NATIONAL INSTITUTE FOR COMMUNICABLE DISEASES
Division of the National Health Laboratory Service

SCIENCE FOCUS

A quarterly nexus of scientific insights

ISSUE 31 | Q2 | 2024

The Science Focus acknowledges NICD members of staff who have published in peer-reviewed journals. This publication is a compilation of scientific publications where an NICD staff member is either the first or last author.

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Disclaimer: Impact factor scores contained in this publication were compiled in Aug - Sep 2024.

MR VUYO SABANI

SENIOR COMMUNICATIONS MANAGER

NICD RESEARCHERS VENTURE BEYOND THE ORDINARY TO UNEARTH DISEASE AND HEALTH INSIGHTS

It is our pleasure to share the second edition of the Science Focus for this current financial year. This issue covers peer-reviewed publications published in Quarter two (July-September). For this period, National Institute for Communicable Diseases (NICD) staff were involved in various research studies, which led to the publication of 50 peer-reviewed articles. This puts us on course to meet our target of 180 publications for the 2024/2025 financial year. Achieving this milestone is no mean feat and demonstrates the NICD researcher's resolve and commitment to knowledge and information generation. In this issue, we profile 25 abstracts of peer-reviewed publications where an NICD staff member was either the first or the last author.

Each abstract shines a light on a health or disease phenomenon and showcases the ingenuity of our researchers and collaborators to find solutions and improve our understanding of it. The NICD researchers don't just study health; they venture beyond the ordinary and develop innovative and creative methods to unearth health diseases and health insights. The study "Metagenomics analysis of sewage for surveillance of antimicrobial resistance in South Africa" is a case in point. In what is believed to be the first study of its kind to be published in South Africa, Prof. Anthony Smith of the Centre for Enteric Disease, together with his colleagues, conducted a 24-month study using metagenomics to investigate antimicrobial resistance (AMR) abundance in raw sewage from wastewater treatment works in two municipalities in Gauteng Province. The analysis of raw sewage and wastewater are innovative adjuncts to current conventional methodologies for the surveillance of antimicrobial resistance in the human population.

Another study that ventures beyond the ordinary is "Attempted Transmission of Marburg Virus by Bat-Associated Fleas Thaumapsylla breviceps (Ischnopsyllidae: Thaumapsyllianae) to the Egyptian Rousette Bat (Rousettus aegyptiacus)," which was led by Prof. Janusz Paweska, of the Centre for Emerging Zoonotic Parasitic Diseases. This study investigated the Marburg virus (MARV) transmission between Egyptian Rousette Bats and Bat-Associated fleas. The researchers caution that "while our findings demonstrate that bat fleas lack the vectorial capacity to transmit MARV biologically, their role in mechanical transmission should not be discounted."

Another publication that ventures beyond the ordinary is "Odyssean Malaria in South Africa (2014-2023): An In-Depth Review," published in the Public Health Bulletin South Africa. This article shares insights about the transmission of Odyssean malaria. Odyssean malaria is caused by malaria parasite-infected mosquitoes that have inadvertently travelled to non-malarious areas via various transport mechanisms (sea, air, rail, road). Even though Odyssean malaria is unusual, it is a recurrent occurrence in South Africa, especially in Gauteng Province.

We invite you to read this edition for more on these and other peer-reviewed publications.

Until the next issue, enjoy the read!

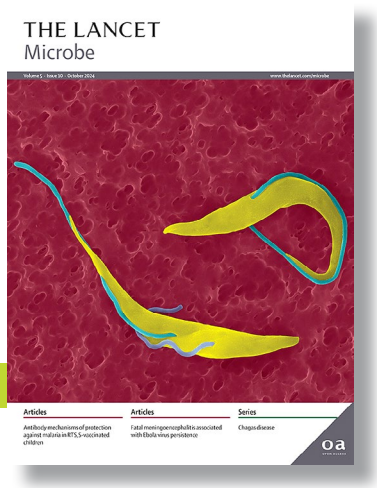
On behalf of the team,

Vuyo Sabani
Senior Communications Manager

DR SHAHEED V. OMAR

WHO global research priorities for antimicrobial resistance in human health

Silvia Bertagnolio, Zlatina Dobreva, Chad M Centner, Ioana Diana Olaru, Daniele Donà, Stefano Burzo, Benedikt D Huttner, Antoine Chaillon, Nebiat Gebreselassie, Teodora Wi, Mateusz Hasso-Agopsowicz, Benedetta Allegranzi, Hatim Sati, Verica Ivanovska, Kavita U Kothari, Hanan H Balkhy, Alessandro Cassini, Raph L Hamers, Kitty Van Weezenbeek; **WHO Research Agenda for AMR in Human Health Collaborators (Shaheed Vally Omar)**



The Lancet Microbe

IMPACT FACTOR: 20.9

https://www.thelancet.com/journals/lanmic/article/PIIS2666-5247(24)00134-4/fulltext

ABSTRACT

The WHO research agenda for antimicrobial resistance (AMR) in human health has identified 40 research priorities to be addressed by the year 2030. These priorities focus on bacterial and fungal pathogens of crucial importance in addressing AMR, including drug-resistant pathogens causing tuberculosis. These research priorities encompass the entire people-centred journey, covering prevention, diagnosis, and treatment of antimicrobial-resistant infections, in addition to addressing the overarching knowledge gaps in AMR epidemiology, burden and drivers, policies and regulations, and awareness and education. The research priorities were identified through a multistage process, starting with a comprehensive scoping review of knowledge gaps, with expert inputs gathered through a survey and open call. The priority setting involved a rigorous modified Child Health and Nutrition Research Initiative approach, ensuring global representation and applicability of the findings. The ultimate goal of this research agenda is to encourage research and investment in the generation of evidence to better understand AMR dynamics and facilitate policy translation for reducing the burden and consequences of AMR.

PROF. ANNE VON GOTTEBERG

PROF. CHERYL COHEN

Long-term effect of pneumococcal conjugate vaccines on invasive pneumococcal disease incidence among people of all ages from national, active, laboratory-based surveillance in South Africa, 2005-19: a cohort observational study

Anne von Gottberg, Jackie Kleynhans, Linda de Gouveia, Stefano Tempia, **Susan Meiring, Vanessa Quan, Mignon du Plessis,** Claire von Mollendorf, Penny Crowther-Gibson, Theunis Avenant, Nicolette du Plessis, Ranmini Kularatne, Vindana Chibabhai, Shabir A Madhi, Keith P Klugman, Cynthia G Whitney, **Cheryl Cohen**; **GERMS-SA**

The Lancet Global Health

IMPACT FACTOR: 19.9

https://www.thelancet.com/journals/langlo/article/PIIS2214-109X(24)00263-8/fulltext

Background: In South Africa, 7-valent pneumococcal conjugate vaccine (PCV7) was introduced in 2009 and 13-valent PCV (PCV13) was introduced in 2011, both in a two plus one schedule. We evaluated the ongoing effects of PCV on the prevention of invasive pneumococcal disease (IPD) over 15 years of sustained surveillance in South Africa before the COVID-19 pandemic.

Method: We conducted national, active, laboratory-based surveillance for IPD among all ages in South Africa, including isolate serotyping and susceptibility testing. We fitted linear regression models with vaccine covariates to imputed IPD case counts each year by serotype and age to compare expected and actual IPD cases in 2019, which was the main outcome. Vaccine effects were set to zero to identify expected incidence after the introduction of PCV7 and PCV13.

Findings: From Jan 1, 2005, to Dec 31, 2019, surveillance identified 52 957 IPD cases. Among the 50 705 individuals with age data available, 9398 (18·5%) were infants aged younger than 2 years. Compared with expected case numbers (no vaccination) predicted using all available data, overall IPD rates among children younger than 2 years declined by 76·0% (percentage risk difference; 95% CI -79·0 to -72·8%) in 2019; notably, PCV7 and additional PCV13 serotype IPD rates declined by 95·5% (-97·0 to -93·4%) and 93·8% (-96·2 to-90·5%), respectively, whereas non-vaccine serotypes (NVTs) did not change significantly. Among adults aged 25-44 years, overall IPD declined by 50·4% (-54·2 to -46·3%), and PCV7 and additional PCV13 serotype IPD rates declined by 86·1% (-88·7 to -83·1%) and 77·2% (-80·9 to -73·0%), respectively, whereas NVTs increased by 78·5% (56·8 to 103·4%). Individuals aged older than 64 years also benefited from declines in IPD (-30·2%; -41·9 to -16·2%), but NVTs increased (234·9%; 138·1 to 379·4%).

Interpretation: We documented sustained direct and indirect benefits of PCV across age groups, and NVT increases in adults older than 24 years. Higher valency PCVs would have the added benefit of preventing this residual disease.

Funding: National Institute for Communicable Diseases of the National Health Laboratory Service (South Africa) and US Agency for International Development Antimicrobial Resistance Initiative, US Centers for Disease Control and Prevention.

MS CEBILE LEKHULENI

DR MIGNON DU PLESSIS

Impact of pneumococcal conjugate vaccines on invasive pneumococcal disease-causing lineages among South African children

Cebile Lekhuleni, Kedibone Ndlangisa, Rebecca A Gladstone, Sopio Chochua, Benjamin J Metcalf, Yuan Li, **Jackie Kleynhans, Linda de Gouveia,** Scott Hazelhurst, Ana D S Ferreira, Happy **Skosana, Sibongile Walaza, Vanessa Quan, Susan Meiring,** Paulina A Hawkins, Lesley McGee, Stephen D Bentley, **Cheryl Cohen,** Stephanie W Lo, **Anne von Gottberg, Mignon du Plessis**

Nature Communications

IMPACT FACTOR: 14.7

https://doi.org/10.1038/s41467-024-52459-3

ABSTRACT

Invasive pneumococcal disease (IPD) due to non-vaccine serotypes after the introduction of pneumococcal conjugate vaccines (PCV) remains a global concern. This study used pathogen genomics to evaluate changes in invasive pneumococcal lineages before, during and after vaccine introduction in South Africa. We included genomes (N = 3104) of IPD isolates from individuals aged <18 years (2005–20), spanning four periods: pre-PCV, PCV7, early-PCV13, and late-PCV13. Significant incidence reductions occurred among vaccine-type lineages in the late-PCV13 period compared to the pre-PCV period. However, some vaccine-type lineages continued to cause invasive disease and showed increasing effective population size trends in the post-PCV era. A significant increase in lineage diversity was observed from the PCV7 period to the early-PCV13 period (Simpson's diversity index: 0.954, 95% confidence interval 0.948-0.961 vs 0.965, 0.962-0.969) supporting intervention-driven population structure perturbation. Increases in the prevalence of penicillin, erythromycin, and multidrug resistance were observed among non-vaccine serotypes in the late-PCV13 period compared to the pre-PCV period. In this work we highlight the importance of continued genomic surveillance to monitor disease-causing lineages post vaccination to support policy-making and future vaccine designs and considerations.

DR NISHI PRABDIAL-SING

Molecular characterisation of hepatitis A in the Western Cape province, South Africa in 2023

Kathleen Subramoney, **Jack Manamela**, Stephen Korsman, **Janine Bezuidenhoudt**, Charlene Lawrence, **Jayendrie Thaver, Keveshan Bhagwandin, Jimmy Khosa**, Zinhle Khalishwayo, **Nishi Prabdial-Sing**

BMC Infectious Diseases

IMPACT FACTOR: 6.4

https://doi.org/10.1186/s12879-024-09738-7

ABSTRACT

In 2023, passive laboratory-based surveillance showed an increase in hepatitis A virus (HAV) infection. We investigated hepatitis A incidence using the notifiable medical condition surveillance system (NMCSS) data and molecularly characterised positive blood samples from the Western Cape province for 2023. All HAV IgM seropositive cases from the NMCSS from 1 January to 31 October 2023 in South Africa were investigated. HAV RNA from blood samples that had tested positive for HAV IgM from Western Cape was amplified in the VP1/P2B junction and sequenced (3500Xl Genetic Analyser). Sequences were assembled, aligned (Sequencher) and analysed (Aliview 1.27 and MEGA11). Statistical analysis was performed using Excel and the CuSum2 Threshold to determine suspected outbreaks. In 2023, the incidence of HAV IgM was 6.28/100,000 in South Africa, with the highest incidence in Western Cape province (15.86/100,000). Children aged 5 to 14 years were affected the most in the Western Cape. The positive cases in the Western Cape were above the CuSum2 threshold from January to May 2023, with the highest incidence observed in the City of Cape Town Metropolitan (14.8/100,000). Genotyping was successfully performed on 92.7% (139/150) of serum samples, for which the IB sub-genotype was detected. Three primary mutations R63K, R71S and M104I were observed in more than 49% of the samples. Most of the samples sequenced belonged to patients residing in areas close to each other within the City of Cape Town Southern, Western, and Mitchells Plain sub-districts. The CuSum2 threshold method allowed the identification of suspected HAV outbreaks in the districts within the Western Cape in 2023 while genotyping identified clusters of sub-genotype IB. Genotyping could assist with determining the common source of infection during an outbreak, especially if coupled with epidemiological and geographical data. Further active surveillance can assist in investigating the HAV risk factors for targeted public health responses.

DR NICOLA CHIWANDIRE

PROF. CHERYL COHEN

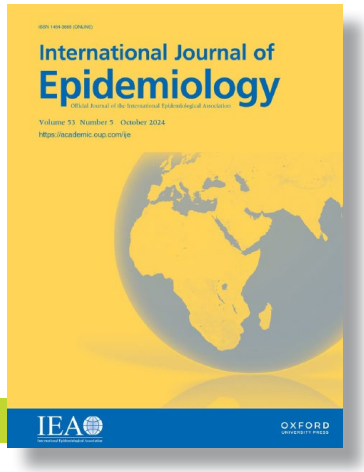
Estimation of vaccine effectiveness against SARS-CoV-2-associated hospitalization using sentinel surveillance in South Africa

Nicola Chiwandire, Sibongile Walaza, Anne von Gottberg, Nicole Wolter, Mignon Du Plessis, Fahima Moosa, Michelle J Groome, Jeremy Nel, Ebrahim Variava, **Halima Dawood, Mvuyo Makhasi,** Leora R Feldstein, Perrine Marcenac, Kathryn E Lafond , Aaron M Samuels, **Cheryl Cohen**

International Journal of Epidemiology

IMPACT FACTOR: 6.4

https://doi.org/10.1093/ije/dyae116



Background: COVID-19 vaccine effectiveness (VE) studies leveraging systematic surveillance in sub-Saharan Africa are limited. We assessed the effectiveness of two vaccines (Pfizer BNT162b2 and Johnson & Johnson Ad26.COV2.S) against SARS-CoV-2-associated hospitalization in South African adults aged ≥18 years.

Method: We conducted a test-negative case-control study using pneumonia surveillance data in South Africa. Inpatients with physician-diagnosed lower respiratory tract infection or suspected COVID-19, testing SARS-CoV-2 positive or negative from June 2021-March 2022, were cases or controls, respectively. Fully vaccinated individuals received one Ad26.COV2.S dose or two BNT162b2 doses ≥14-days before enrollment. VE was estimated using multivariable logistic regression for Delta- and Omicron BA.1/BA.2-predominant periods, stratified by age and HIV status.

Results: The study included 925 cases and 1890 controls; 38 (4%) cases and 186 (10%) controls were fully vaccinated with BNT162b2, and 30 (3%) cases and 94 (5%) controls with Ad26.COV2.S.

The vaccine effectiveness of BNT162b2 against SARS-CoV-2-associated hospitalization over Delta and Omicron BA.1/BA.2 periods was 91% (95% CI: 52%, 98%) and 33% (-16%, 86%), respectively. The vaccine effectiveness of Ad26.COV2.S against hospitalization over Delta and Omicron BA.1/BA.2 periods was 72% (-36% ,94%), and -19% (-130%, 39%), respectively. The vaccine effectiveness of BNT162b2 against hospitalization over the Delta period was 94% (50%, 99%) and 89% (27%, 98%) among adults aged ≥60 years and HIV-uninfected, respectively.

Conclusions: The BNT162b2 vaccine was effective against SARS-CoV-2-associated hospitalization during the Delta period for adults aged ≥18 years, ≥60 years and those HIV-uninfected. VE for Ad26.COV2.S was inconclusive, potentially due to limited sample size or residual confounding. These findings highlight the utility of sentinel surveillance for estimating VE.

Keywords: COVID-19; SARS-CoV-2; sentinel surveillance; test-negative case control; vaccine effectiveness.

DR SHAHEED V. OMAR

MS LAVANIA JOSEPH

Performance evaluation of the Xpert MTB/XDR test for the detection of drug resistance to *Mycobacterium tuberculosis* among people diagnosed with tuberculosis in South Africa

Shaheed Vally Omar, Gail Louw**, Farzana Ismail,** Xiaohong Liu, **Dumsani Ngcamu, Thabisile Gwala, Minty van der Meulen, Lavania Joseph**

Journal of Clinical Microbiology

IMPACT FACTOR: 6.1

https://doi.org/10.1128/jcm.00229-24

ABSTRACT

Drug-resistant tuberculosis (TB) poses a significant public health concern in South Africa due to its complexity in diagnosis, treatment, and management. This study assessed the diagnostic performance of the Xpert MTB/XDR test for detecting drug resistance in patients with TB by using archived sputum sediments. This study analyzed 322 samples collected from patients diagnosed with TB between 2016 and 2019 across South Africa, previously characterized by phenotypic and genotypic methods. The Xpert MTB/XDR test was evaluated for its ability to detect resistance to isoniazid (INH), ethionamide (ETH), fluoroquinolones (FLQ), and second-line injectable drugs (SLIDs) compared with phenotypic drug susceptibility testing (pDST) and whole-genome sequencing (WGS). Culture, Xpert MTB/RIF Ultra, and Xpert MTB/RIF (G4) tests were performed to determine sensitivity and agreement with this test for TB detection. The sensitivities using a composite reference standard, pDST, and sequencing were >90% for INH, FLQ, amikacin (AMK), kanamycin (KAN), and capreomycin (CAP) resistance, meeting the WHO target product profile criteria for this class. A lower sensitivity of 65.9% (95% CI: 57.1-73.6) for ETH resistance was observed. The Xpert MTB/XDR showed a sensitivity of 98.3% (95% CI: 96.1-99.3) and specificity of 100% (95% CI: 86.7-100) compared with culture, a positive percent agreement (PPA) of 98.8% (95% CI: 93.7-99.8) and negative percent agreement (NPA) of 100.0% (95% CI: 78.5-100.0) compared with G4, and a PPA of 99.5% (95% CI: 97.3-99.9) and NPA of 100.0% (95% CI: 78.5-100.0) compared with Xpert MTB/RIF Ultra for detecting *Mycobacterium tuberculosis*. The test offers a promising solution for the rapid detection of drug-resistant TB and could significantly enhance control efforts in this setting.

DR MICHELLE LOWE

PROF. OLGA PEROVIC

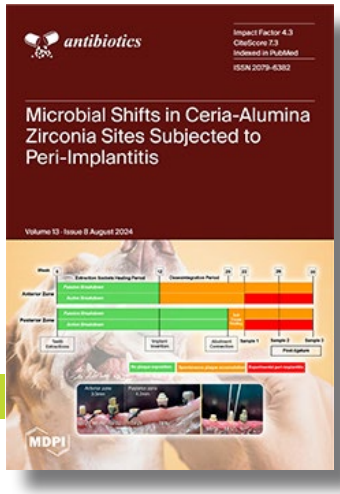
Bacterial and genetic features of raw retail pork meat: integrative analysis of antibiotic susceptibility, whole-genome sequencing, and metagenomics

Michelle Lowe, Wilhelmina Strasheim, Wai Yin Chan, **Olga Perovic**

Antiboitics (Basel, Swaziland)

IMPACT FACTOR: 4.6

https://doi.org/10.3390/antibiotics13080700



ABSTRACT

The global antibiotic resistance crisis, driven by overuse and misuse of antibiotics, is multifaceted. This study aimed to assess the microbiological and genetic characteristics of raw retail pork meat through various methods, including the isolation, antibiotic susceptibility testing (AST), whole-genome sequencing (WGS) of selected indicator bacteria, antibiotic residue testing, and metagenomic sequencing. Samples were purchased from 10 pre-selected retail stores in Gauteng, South Africa. The samples were aseptically separated, with portions sent to an external laboratory for isolating indicator bacteria and testing for antibiotic residues. Identification of the isolated bacteria was reconfirmed using matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS). AST was performed using the Microscan Walkaway system (Beckman Coulter, Brea, CA, USA). WGS and metagenomic sequencing were performed using the Illumina NextSeq 550 instrument (San Diego, CA, USA). The isolated E. coli and E. faecalis exhibited minimal phenotypic resistance, with WGS revealing the presence of tetracycline resistance genes. Both the isolated bacteria and meat samples harboured tetracycline resistance genes and the antibiotic residue concentrations were within acceptable limits for human consumption. In the metagenomic context, most identified bacteria were of food/meat spoilage and environmental origin. The resistome analysis primarily indicated beta-lactam, tetracycline and multidrug resistance genes. Further research is needed to understand the broader implications of these findings on environmental health and antibiotic resistance.

DR SIMONE I. RICHARDSON

PROF. PENNY MOORE

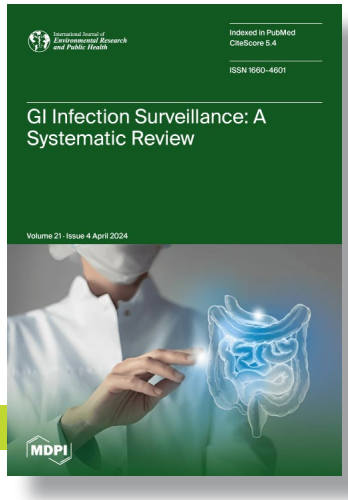
SARS-CoV-2 BA.4/5 infection triggers more cross-reactive FcγRIIIa signaling and neutralization than BA.1, in the context of hybrid immunity

Simone I Richardson, Nonkululeko Mzindle, Thopisang Motlou, Nelia P Manamela, Mieke A van der Mescht , Bronwen E Lambson, Josie Everatt , Daniel Gyamfi Amoako, Sashkia Balla, **Anne von Gottberg, Nicole Wolter,** Zelda de Beer, Talita Roma de Villiers, Annie Bodenstein , Gretha van den Berg, Fareed Abdullah, Theresa M Rossouw, Michael T Boswell, Veronica Ueckermann 7, **Jinal N Bhiman , Penny L Moore**

Journal of Virology

IMPACT FACTOR: 4.0

https://doi.org/10.1128/jvi.00678-24



ABSTRACT

SARS-CoV-2 variants of concern (VOCs) differentially trigger neutralising and antibody-dependent cellular cytotoxic (ADCC) antibodies with variable cross-reactivity. Omicron BA.4/5 was approved for inclusion in bivalent vaccination boosters, and therefore the antigenic profile of antibodies elicited by this variant is critical to understand. Here, we investigate the ability of BA.4/5-elicited antibodies following the first documented (primary) infection (n = 13) or breakthrough infection after vaccination (n = 9) to mediate neutralisation and FcγRIIIa signaling across multiple SARS-CoV-2 variants including XBB.1.5 and BQ.1. Using a pseudovirus neutralisation assay and a FcγRIIIa crosslinking assay to measure ADCC potential, we show that unlike SARS-CoV-2 Omicron BA.1, BA.4/5 infection triggers highly cross-reactive functional antibodies. Cross-reactivity was observed both in the absence of prior vaccination and in breakthrough infections following vaccination. However, BQ.1 and XBB.1.5 neutralisation and FcγRIIIa signaling were significantly compromised compared to other VOCs, regardless of prior vaccination status. BA.4/5 triggered FcγRIIIa signaling was significantly more resilient against VOCs (<10-fold decrease in magnitude) compared to neutralisation (10- to 100-fold decrease). Overall, this study shows that BA.4/5 triggered antibodies are highly cross-reactive compared to those triggered by other variants. Although this is consistent with enhanced neutralisation and FcγRIIIa signaling breadth of BA.4/5 vaccine boosters, the reduced activity against XBB.1.5 supports the need to update vaccines with XBB sublineage immunogens to provide adequate coverage of these highly antibody evasive variants.

Importance: The continued evolution of SARS-CoV-2 has resulted in a number of variants of concern. Of these, the Omicron sublineage is the most immune evasive. Within Omicron, the BA.4/5 sublineage drove the fifth wave of infection in South Africa prior to becoming the dominant variant globally. As a result this spike sequence was approved as part of a bivalent vaccine booster, and rolled out worldwide. We aimed to understand the cross-reactivity of neutralising and Fc mediated cytotoxic functions elicited by BA.4/5 infection following infection or breakthrough infection. We find that, in contrast to BA.1 which triggered fairly strain-specific antibodies, BA.4/5 triggered antibodies that are highly cross-reactive for neutralisation and antibody-dependent cellular cytotoxicity potential. Despite this cross-reactivity, these antibodies are compromised against highly resistant variants such as XBB.1.5 and BQ.1. This suggests that next-generation vaccines will require XBB sublineage immunogens in order to protect against these evasive variants.

PROF. JANUSZ T PAWĘSKA

Detection of dengue virus 1 and mammalian orthoreovirus 3, with novel reasosortments, in a South African family returning from Thailand, 2017

Petrus Jansen van Vuren, Rhys H. parry, **Janusz T. Paweska**

Viruses

IMPACT FACTOR: 3.8

https://doi.org/10.3390/v16081274

ABSTRACT

In July 2017, a family of three members, a 46-year-old male, a 45-year-old female and their 8-year-old daughter, returned to South Africa from Thailand. They presented symptoms consistent with mosquito-borne diseases, including fever, headache, severe body aches and nausea. Mosquito bites in all family members suggested recent exposure to arthropod-borne viruses. Dengue virus 1 (Genus Orthoflavivirus) was isolated (isolate no. SA397) from the serum of the 45-year-old female via intracerebral injection in neonatal mice and subsequent passage in VeroE6 cells. Phylogenetic analysis of this strain indicated close genetic identity with cosmopolitan genotype 1 DENV1 strains from Southeast Asia, assigned to major lineage K, minor lineage 1 (DENV1I_K.1), such as GZ8H (99.92%) collected in November 2018 from China, and DV1I-TM19-74 isolate (99.72%) identified in Bangkok, Thailand, in 2019. Serum samples from the 46-year-old male yielded a virus isolate that could not be confirmed as DENV1, prompting unbiased metagenomic sequencing for virus identification and characterisation. Illumina sequencing identified multiple segments of a mammalian orthoreovirus (MRV), designated as Human/SA395/SA/2017. Genomic and phylogenetic analyses classified Human/SA395/SA/2017 as MRV-3 and assigned a tentative genotype, MRV-3d, based on the S1 segment. Genomic analyses suggested that Human/SA395/SA/2017 may have originated from reassortments of segments among swine, bat, and human MRVs. The closest identity of the viral attachment protein σ1 (S1) was related to a human isolate identified from Tahiti, French Polynesia, in 1960. This indicates ongoing circulation and co-circulation of Southeast Asian and Polynesian strains, but detailed knowledge is hampered by the limited availability of genomic surveillance. This case represents the rare concurrent detection of two distinct viruses with different transmission routes in the same family with similar clinical presentations. It highlights the complexity of diagnosing diseases with similar sequelae in travelers returning from tropical areas.

PROF. JANUSZ T PAWĘSKA

MR ALAN KEMP

Attempted Transmission of Marburg Virus by Bat-Associated Fleas *Thaumapsylla breviceps* (Ischnopsyllidae: Thaumapsyllianae) to the Egyptian Rousette Bat (*Rousettus aegyptiacus*)

Janusz T Pawęska, Nadia Storm, Petrus Jansen van Vuren, Wanda Markotter, **Alan Kemp**

Viruses

IMPACT FACTOR: 3.8

https://doi.org/10.3390/v16081197

ABSTRACT

Egyptian rousette bats (ERBs) are implicated as reservoir hosts for Marburg virus (MARV), but natural mechanisms involved in maintenance of MARV in ERB populations remain undefined. A number of hematophagous ectoparasites, including fleas, parasitize bats. Subcutaneous (SC) inoculation of ERBs with MARV consistently results in viremia, suggesting that infectious MARV could be ingested by blood-sucking ectoparasites during feeding. In our study, MARV RNA was detected in fleas that took a blood meal during feeding on viremic bats on days 3, 7, and 11 after SC inoculation. Virus concentration in individual ectoparasites was consistent with detectable levels of viremia in the blood of infected host bats. There was neither seroconversion nor viremia in control bats kept in close contact with MARV-infected bats infested with fleas for up to 40 days post-exposure. In fleas inoculated intracoelomically, MARV was detected up to 14 days after intracoelomic (IC) inoculation, but the virus concentration was lower than that delivered in the inoculum. All bats that had been infested with inoculated, viremic fleas remained virologically and serologically negative up to 38 days after infestation. Of 493 fleas collected from a wild ERB colony in Matlapitsi Cave, South Africa, where the enzootic transmission of MARV occurs, all tested negative for MARV RNA. While our findings seem to demonstrate that bat fleas lack vectorial capacity to transmit MARV biologically, their role in mechanical transmission should not be discounted. Regular blood-feeds, intra- and interhost mobility, direct feeding on blood vessels resulting in venous damage, and roosting behaviour of ERBs provide a potential physical bridge for MARV dissemination in densely populated cave-dwelling bats by fleas. The virus transfer might take place through inoculation of skin, mucosal membranes, and wounds when contaminated fleas are squashed during auto- and allogrooming, eating, biting, or fighting.

PROF. ANTHONY M. SMITH

MR PHUTI SEKWADI

Metagenomics analysis of sewage for surveillance of antimicrobial resistance in South Africa

Anthony M. Smith, Masindi Ramudzulu, Patrick Munk, Baptiste J. P. Avot Kerneels C. M. Esterhuyse, Nico van Blerk, **Stanford Kwenda, Phuti Sekwadi**

PLoS One

IMPACT FACTOR: 2.9

https://doi.org/10.1371/journal.pone.0309409

ABSTRACT

Our 24-month study used metagenomics to investigate antimicrobial resistance (AMR) abundance in raw sewage from wastewater treatment works (WWTWs) in two municipalities in Gauteng Province, South Africa. At the AMR class level, data showed similar trends at all WWTWs, showing that aminoglycoside, beta-lactam, sulfonamide and tetracycline resistance was most abundant. AMR abundance differences were shown between municipalities, where Tshwane Metropolitan Municipality (TMM) WWTWs showed overall higher abundance of AMR compared to Ekurhuleni Metropolitan Municipality (EMM) WWTWs. Also, within each municipality, there were differing trends in AMR abundance. Notably, within TMM, certain AMR classes (macrolides and macrolides_streptogramin B) were in higher abundance at a WWTW serving an urban high-income area, while other AMR classes (aminoglycosides) were in higher abundance at aWWTW serving a semi-urban low income area. At the AMR gene level, all WWTWs samples showed the most abundance for the sul1 gene (encoding sulfonamide resistance). Following this, the next 14 most abundant genes encoded resistance to sulfonamides, aminoglycosides, macrolides, tetracyclines and beta-lactams. Notably, within TMM, some macrolide-encoding resistance genes (mefC, msrE, mphG and mphE) were in highest abundance at a WWTW serving an urban highincome area; while sul1, sul2 and tetC genes were in highest abundance at a WWTW serving a semi-urban low income area. Differential abundance analysis of AMR genes at WWTWs, following stratification of data by season, showed some notable variance in six AMR genes, of which blaKPC-2 and blaKPC-34 genes showed the highest prevalence of seasonal abundance differences when comparing data within a WWTW. The general trend was to see higher abundances of AMR genes in colder seasons, when comparing seasonal data within a WWTW. Our study investigated wastewater samples in only one province of South Africa, from WWTWs located within close proximity to one another. We would require a more widespread investigation at WWTWs distributed across all regions/provinces of South Africa, in order to describe a more comprehensive profile of AMR abundance across the country.

PROF. CHERYL COHEN

Demographic and pathogen characteristics of incident bacterial meningitis in infants in South Africa: A cohort study

Yannick Nkiambi Kiakuvue, Sumaya Mall, **Nelesh Govender, Anne von Gottberg, Rudzani Mashau, Susan Meiring, Cheryl Cohen**

PLoS One

IMPACT FACTOR: 2.9

https://doi.org/10.1371/journal.pone.0310528

Introduction: Bacterial meningitis is a major cause of death, with an approximate case fatality rate of 37% across all age groups in South Africa. This study aimed to describe the demographic and pathogen characteristics of incident meningitis in children aged <1 year in South Africa from 2014 through 2018, during a period when *Haemophilus influenzae* type b vaccine and pneumococcal conjugate vaccines (PCV) were both included in the expanded program on immunization (EPI).

Method: We conducted a cohort study of routine laboratory data in the National Health Laboratory Service Corporate Data Warehouse, which covers approximately 80% of the South African population. We defined a case of laboratory-confirmed bacterial meningitis as any person aged <1 year with meningitis diagnosed by culture and identification of a pathogen documented as being a common cause of meningitis in CSF. The cause-specific incidence risks were calculated by dividing the number of positive specimens in each age group and year by the corresponding mid-year population for children under 1 year old and those in the post-neonatal period (≥ 28 days to 365 days old). For children under 28 days old, the annual numbers of registered livebirths were used. We used Poisson regression to compare the incidence of meningitis by year.

Results: We identified 3575 (1.5%) cases of culture-confirmed bacterial meningitis from the 232,016 cerebrospinal fluid (CSF) specimens tested from 2014-2018. The highest number of cases were recorded in children aged <28 days (1873, 52.4%), male children (1800, 50.4%) as well as in the Gauteng Province (2014, 56.3%). *Acinetobacter baumannii* (14.9%), followed by *Klebsiella pneumoniae* (13.5%), and group B *streptococcus* (GBS) (10.7%), were the most common pathogens detected. Overall, *A. baumannii* had the highest incidence risk, occurring at 9.8 per 100,000 persons in children aged <1 year in 2018. Among neonates, *A. baumannii* peaked at 14.9 per 100,000 livebirths in 2018, while *Streptococcus pneumoniae* was most common in the post-neonatal period (≥ 28 days to 365 days old), peaking at 9.8 per 100,000 persons in 2014. There was an increase in the annual incidence of most pathogens over the study period.

Conclusion: There was an increasing trend in the annual incidence of bacterial meningitis in infants caused by most pathogens, particularly *A. baumannii*, *K. pneumoniae* and GBS. In addition to increased uptake of vaccination, prevention measures to reduce nosocomial and mother-to-child transmission of bacteria could include antenatal screening for GBS in pregnant women, rigorous hygiene in the hospital environment as well as rational antibiotic use.

DR TENDESAYI KUFA-CHAKEZHA

PROF. ADRIAN PUREN

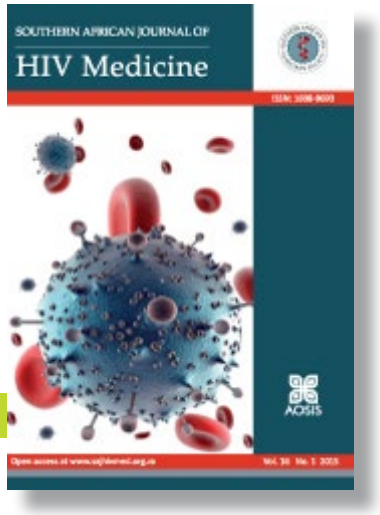
Acceptability and performance of dual HIV/syphilis testing in male circumcision clients, 2021

Kufa Tendesayi, Tobaiwa Ocean, **Cutler Ewaldé, Singh Beverley, Brukwe Zinhle**, Maseko Venessa, Pillay Erushka, Dorrell Philip, Moyo Khumbulani, Zondi Lindokuhle, Pillay Yogan, Patrick Sean, **Puren Adrian**

Southern African Journal of HIV Medicine

IMPACT FACTOR: 2.75

https://doi.org/10.4102/sajhivmed.v25i1.1571



Background: Dual HIV/syphilis testing may be an acceptable intervention to identify men with sexually transmitted infections (STIs) and at risk of HIV acquisition.

Objective: We sought to determine the acceptability, and performance of dual HIV/syphilis testing among men attending voluntary medical male circumcision (VMMC) services at six public sector facilities in Gauteng.

Method: This was a cross-sectional study at VMMC facilities. Men ≥ 18 years were enrolled. The men had (1) a questionnaire administered, (2) on-site dual HIV/syphilis testing with First Response HIV1+2/Syphilis Combo Card Test by routine lay counsellors, and (3) a blood specimen collected for centralised laboratory testing for HIV and syphilis serology. We evaluated pre-test and post-test acceptability and performance compared to serological testing.

Results: Of the 679 men analysed (median age 32.1 years), 96.7% of HIV-negative men preferred testing for HIV and syphilis simultaneously. Of the 675 men tested for syphilis, 28 (4.7%) tested positive (past or recent). In the laboratory, 43/609 (7.1%) had syphilis infection detected, with 9/609 (1.5%) having recent syphilis. There was sub-optimal sensitivity for HIV detection (90.9%; 95% confidence interval [CI]: 88.5% – 93.3%), and for past/recent syphilis (55.8%; 95% CI: 51.9% – 59.8%), improving to 88.9% (95% CI: 86.4% – 91.4%) for recent syphilis. Specificities were > 99% for HIV and syphilis (past or recent). Post-test acceptability was 96.6% and willingness to pay for future testing was 86.1%.

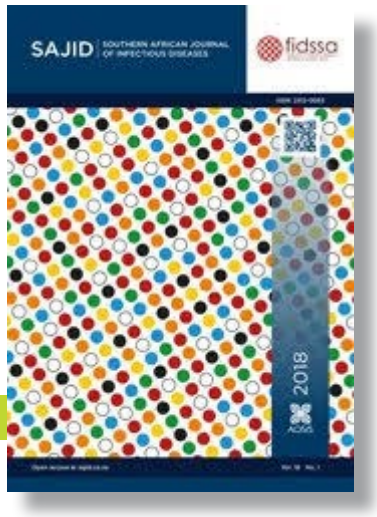
Conclusion: Dual HIV/syphilis testing was acceptable but had sub-optimal sensitivity for HIV and syphilis. Syphilis detection was adequate for recent infection.

DR FIONA ELS

DR SIBONGILE WALAZA

Comparing adults with severe SARS-CoV-2 or influenza infection: South Africa, 2016-2021

Fiona Els, Jackie Kleynhans, Nicole Wolter, Mignon du Plessis, Fahima Moosa, Stefano Tempia, **Mvuyo Makhasi**, Jeremy Nel, Halima Dawood, **Susan Meiring, Anne von Gottberg, Cheryl Cohen, Sibongile Walaza**



Southern African Journal of Infectious Diseases

IMPACT FACTOR: 2.5

https://doi.org/10.4102/sajid.v39i1.574

Background: Comparisons of the characteristics of individuals hospitalised with severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) or seasonal influenza in low-to middle-income countries with high human immunodeficiency virus (HIV) prevalence are limited.

Objectives: Determine the epidemiological differences with those hospitalised with influenza or SARS-CoV-2 infection.

Method: We investigated hospitalised individuals ≥18 years of age testing positive for seasonal influenza (2016-2019) or SARS-CoV-2 (2020-2021). We used random effects multivariable logistic regression, controlling for clustering by site, to evaluate differences among adults hospitalised with influenza or SARS-CoV-2 infection.

Results: Compared to individuals with influenza, individuals with SARS-CoV-2 infection were more likely to be diabetic (adjusted odds ratio [aOR]: 1.70, 95% confidence interval [CI]: 1.11-2.61) or die in hospital (aOR: 2.57, 95% CI: 1.61-4.12). Additionally, those with SARS-CoV-2 infection were less likely to be living with HIV (not immunosuppressed) (aOR: 0.50, 95% CI: 0.34-0.73) or living with HIV (immunosuppressed) (aOR: 0.27, 95% CI: 0.18-0.39) compared to not living with HIV and less likely to be asthmatic (aOR: 0.21, 95% CI: 0.13-0.33) rather than those living with influenza.

Conclusion: Individuals hospitalised with SARS-CoV-2 had different characteristics to individuals hospitalised with influenza before the coronavirus disease 2019 (COVID-19) pandemic. Risk factors should be considered in health management especially as we move into an era of co-circulation of SARS-CoV-2 and influenza pathogens.

Contribution: Identifying groups at high risk of severe disease could help to better monitor, prevent and control SARS-CoV-2 or influenza severe disease.

MS YAMKELA QUMBELO

DR SHAHEED V. OMAR

Extended clinical sample incubation in the cepheid Xpert MTB/XDR test sample reagent: Enhancing flexibility and workflows in high-volume laboratories

Yamkela Qumbelo, Elizabeth Kachingwe, **Shaheed Vally Omar**

Diagnostic Microbiology and Infectious Disease

IMPACT FACTOR: 2.1

https://doi.org/10.1016/j.diagmicrobio.2024.116504

ABSTRACT

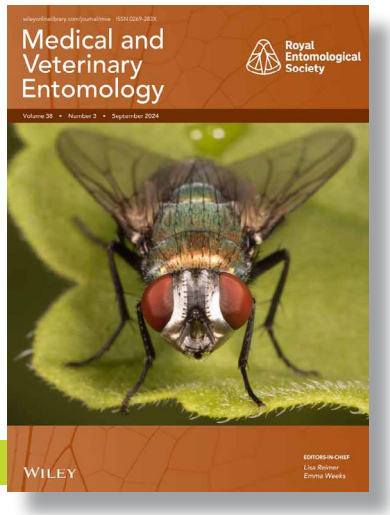
Cepheid Xpert MTB/RIF ULTRA (ULTRA) and Xpert MTB/XDR are tests for detecting Mycobacterium tuberculosis (MTB) and drug resistance. Both tests involve a sample pre-processing step using the test's sample reagent (SR). The manufacturer recommends a four-hour limit for SR-treated samples prior to testing, posing challenges for high-volume laboratories conducting both tests. Implementing the XDR test as a follow-on to ULTRA positive specimen can be challenging in high-volume laboratories due to the time constraints imposed by the manufacturer's recommendations. To address this issue, this study investigated the impact of extended sample incubation in SR for durations longer than four hours at varying temperature conditions. Pre-characterized MTB isolates with diverse drug susceptibility profiles were incubated up to 36 hours at different temperatures including room temperature (RT), 2-8°C, and -20°C and tested using Xpert MTB/XDR. The study results indicate no adverse effects on sample stability or drug susceptibility detection. This suggests extended incubation could offer flexibility for conducting both tests on a single specimen, benefiting high-throughput laboratories.

MS KAYLA P. NOETH

DR SHÜNÉ V. OLIVER

A review of historical trends in *Anopheles gambiae* Giles (Diptera: Culicidae) complex composition, collection trends and environmental effects from 2009 to 2021 in Mpumalanga province, South Africa.

Kayla P. Noeth, Maria L. Kaiser, Thabo Mashatola, Yael L. Dahan-Moss, P. Avhatakali Matamba, Belinda Spillings, **Riaan Christian**, Erika Erlank, B. Power Tshikae, **Eunice Jamesboy**, Silindile Sibambo, Busisiwe G. Nkosi, Brian T. Silawu, Lazarus J. Mkhabela, Fanuel S. Ndlovu, Thembekile P. Mgwenya, Maureen Coetzee, **Basil D. Brooke, Lizette L. Koekemoer, Givemore Munhenga, Shüné V. Oliver**



Medical and Veterinary Entomology

IMPACT FACTOR: 1.6

https://doi.org/10.1111/mve.12761

ABSTRACT:

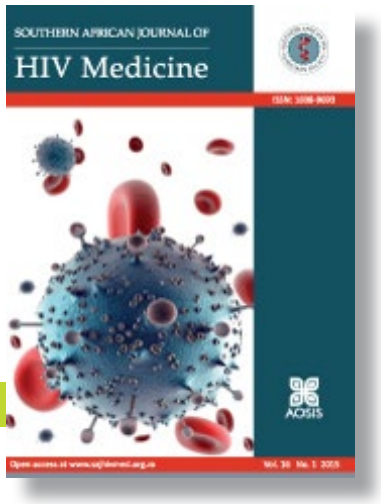
South Africa is a frontline country for malaria elimination in the southern African region. It has three malaria-endemic provinces, each with its own transmission pattern. The elimination of malaria depends, in part, on controlling and/or eliminating vectors responsible for transmission. Sustained entomological surveillance is an important factor to consider when shifting from a control to elimination framework. The Ehlanzeni district in Mpumalanga province is a key entomological sentinel surveillance area. It is one of the malaria-endemic districts in South Africa with higher rates of malaria incidences. As such, entomological data about the Anopheles gambiae Giles (Diptera: Culicidae) complex have been collected in this province over a substantial period. These data are stored in a pre-existing institutional database. An analysis of the trends that can be observed from this database has not been performed before. This retrospective (longitudinal) analysis provides a summary of the *An. gambiae* complex vector composition in this region from 2009 to 2021.

Routine surveillance data were correlated with climatic data (obtained from the NASA LaRC POWER project database) for the same period to assess the role of climatic factors in vector dynamics. This review also identifies a number of limitations in the data collection process across the sampling period and provides recommendations on how to strengthen the database going forward. The most abundant member of the *An. gambiae* complex since 2009 in the province was An. merus Dönitz followed by *An. arabiensis* Patton. Collection methods used showed that human landing catches were successful for collecting *An. arabiensis*, while pit traps were the most effective in collecting *An. merus* and *An. quadriannulatus* Theobald. The latter two species were mainly collected in spring, whereas *An. arabiensis* abundance was larger during autumn collections. Vector abundance was not significantly correlated with annual climatic data. The information gained from this database provides insights into the vector dynamics of the Ehlanzeni district of the Mpumalanga province.

DR SHAHEED V. OMAR

Missed rifampicin and isoniazid resistance by commercial molecular assays

Richards L, **Ismail F**, Nel J, **Omar Shaheed V.**



South African Medical Journal

IMPACT FACTOR: 1.5

https://doi.org/10.7196/SAMJ.2024.v114i17.1779

ABSTRACT:

The Drug-resistant tuberculosis (TB) has poor outcomes unless resistance is detected early, ideally by commercially available molecular tests. We present a case of occult multidrug-resistant TB where both rifampicin and isoniazid resistance were missed by molecular testing and were only identified by phenotypic testing.

DR JAISHREE RAMAN

The prevalence and distribution of malaria in Mpumalanga Province before and during COVID-19 (2017 - 2022)

I Kleinhans, S Mahanjana, **F Els, M Mabona,** L A Pitso, G Malatje, G Kok, **J Raman**

South African Medical Journal

IMPACT FACTOR: 1.5

https://scielo.org.za/scielo.php?script=sci_arttext&pid=S0256-95742024000900009

Background: South Africa (SA) has committed to eliminating malaria by 2028. However, the initial target was set for 2023. Additionally, the ongoing COVID-19 pandemic and the emergence of drug and insecticide resistance have been identified as potential stumbling blocks in the achievement of this goal. The impact of COVID-19 on the prevalence and distribution of malaria in SA is unclear.

Objectives: To describe the trends and distribution of malaria before and during the pandemic and its associated lockdown strategies in one of the country's malaria-endemic provinces, Mpumalanga Province.

Method: A descriptive, retrospective and cross-sectional study was conducted using Mpumalanga provincial malaria case data extracted from the provincial District Health Information System 2. The impact of COVID-19 on the prevalence and distribution of malaria was assessed in Mpumalanga Province between 2017 and 2022 using descriptive trend analysis. Malaria cases before (2017 - 2019) and post-COVID-19 (2020 - 2022) were cross-tabulated using Stata version 17. We used $\chi 2$ tests to test for significant differences, set at $p<0.05$.

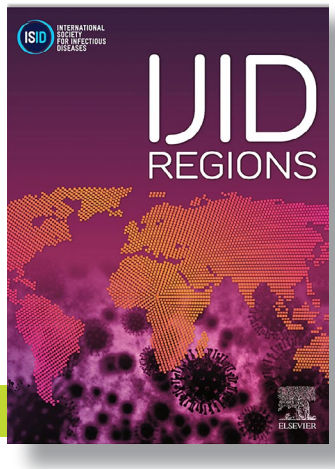
Results: During the study period, 25 380 malaria cases were reported, with the majority men (61%) >26 years old, with reported international travel, primarily to Mozambique. Limpopo Province (93%) accounted for most of the locally imported cases. Headaches and fever were the most common symptoms before and post COVID-19, while asymptomatic malaria carriage was higher during and post COVID ($p<0.05$). Prior to the pandemic reporting of the preferred treatment for uncomplicated malaria, Coartem use was at 53%, declining to 21% thereafter. Although COVID-19-related restrictions on human movement greatly reduced the malaria burden in Mpumalanga Province, the high-risk group (young mobile men) remained unchanged over the study period. Of concern were the marked reduction in the reporting of Coartem doses administered and the increased prevalence of asymptomatic carriage since 2020. The importation of malaria poses one of the biggest challenges to malaria elimination in Mpumalanga Province.

Conclusion: This study highlighted the impact of COVID-19 and its related lockdown restrictions on the delivery of malaria health services in Mpumalanga Province. If malaria elimination is to be achieved, all aspects of the malaria programme must be strengthened urgently. Additionally, the health system and cross-border collaborations must also be strengthened.

PROF. LUCILLE BLUMBERG

The 2023 - 2024 multi-source mpox outbreaks of Clade I MPXV in sub-Saharan Africa: Alarm bell for Africa and the World

Muge Cevik, Oyewale Tomori, Placide Mbala, Alessandra Scagliarini, Eskild Petersen, Nicola Low, David Heymann, Shui Shan Lee, **Lucille Blumberg**



IJID Regions

IMPACT FACTOR: 1.5

https://doi.org/10.1016/j.ijregi.2024.100397

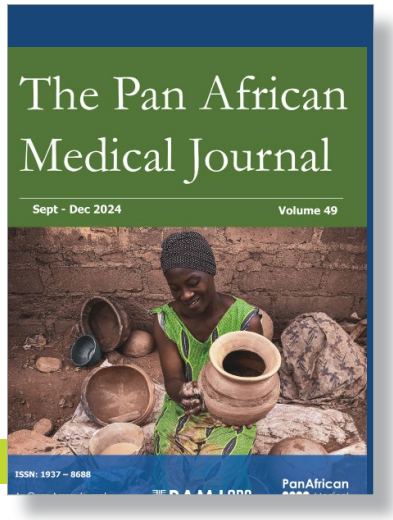
ABSTRACT:

Human mpox (formerly monkeypox) has historically received little attention until 2022, when we saw a reemergence beyond endemic countries [1,2]. In this global outbreak, mpox caused by Clade IIb monkeypox virus (MPXV) was introduced to countries that had never experienced mpox or had collectively reported fewer than ten imported cases, with few secondary cases. This global outbreak was characterised by unique patterns of person-to-person transmission [3] sustained within sexual networks among men who have sex with men (MSM) [4]. Few clinical cases in women were reported [5]. This outbreak of Clade IIb MPXV decelerated at the beginning of 2023; [6] however, in April 2024, 27 countries still reported new cases to the World Health Organization, including the growing Clade IIb outbreak in South Africa mainly affecting MSM. Meanwhile, the increasing frequency of outbreaks with Clade I MPXV in endemic regions, especially in the Democratic Republic of Congo (DRC), has become a major source of concern.

MPXV is subdivided into two distinct clades: Clade I (formerly known as the Congo Basin or Central African clade) and Clade II (formerly known as the West African clade) [7]. Clade II is subdivided into two subclades, IIa and IIb, the latter being responsible for the 2022 – 2024 ongoing multi-country outbreak having originated in Nigeria.

MS TERESA MASHUDU LAMOLA

The epidemiology of laboratory-confirmed Hepatitis B Virus infection in the general population of South Africa, 2016-2018



Mashudu Teresa Lamola, Alfred Musekiwa, Alex de Voux, **Carl Reddy,** Portia Chipo Mutevedzi

Pan African Medical Journal

IMPACT FACTOR: 1.2

https://www.panafrican-med-journal.com//content/article/48/172/full

Introduction: Despite the introduction of the Hepatitis B Virus (HBV) vaccine in South Africa in 1995, HBV remains endemic. South Africa's HBV vaccine coverage for the third dose was 71% in 2015. Information on the HBV prevalence in South Africa in recent years is limited, therefore, we estimated HBV prevalence and described annual trends.

Method: We conducted a retrospective descriptive study of data extracted from the Notifiable Medical Conditions Surveillance System, and estimated HBV prevalence per 100 000 population using the mid-year population estimates obtained from Statistics South Africa, for the 2016-2018 period.

Results: In total, 105 308 laboratory-confirmed HBV cases were analysed, of which 50.2%(53 895/105 308), 95%CI (49.9-50.5) were males. HBV prevalence for males was 34.1 in 2016, 84.1 in 2017, and 72.3 per 100 000 population in 2018. The age group with the highest HBV cases and prevalence were ages 15-49 years having 80.5%(n=84 718), with 52.2 in 2016, 123.3 in 2017, and 99.6 per 100 000 population in 2018. Between 2016 and 2018, South Africa had an overall HBV prevalence of 33.8, 82.6, and 68.8 per 100 000 population, respectively. KwaZulu-Natal province had the highest number of HBV cases with 37.8%(n=39 851) however, Mpumalanga province had the highest HBV prevalence with 73.2 in 2016, 188.8 in 2017, and 126.5 per 100 000 population in 2018.

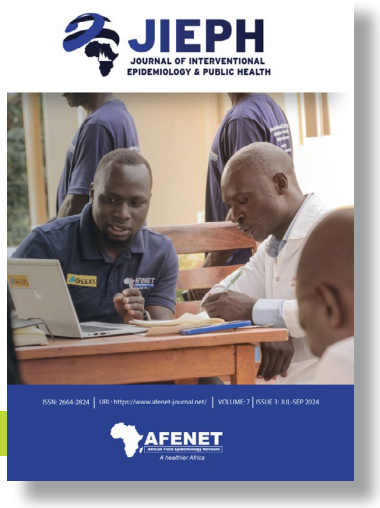
Conclusion: Our results indicated a high HBV prevalence is reflective of the group prior to the HBV vaccine introduction in South Africa.

DR FIONA ELS

DR JACKIE KLEYNHANS

An influenza outbreak in a South African mine, following the relaxation of COVID-19 pandemic restrictions, September – December 2021

Fiona Els, Mariana Khoza, Inge Kleinhans, **Hetani Mdose, Sibongile Walaza, Cheryl Cohen, Anne von Gottberg, Fahima Moosa, Mignon du Plessis, Nicole Wolter,** Chijioke Umunnakwe, Zinhle Makatini, **Genevie Ntshoe,** Andronica Shonhiwa, **Nevashan Govender,** Hugo Tempelman, Lourens Duvenhage, Charles Mandivenyi, Freda Ngobeni, **Jackie Kleynhans**



Journal of Interventional Epidemiology and Public Health

IMPACT FACTOR: N/A

https://www.afenet-journal.net/content/article/7/40/full

Introduction: In November 2021, two months after lifting COVID-19 restrictions, a cluster of laboratory-confirmed influenza cases was detected outside of the normal influenza season at a mine in South Africa. We aimed to determine factors associated with influenza infection.

Method: A suspected influenza case was an employee presenting with acute onset of ≥1 symptom (fever, cough, rhinorrhoea, sore throat, shortness of breath, loss of smell or taste, myalgia, diarrhoea, nausea, vomiting) or any employee returning from leave or newly recruited. A confirmed influenza case was any person with laboratory-confirmed influenza. We calculated the influenza attack rate among 10 030 mine employees and assessed factors associated with influenza infection from 1 September–13 December 2021 using logistic regression.

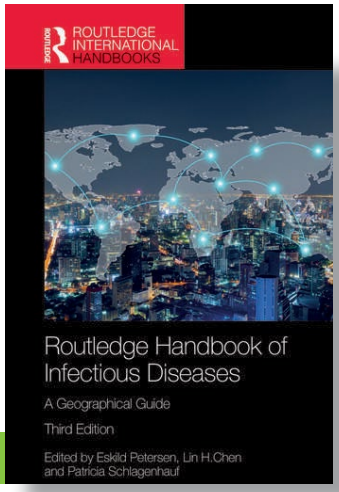
Results: There were 3,534 suspected influenza cases of which 161 tested influenza positive (influenza attack rate 1.6%, 161/10 030). Of the suspected influenza cases, 82% (2,886/3,534) were male and the mean age was 40-years. Among the confirmed cases, 87% (140/161) were male and the mean age was 39-years (IQR:31-45). Factors associated with laboratory-confirmed influenza were age 18-35-years (aOR 2.09; 95%CI 1.21-3.60) or 36-49 years (aOR 1.68, 95% CI: 1.02-2.79) vs. ≥50 years and working as an operator (aOR 3.47; 95%CI 1.23-9.75) or in engineering (aOR 3.20; 95%CI 1.03-9.98) vs. in the office. Of the 118 samples that were subtyped, 88 (74.6%) were influenza A(H1N1)pdm09.

Conclusion: Out-of-season influenza outbreaks can occur in semi-closed communities. Influenza vaccines could help reduce illness and work absenteeism. Immediate recommendations included isolation of infected individuals and more personalized education to increase adherence to non-pharmaceutical interventions.

PROF. OLGA O. PEROVIC

PROF. LUCILLE BLUMBERG

Routledge Handbook of Infectious Diseases: A Geographical Guide (3rd Edition)



Perovic O, Olga, Nectarios Papavarnavas, **Lucille Blumberg**

Routledge Handbook of Infectious Diseases, Chapter in the book, published online

IMPACT FACTOR: N/A

https://www.routledge.com/Routledge-Handbook-of-Infectious-Diseases-A-Geographical-Guide/Petersen-Chen-Schlagenhauf/p/book/9781032856612

ABSTRACT:

The new edition of this unique resource, ground on an understanding that our global world is more connected than it has ever been, provides an essential survey of infectious diseases based on both clinical presentation and geographical area of exposure. Thoroughly updated through the latest clinical data, and featuring some of the leading scholars and clinicians in the field, this is a timely and important resource for practitioners and scholars across Clinical Medicine, Epidemiology and Public Health.

DR BIANCA DA COSTA DIAS

MR FRANS RADEBE

Sexually transmitted infections surveillance among a high-risk men who have sex with men (MSM) cohort in Johannesburg, South Africa, 2023

Bianca Da Costa Dias, Mpumelelo Sibanda, Mahlape P Mahlangu, Johanna ME Venter, Lindy Gumede, Duduzile Valashiya, Maurice Greeves, **Etienne E Müller, Dumisile Maseko, Thabitha Mathega, Portia Baloyi, Tendesayi Kufa, Frans Radebe**

Public Health Bulletin South Africa

IMPACT FACTOR: N/A

https://www.phbsa.ac.za/wp-content/uploads/2024/08/sti-surveillance-among-msm-cohort-in-johannesburg-2023.pdf

ABSTRACT:

In South Africa, screening for sexually transmitted infections (STIs) among men who have sex with men (MSM) is not routinely available in the public sector, and current STI management guidelines do not include algorithms for screening or treatment of extragenital infections. This report summarises the first year of comprehensive STI surveillance among high-risk members of this key population from a single NGO partner site in Johannesburg. Participants were stratified based on the presence or absence of urethral discharge at enrolment. Among the 131 participants recruited, the prevalence of extragenital (pharyngeal and/or rectal) STIs was 35% and 41% among MSM with and without urethral discharge, respectively. Overall, 17.6% of participants were reactive for non-treponemal rapid plasma reagin (RPR) and approximately a quarter (24.4%) were reactive for HIV. *Neisseria gonorrhoeae* antimicrobial susceptibility testing revealed all isolates were susceptible to the third-generation cephalosporins, ceftriaxone, and cefixime, whilst one urethral isolate was resistant to azithromycin. These findings highlight the importance of continued and expanded aetiological STI surveillance, with a specific focus on *N. gonorrhoeae* antimicrobial susceptibility testing, amongst all high-risk members of this key population, regardless of symptoms. Furthermore, national STI management guidelines should be updated to include aetiological screening and pathogen-directed treatment recommendations for extragenital infections among MSM.

DR CHARLOTTE SRIRUTTAN-NEL

PROF. JOHN FREAN

Odyssean malaria in South Africa, 2014 -2023

Charlotte Sriruttan-Nel, Basil Brooke, Yael Dahan-Moss, Maxwell Mabona, Ramokone Ednah Baloyi, **Lucille Blumberg, John Frean**

Public Health Bulletin South Africa

IMPACT FACTOR: N/A

https://www.phbsa.ac.za/odyssean-malaria-in-south-africa-2014-2023/

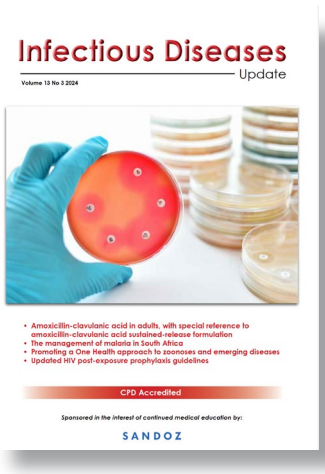
ABSTRACT:

Odyssean malaria is caused by malaria parasite-infected mosquitoes that have inadvertently travelled to non malarious areas via various transport mechanisms (sea, air, rail, road). A person/s bitten by such a mosquito may result in a case/s of malaria in the absence of travel to an endemic area. In South Africa (SA), active malaria transmission predominantly occurs in the north-eastern regions bordering on Mozambique and Zimbabwe. Local acquisition of malaria outside of these areas is unexpected, often leading to delayed diagnosis, complications and death. Malaria is a notifiable medical condition in SA, and notified cases from non-endemic areas in individuals with no recent travel history warrant further investigation of their clinical, epidemiological and entomological aspects. Here we describe odyssean malaria investigations from 2014 to 2023 in SA with which the National Institute for Communicable Diseases (NICD) assisted.

DR JAISHREE RAMAN

PROF. JOHN FREAN

The management of malaria in South Africa



Jaishree Raman, John Frean

Infectious Diseases Update

IMPACT FACTOR: N/A

ABSTRACT:

According to the World Health Organization's (WHO) latest World Malaria Report (2023), sub-Saharan Africa remains the region most affected by malaria, with four African countries, namely Nigeria, the Democratic Republic of Congo, Uganda and Mozambique, accounting for nearly 50% of the global burden[1] The WHO estimated that 233 million cases were reported from the sub-Saharan region in 2022, constituting about 94% of the global malaria total.[1] South Africa (SA) recorded around 10 000 malaria cases, with 91 deaths, in 2023. Malaria is a notifiable medical condition in SA; although there is under-notification, an analysis of these data confirms that the country's malaria-endemic districts are in Limpopo, Mpumalanga, and KwaZulu-Natal provinces, all of which share borders with neighbouring countries.

Transmission is absent in Gauteng Province, but it notifies about 19% of cases, all imported[2] South Africa is a low-transmission area, and semi- immunity to malaria does not develop with increasing age in local populations, as it does elsewhere in Africa; this means that all South Africans are at risk for severe and complicated malaria. Most cases of malaria in sub-Saharan Africa, including South Africa, are due to infection with Plasmodium falciparum, the parasite species associated with the most severe disease. Critical factors in the successful management of malaria are early recognition, urgent and accurate diagnosis, and prompt treatment with effective drugs. In this article important messages about diagnosing and treating malaria are shared, which if followed, will reduce the risk of severe illness and death from malaria. South African national guidelines for the treatment of malaria are available online[3].

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