveillance enrolled 7077 patients, of which 69.2% (4895) for SARI and 30.8% (2182) for ILI. The median patient age was 2.9 (IQR, 1.0-8.8) years. Overall, 614 (8.7%) patients were positive for influenza with a median age of 5.0 (IQR, 1.8-12.0 years). ILI patients were more likely to be positive for influenza (16.5% [360/2181] when compared to SARI patients (5.2% [254/4884]). Of those tested for RSV, 21.6% (434/2010) were positive and had a median age of 0.6 (IQR, 0.2-1.1 years). The SARI patients were more likely to be RSV positive (32.4% [356/1099] vs. 8.6% [78/911]) and to be younger (median age of 0.6 years [IQR, 0.2-1.1] years vs. 1.0 years [IQR, 0.5-2.0]) than those with ILI. Adjusted multivariable analysis revealed that decreasing age (aOR=0.30; 95% CI: 0.12-0.63) increases odds for influenza-associated hospitalizations and breathing difficulty (aOR=16.1; 95% CI: 2.19-236) were associated with increased odds of influenza-associated hospitalization. Rhinorrhea (aOR=5.46 95% CI: 1.64-20.5) and general malaise (aOR=33.9; 95% CI: 1.6-1957) were associated with increased odds of RSV-associated hospitalization.

Conclusion: Risk factors and symptoms associated with severe influenza and RSV infections were determined, highlighting the need for addressing control measures to people with these demographic, clinical and virological conditions during epidemic seasons.

Keywords: Hospitalization, risk factors, influenza, RSV, severe acute respiratory illness, Mozambique.

Impact of COVID-19 pandemic on Acute Respiratory Infection sentinel surveillance in Mozambique

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Biography:

Graduated in Veterinary Medicine, has been working with the respiratory viruses (Influenza, RSV and SARS-Cov-2), currently works as coordinator for the epidemiology area of the sentinel posts in the acute respiratory infections (ARI) surveillance.

Introduction: The COVID-19 pandemic significantly impacted routine health systems, including Mozambique's acute respiratory infection (ARI) sentinel surveillance system. We describe the impacts of COVID-19 on and actions taken to revive the ARI sentinel surveillance activities in Maputo.

Methods: We compared the primary performance indicators of ARI surveillance during the pandemic phase to the pre-pandemic phase (January 2018 to March 2020). We identified actions that may have contributed to changes in performance and interventions adopted to resume the system.

Results: During the pre-pandemic phase, the ARI system consisted of two pediatric SARI sentinel sites, from which an average of 56 samples were collected per site per month. Following the COVID-19 pandemic declaration on March 11, 2020, ARI sentinel surveillance and laboratory testing for influenza and RSV was interrupted in weeks 12-47, 2020. During this time, reagents were not available for influenza and RSV testing as they were prioritized for SARS-CoV-2 testing, newly deployed staff were not trained on ARI sentinel surveillance procedures, and patient and specimens flows were changed as tents and isolation centers were established to receive patients. Gradually, ARI surveillance activities were restarted beginning in week 48 of 2020 through an integrated surveillance approach recommended by WHO. Surveillance focal points were repositioned at sentinel sites, and ARI sentinel surveillance was re-established to its pre-pandemic form from July 2022 after the receipt of Pan-Respiratory Disease Surveillance funds. Between June-September 2022, 5 new sites were added to the sentinel surveillance, all of which enrolled pediatric and adult cases. Subsequently, 95 specimens were collected per site per month.

Conclusion: COVID-19 pandemic response actions resulted in the interruption of routine surveillance activities in Mozambique. Subsequent emergency funding was pivotal in restoring the ARI surveillance system to its pre-pandemic levels and allowed for expansion.

West Africa as an emerging influenza epicenter: genomic, serological, and phylogenetic evidence reveal considerable interspecies transmission of influenza viruses at the human-swine interface

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Biography:

Dr. Oluwagbenga A. Adeola has broad background in infectious diseases, with specific training and expertise in virology, molecular diagnostics, genomics, phylogenetic analysis, and clinical and epidemiological studies. His research interest includes genomics and phylogenetics of emerging viral diseases, mechanisms of evolution of RNA viruses, molecular and sero-epidemiological studies of viral infections, viral zoonoses, and One Health research. He is currently an Associate Professor of Medical Microbiology (Virology) at the College of Medicine of Bingham University, Nigeria.

Background

In order to understand the nature and transmission patterns of influenza virus infections at the human-swine interface in West Africa, we conducted various studies, between 2007 and 2022, in selected cities in three West African countries: Nigeria (Ibadan), Ghana (Kumasi), and Liberia (Buchanan).

Methods

Syndromic, serological (HI assay and quantitative antigen-detection ELISA), molecular (RT-PCR), genetic (matrix gene-based), phylogenetic (Neighbour Joining and Maximum Likelihood), and spatial epidemiological (spatial lag and Poisson regression models) tools were used to investigate the nature and transmission patterns of influenza viruses at the human-swine.

Results

Serological studies revealed presence of HI antibodies against human H1 and H3 strains of influenza A viruses in Nigerian pigs. Human strain of influenza A(H3N2) was also detected among swine populations in Nigeria and Ghana, and were found to have co-circulated with other influenza viruses. Molecular analyses revealed presence of the pandemic influenza strain (A/H1N1/pdm09) in Nigerian and Ghanaian swine populations, and among humans who regularly handled live pigs (termed "pig handlers"). Genetic and phylogenetic analyses of the matrix gene of some influenza A(H1N1)pdm09 viruses detected among pig handlers and swine populations suggest human-swine bi-directional interspecies transmission of influenza A(H1N1)pdm09 virus in Nigeria and Ghana. Results from spatial epidemiological studies and risk factor analyses conducted revealed risk factors associated with influenza virus transmission at the human-swine interface in West Africa.

Conclusions

The domestic pig remains an important mixing vessel for genetic reassortment of influenza viruses and generation of novel reassortants. Continual interspecies transmission of influenza viruses at the human-animal interface was important for emergence of influenza epicenters in South-East Asia. Considering the risk factors identified and other findings from our studies, the human-swine interface in West Africa may gradually evolve into another influenza epicenter, if adequate polices, preventive strategies, and biosecurity measures are not put in place and enforced.

RESPIRATORY PATHOGENS SENTINEL SURVEILLANCE : GABON EXPERIENCE

Madame Oriane Cordelia Aboumegone Biyogo[1]
[1]Ministere De Santé Publique

Biography:

Biologiste avec un master 2 recherche en Infectiologie tropicale j'ai 10 ans de service au ministère de la sante précisément au Laboratoire de santé je suis publique et au Centre Hospitalier Universitaire de Libreville. je suis spécialiste des infections respiratoires basse et haute. j'ai énormément travaillé dans le renforcement des capacités des laboratoires de tuberculose, de la covid19 et de la grippe.

Je suis formateur sur les différentes technique de biologie moléculaire dans le diagnostique de la tuberculose, de Sars Cov2, des Influenza A et B et les autres pathogènes

RESPIRATORY PATHOGENS SENTINEL SURVEILLANCE : GABON EXPERIENCE

Background

Respiratory pathogens remain a public health threat, despite worldwide efforts to control the strain responsible. In this context, Gabon has been selected by the WHO regional office's Health security and Emergencies (WHE) program as one of the countries to be supported to implement influenza viruses sentinel surveillance. The main objective was to describe patients proportion and distribution with Influenza Like-Illness (ILI) or Severe Acute Respiratory Infection (SARI).

Methods

From May 2022 to May 2023, for 620 patients with ILI or SARI nasopharyngeal or nasopharyngeal aspirates samples were collected. We tested by Real-time RT-PCR, Influenza Viruses A and B (IAV/ IBV), Sars-Cov-2 and RNase P with Influenza FluSC2 Multiplex kit from CDC-Atlanta, US. Samples tested positive for IAV or IBV, were subtyped for Influenza A(H3N2), A(H1N1) pdm09, B lineage Victoria and Yamagata. In addition, negative samples were tested for the detection of thirty-three respiratory pathogens in a single reaction mixture by real-time RT-PCR using Fast Track Diagnosis (FTD) Respiratory pathogens 33.

Results

Out of 620 enrolled patients, 592 (95.5 %) were ILI and 28 (4.5 %) were SARI cases. Forty-seven individuals (7.6%) were positive for IAV. Of 47 IAV, 20 were seasonal H3N2, 10 were H1N1pdm09 and 17 were non-subtypable. Twenty-six individuals (4.2%) were positive for IBV. Of 26 IBV, 12 were lineage victoria, 14 were non-subtypable. Fifty-nine individuals (9.5%) were positive for Sars-CoV-2, less than 1% were infected with one pathogen and 13% were co-infected. Strains of Adenovirus, Haemophilus influenzae, Bordetella pertussis, Bocavirus, Streptoccocus pneumoniae, Rhinovirus, coronavirus HCoV OC43, Moraxella catarrhalis, Klebsiella pneumoniae, Chlamydia pneumoniae, Staphyloccocus aureus, Syncytial Virus A/B were identified.

Conclusion

Observed trends in influenza virus A/B-positive cases and respiratory pathogens circulating in Gabon allow timely public health interventions for high-risk groups.

Keywords
Sentinel surveillance, Respiratory pathogens, ILI, SARI, Gabon.

Molecular Epidemiology of Seasonal Influenza A Viruses Circulating in Mozambique from 2015-2022

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Biography:

As an early-stage investigator, my role is to support the detection, diagnosis, and monitoring of influenza. With a passion for providing reliable care, I ensure precise sample preparation and accurate laboratory testing. I maintain confidential patient data and prioritize equipment maintenance. To stay updated, I actively participate in training and continuing education. Whether working independently or in a team, I am dedicated to contributing to the laboratory's success. Driven by my commitment to delivering the best care, I strive for excellence in routine tests and process improvement. My goal is to make a positive impact in influenza research.

Introduction: Molecular surveillance for influenza is crucial for detecting novel variants with epidemiological and clinical significance. This study describes the molecular epidemiology of influenza A in Maputo, Mozambique between 2015 and 2022.

Methods: Phylogenetic and evolutionary trees of hemagglutinin (HA) and neuraminidase (NA) gene sequences were constructed from influenza A viruses collected through the Mozambique respiratory infection sentinel surveillance from 2015– 2022. Vaccine, reference, and other global sequences were obtained from the Global Initiative on Sharing Avian Influenza Data (GISAID).

Results: Based on HA, the A(H1N1)pdm09 sequences changed from predominantly clade 6.B.1 from 2015–2018,to clade 5a.1.1 from 2019–2022 . This temporal variation suggests evolving viral lineages within the country. In contrast, from 2015–2022 all A(H3N2) sequences belonged to clade 3c.2 with, many showing similarity to sequences from the African region or global sequences . This suggests a mix of regionally circulating strains and strains that are more widely distributed. Amino acid substitutions were most frequently found in the head domain of HA gene of A(H1N1)pdm09 viruses, mainly during higher activity seasons and in the stem region in A(H3N2). Nucleotide variations were lower at the antigenic sites of A(H3N2) than of A(H1N1)pdm09, which experienced higher variability at the antigenic sites, reflecting increased immunological pressure due to longer circulation and continuous vaccine changes. Analysis of the NA gene of both subtypes revealed no mutation associated to with resistance or reduced susceptibility to NA inhibitors.

Conclusions:

The A(H1N1)pdm09 viruses showed evidence of multiple introductions into Mozambique, with different clades dominating during distinct time periods. This suggests ongoing viral circulation and potential importation of strains from various sources. In contrast, the A(H3N2) viruses exhibited a more consistent clade classification, indicating a relatively stable lineage within the country, with a mix of locally circulating strains and those more widely distributed in the region.

Biological specimen quality and the success on the influenza virus genetic and antigenic analyses– Mozambique, 2015 to 2022

Miss Rassula Zimba[1], Miss Jessica Monjane[1], Mr Pedro Inguana[1], Mr Almiro Tivene[1], Mr Osvaldo Inlamea[1], Miss Bibiana Melchior[1], Mr Daniel Owuso[2], Mr Aaron Samul[3], Mr Paulo Notico[1]
[1]National Institute of Health, [2]2Influenza Division, National Center for Immunization and Respiratory Diseases, US , [3]3Influenza Program, National Center for Immunization and Respiratory Diseases, US Centers for Disease Control and Prevention, Pretoria, South Africa

Biography:

Rassula Arone Dzimba, Graduated in BIomedicine, from the High Institute of Health Science, in 2021, currently working in the IRA Survaillence at the National Institute of Health, in Mozambique.

Introduction: The viability of influenza virus and viral RNA (vRNA) in clinical specimens collected by countries underpin antigenic and sequence analysis and accuracy of the recommendations released by WHO for influenza control. Knowing that failures in this process may compromise the WHO influenza vaccine recommendation for these countries, this study sought to identify the potential reasons for failure to recover vRNA and influenza virus in specimens submitted by Mozambique to WHO reference laboratories between 2015 and 2022.

Methods: We compared the characteristics and handling conditions of specimens from which virus recovery (antigenic results) and vRNA (sequence results) failed to those with successful recovery. We also discuss potential impacts of the results on influenza control in Mozambique and other African settings. Statistical analysis were performed using chi-square and Student's t test, $p< 0.05$ was considered significant.

Results: Of the142 specimens analyzed, 97.6%, 78.9% and 48.6% had successful PCR detection, genome sequencing and antigenic analyses completed, respectively. Virus recovery rate varied from 95% in 2015 to 0% in 2019 (0/42) and 2022 (0/22). Antigenically analyzed specimens had lower mean Cycle threshold (Ct) values (23.9 vs 26.4;$p=0.002$) and fewer numbers of temperature excursions during the storage (0.5 vs 2.1 days; $p=0.02$) than those in which virus couldn't be recovered. Those that were successfully sequenced also had lower mean Ct values (24.0 vs 27.9: $P=0,001$) than those that failed. Failure on virus recovery was observed in many African countries, except in South Africa, thus vaccine composition recommendation could be inferred through phylogenetic analysis.

Conclusion: lower viral loads and improper specimen's storage might be associated with failure in antigenic and genetic analysis at WHO-CC, highlighting the need to improve sample management for more realistic vaccine composition for African countries.

Keywords: influenza, specimens handling, virus recovery, Mozambique, non-conformity.

SARS-CoV-2 Wastewater Based Surveillance in LMICs

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[1]Institut Pasteur de Tunis, [2]Mount Kenya University, School of Medicine

Biography:

Dhafer Laouini is a scientist at Institut Pasteur de Tunis. After obtaining his PhD in Immunology and Molecular Biology, he held several postdoctoral positions (Institute Pasteur, Paris, France and Harvard Medical School, Boston, USA), specializing in Immunology. He is currently heading the Group Immunobiology of Infections that focuses on the identification of correlates of protection in individuals at risk, the use of omics approaches to investigate host-pathogen interactions and the study of innate and adaptive immune responses.

Background

The global COVID-19 pandemic, caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), has disrupted all national health systems. Epidemiological surveillance is one of the essential tools to contain it. Shedding of non-infectious fragments of SARS-CoV-2 by infected individuals, even asymptomatic, allows the use of sewage monitoring to track its spread within a community.

This approach is particularly interesting for Low- and Middle-Income countries (LMICs) where surveillance capacity at the individual level is limited, provided that methodological aspects are validated to make surveillance data quickly usable in public health.

Methods

We aimed to show the presence of SARS-CoV-2 in samples from wastewater treatment plants in Tunis, Tunisia and Thika, Kenya.

Total nucleic acid (TNA) was purified from samples collected over 24h (solid membrane “swab”) or instantaneous (liquid “grab”) of undischarged wastewater collected between December 2021 and September 2022. TNA isolated from wastewater was used to perform RT-qPCR targeting the nucleocapsid (N1, N2) and envelope (E) regions of the SARS-CoV-2 genome.

Results

Results show the presence of SARS-CoV-2 fragments in our samples and the detection of an increase in viral levels several days before their clinical appearance. Our study not only emphasizes the importance of the contribution of molecular monitoring of wastewater, but also on the choice of sampling methods which proves to be crucial for the effective use of this surveillance.

Conclusions

Our next step is to translate these findings into action to inform decision makers and engage communities and stakeholders to adapt such Wastewater-based surveillance (WBS) as a routine and useful approach.

Circulation Patterns of Other Respiratory Viruses in Maputo, Mozambique in 2022

Mr Domingos Mulungo[1], Ms Jennifer Cumbana[1], Mr Dércio Chauque[1], Ms Claúdia Manguel[1], Mr Cândido Luis[1], Ms Neuza Nguenha[1], Ms Bibiana Melchior[1], Ms Jorfélia Chilaule[1], Ms Sádia Pereira[1], Mr Daniel Owusu[2], Mr Aaron Samuels[2,3], Mr Almiro Tivane[1]

[1]Instituto Nacional de Saúde, [2]US Centers for Disease Control and Prevention, Atlanta, Georgia, [3]US Centers for Disease Control and Prevention, Pretoria

Biography:

I am Domingos Mulungo, graduated in Applied Biology from Eduardo Mondlane University. Currently, I am part of the National Institute of Health, specifically the Virology Laboratory.

Background: Epidemiological studies and control actions have historically prioritized Seasonal influenza, RSV, and recently, SARS-CoV-2 over other respiratory viruses (ORV). The COVID-19 pandemic has reinvigorated interest in understanding the impact of non-pharmaceutical interventions in respiratory virus control beyond SARS-CoV-2. This study aimed to detect and determine the circulation of ORVs in Maputo in 2022.

Methodology: A total of 4280 specimens were available, but only 430 negative specimens for SARS-CoV-2 and influenza were selected for analysis. These specimens were collected from children aged 0-14 years and older adults ≥60 years old from the sentinel surveillance for acute respiratory infections were retrospectively and randomly selected and screened for Parainfluenza (1-3), Metapneumovirus, Adenovirus, and Seasonal Coronaviruses (OC43, 229E and NL63) using real-time RT-PCR. Frequencies were calculated and associations of variables including non-pharmaceutical interventions to control SARS-CoV-2 and massive vaccination periods, were examined.

Results: Preliminary results found that in 2022, Adenovirus (7.21%, 31/430), Metapneumovirus (3,02%, 13/430), Parainfluenza 1 (1.63%, 7/430), Parainfluenza 2 (0.47%, 2/430), Parainfluenza 3 (2.33%, 10/430) and Coronavirus NL63 (0.7%, 3/430) were detected among the study sample. Of the positive samples, 87.9% (58/66) were from children ≤3 years old and 12.1% (8/66) were from children older than 3 years and older adults. All viruses were detected throughout the year without apparent epidemic period, except for Adenovirus which showed high activity (61.29%, 17/31) between July and September. The lowest detections of the tested viruses were observed between January and April, coinciding with the 4th wave of SARS-CoV-2 and after massive vaccination for SARS-CoV-2 in the country.

Conclusion: Other respiratory viruses were present throughout the year without clear epidemic periods and appeared to be more common in children ≤3 years old than older adults. The data suggests that waves of SARS-CoV-2, non-pharmaceutical interventions and vaccination campaigns might have significantly impacted the circulation of ORV.

Leveraging on one-health approach for human case search in a recent avian influenza outbreak in Nigeria, 2021

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Biography:

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Background

An avian influenza outbreak started on 25th January 2021 from a backyard farm of different birds in Kano, Nigeria. The outbreak later spread to eight northern States. Consequently, national one-health Rapid Response Team (RRT) was deployed to Kano and some states to investigate for early detection of highly pathogenic avian influenza (HPAI) transmission from bird to human and in humans.

Method

We conducted a cross-sectional study with focus on the human population that was infected birds' contact during the outbreaks of HPAI. We used Influenza-like Illness (ILI) and Severe Acute Respiratory Infection (SARI) case definitions to search for suspected cases, obtained detailed contact information and followed-up individuals exposed to sick and/or dead birds over 14 days of case detection. Naso-and-oropharyngeal swabs were collected from exposed individuals at the backyard and commercial farms, and Live Bird Markets in Kano, Plateau, Bauchi and Gombe States. Swabs subjected to RT-PCR testing and positive samples were shipped to the United States WHO Collaborating Centre (WHO CC) for confirmation and sequencing.

Results

Eighty-Two (82) Exposed Individuals were asymptomatic, and one (1) had catarrh during the visit. Seven (10.9%) of the 83 samples were positive for Flu A (CT value, 34.9 – 38.4), 6 (7.2%) were subtype A/H5 while 1 (1.2%) was unsub-typable. Seven positive samples were referred to WHO CC. Of these samples, 5 (71.4%) were positive for Flu A, and A/H5 (CT value, 36.3 – 43.8), 2 (28.6%) were positive for both A/H5 and A/H9 (39.2 – 40), and 3 (42.9%) had sequence clade 2.3.4.4b like that of HPAI H5.

Conclusion

Early detection of HPAI is critical to mitigate and prevent transmission to humans. There is a need to collect blood samples in parallel with the swabs, follow up with the contact and later collect another set of blood for a convalescent study.

AFRO-MoVE: African network to monitor vaccine effectiveness for COVID-19 and other respiratory pathogens

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none

Background
Vaccine effectiveness (VE) studies provide essential post-licensure evidence of the performance of vaccines in real-world conditions. There is a lack of real-world data on COVID-19 vaccine effectiveness, especially in the African Region due to inadequate Government funding, lack of prioritization of research and capacity to conduct vaccine effectiveness studies. In March 2021, the World Health Organization Regional Office for Africa and partners launched the AFRO-Monitoring Vaccine Effectiveness (AFRO-MoVE) network to establish a network of partners conducting COVID-19 VE studies, to promote sharing of resources and experience across the region, to build capacity to conduct VE and related studies.

Methods
AFRO MoVE supports the implementation and activities for COVID-19 vaccine effectiveness studies, using a multi-pronged approach: technical assistance to countries, advocacy and co-ordination, implementing network webinars and workshops and building on experience. AFRO-MoVE has adapted two generic protocols developed by EURO, to measure COVID-19 VE in the region: a prospective cohort study among health workers and a test-negative design nested in existing surveillance system of hospitalized patients with Severe Acute Respiratory Infections (SARI).

Results
AFRO-MoVE includes partners from 19 AFRO countries and 30 organisations. Twenty-two COVID-19 VE studies are ongoing or planned in AFRO across 13 countries, and six have published estimates so far. Among AFRO MOVE pooling studies, 6 countries have adapted the SARI protocol, 2 have adapted the health workers protocol to local context and 2 countries are conducting cohort studies in populations with comorbidities (e.g. HIV, diabetes, and hypertension). Eleven technical CVE meetings have been organised with participation of 18 countries, a central database and data management support have been operationalised.

Conclusions
AFRO-MoVE provides a platform to pool data across sites to estimate regional CVE by sub-groups or products which enhance comparability of results, facilitate interpretation and build technical expertise and collaborations in the African region.

PROFILES AND DETERMINANTS OF INTENSIVE CARE ADMISSION AND CASE FATALITY OF PATIENTS WITH SEVERE ACUTE RESPIRATORY INFECTIONS IN TUNISIA, 2015-2019, PRIOR TO COVID-19 PANDEMIC

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Biography:

With a PhD in infection diseases surveillance and epidemiology, I work in the medical epidemiology department at the Pasteur Institute in Tunis. Also, I am GOARN-WHO Partner in Capacities Building and Training.

Objectives: Although Severe Acute Respiratory Infection (SARI) causes substantial mortality and morbidity worldwide, data on risk factors for SARI cases in low- and middle-income countries remain limited.

Methods: We conducted a retrospective analytical study of SARI patients admitted in two sentinel surveillance sites in Tunisia prior to COVID-19 pandemic (2015-2019) in order to describe their profile and to elucidate the risk factors associated with severe outcomes. Medical and socio-demographic information of 564 eligible patients with SARI have been compiled and analyzed.

Results: Fifty-eight percent (n= 329) were male and the average age was 53.9 years (SD=19.4). Among all patients, 42% (n=241) were smokers, whereas only 5.8% (n=32) received seasonal influenza vaccine. At least one pathogen was found in 42.4% of tested cases. Influenza virus was the most commonly identified (28.3%) followed by Haemophilus influenzae (5%) and Streptococcus pneumoniae (4.8%). Factors found to be significantly associated with admission to intensive care were history of chronic respiratory diseases (AOR=16.50 [8.86-30.74]) and smoking (AOR= 1.94 [1.20-3.11]). However, case fatality was significantly associated to ICU admission, influenza virus infection and older age (≥60) (AOR=8.31 [4.33-15.92]; $p<0.001$; AOR=8.31 [4.33-15.92]; $p<0.001$ and AOR=8.31 [4.33-15.92]; $p<0.001$ respectively).

Conclusions: These findings highlight the main determinants of severe SARI outcomes prior to COVID-19 pandemic and provided evidence-based information for targeted prevention strategies to reduce the burden of severe respiratory infections in Tunisia.