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

SCIENCE FOCUS

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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.

MS SINENHLANHLA JIMOH

SENIOR COMMS MANANGER

EDITOR'S NOTE

Dear readers,

Welcome to the third quarter edition of the Science Focus, where we continue to bring you the latest and most insightful scientific research from our exceptional and hardworking researchers at the National Institute for Communicable Diseases.

This quarter, we produced 23 publications, and in this edition, we're thrilled to showcase some of those published as first/last authors. Among others, we're delighted to feature the remarkable work of Dr Anthony Smith, whose pioneering research has been published in the prestigious American Society for Microbiology journal. The study on Multiplex PCR Assay for Clade Typing of Salmonella enterica Serovar Enteritidis is a major breakthrough in the development of a high-quality molecular classification assay for clade typing of S. Enteritidis, which can be effectively used in public health laboratories in resource-limited settings.

As we reflect on World Malaria Day, we are honoured to feature an insightful piece published in the Tropical Medicine and Infectious Disease Journal on Malaria vector surveillance and control in an elimination setting in South Africa authored by Professor Basil Brooke. The article highlights South Africa's ambitious malaria elimination plans that are aligned with the World Health Organization's objective of achieving a malaria-free world.

We also feature an timeous study by Ms Siobhan Johnstone and Dr Juno Thomas, published in the BMC Infectious Diseases Journal, on Diagnostic Testing Practices for Diarrhoeal Cases in South African Public Hospitals. The study aims to understand biases in surveillance data and inform guidelines, diagnostic and laboratory practices to improve clinical management. The study examines diarrhoeal diagnostic practices and aetiological agents of diarrhoea in patients admitted to three South African public hospitals.

Take a deep dive into the latest research and cutting-edge solutions driving public health forward. With so many abstracts covered in this edition, you're sure to find something that piques your interest.

We hope you enjoy reading this edition of the Science Focus and look forward to bringing you more exciting and insightful scientific research from quarter 4.

On behalf of the Science Focus Editorial Team,
Sinenhlanhla Jimoh

EXCEPTIONAL RESEARCH STATISTICS

Top Published Authors for Q3 2022/2023

1

PROF CHERYL COHEN

2

DR SIBONGILE WALAZA

DR MIGNON DU PLESSIS

PROF ANNE VON GOTTBERG

3

DR WAASILA JASSAT

DR NICOLE WOLTER

DR MICHELLE J GROOME

DR SUSAN MEIRING

4

DR JINAL N BHIMAN

DR HARRY MOULTRIE

Disclaimer: Impact factor scores contained in this publication were compiled in November/December 2022.

PROF PENNY MOORE

Triggering rare HIV antibodies by vaccination

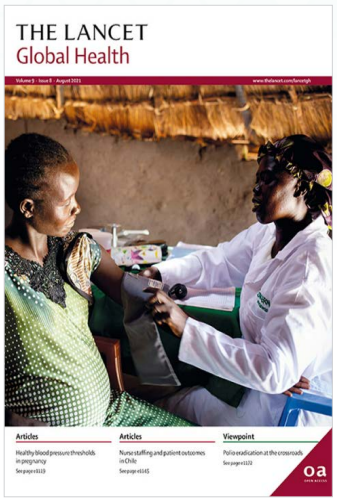
MOORE PL

Science IMPACT FACTOR: 63,235

ABSTRACT

An HIV vaccine is urgent: A recent UNAIDS report entitled "In Danger" showed that in 2021, one adolescent girl or young woman became infected with HIV every 2 min, especially in sub-Saharan Africa (1). A vaccine will likely need to elicit broadly neutralizing antibodies (bnAbs), which are able to recognize globally diverse HIV strains and can prevent HIV infection (2). However, triggering bnAbs by vaccination has proven impossible so far. A key challenge is that bnAbs rarely develop, even during infection. Furthermore, bnAb precursors (or germlines) are uncommon in human immunological repertoires. Devising vaccines specifically aimed at recruiting these rare precursors, an approach referred to as "germline targeting," has driven major immunological advances with broad applicability for other pathogens. On page 964 of this issue, Leggat et al. (3) provide clinical proof of concept for the germline-targeting approach for HIV vaccination and detailed immunological insights upon which future vaccine trials can be designed.

DR HARRY MOULTRIE



Underestimated COVID-19 mortality in WHO African region

BRADSHAW DEBBIE, DORRINGTON ROBERT, MOULTIRE TOM, GROENEWALD PAM, **MOULTRIE HARRY**

The Lancet Global Health IMPACT FACTOR: 38,927

ABSTRACT

Joseph Cabore and colleagues (August, 2022)1 developed a SEIRD model (denoting susceptible, exposed, infected, recovered, and dead) to estimate the number of SARS-CoV-2 infections across 47 countries in the WHO African region between Jan 1, 2020, and Dec 31, 2021. Although the model highlighted large variation across the region, we are concerned about the number of deaths from COVID-19 that was estimated by the model for South Africa.

The model estimated 92 118 deaths from COVID-19 in South Africa, close to the 91 061 deaths reported by the end of 2021 by the National Department of Health to WHO. The authors assumed that, because South Africa's vital statistics are considered to be well developed in terms of the SCORE health data assessment,2 the numbers of reported COVID-19 deaths are from these vital statistics and, hence, are the true numbers. However, this is not the case. The reported number of COVID-19 deaths in South Africa is provided by a new surveillance system, which was rapidly set up by the Ministry of Health at the start of the COVID-19 pandemic, and not from vital statistics, which currently lag the number of deaths by over 3 years. To read the full study please click on the following link : https://www.sciencedirect.com/science/article/pii/S2214109X22004259?via%3Dihub

DR SUSAN MEIRING

Prolonged Shedding of Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) at High Viral Loads Among Hospitalized Immunocompromised Persons Living With Human Immunodeficiency Virus (HIV), South Africa

MEIRING S, TEMPIA S, BHIMAN JN, BUYS A, KLEYNHANS J, MAKHASI M, MCMORROW M, MOYES J, QUAN V, WALAZA S, DU PLESSIS M, WOLTER N, VON GOTTBERG A, COHEN C; COVID-19 SHEDDING STUDY GROUP

Clin Infect Dis IMPACT FACTOR: 20,999

BACKGROUND

We assessed severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) RNA shedding duration and magnitude among persons living with human immunodeficiency virus (HIV, PLHIV).

METHODS

From May through December 2020, we conducted a prospective cohort study at 20 hospitals in South Africa. Adults hospitalized with symptomatic coronavirus disease 2019 (COVID-19) were enrolled and followed every 2 days with nasopharyngeal/oropharyngeal (NP/OP) swabs until documentation of cessation of SARS-CoV-2 shedding (2 consecutive negative NP/OP swabs). Real-time reverse transcription-polymerase chain reaction testing for SARS-CoV-2 was performed, and cycle-threshold (Ct) values < 30 were considered a proxy for high SARS-CoV-2 viral load. Factors associated with prolonged shedding were assessed using accelerated time-failure Weibull regression models.

RESULTS

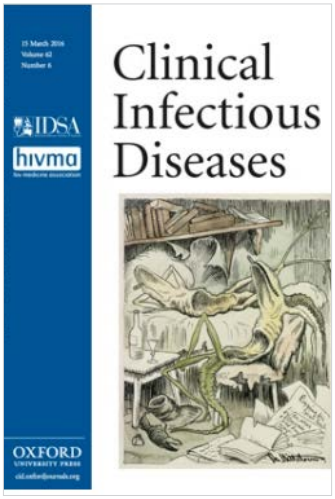
Of 2175 COVID-19 patients screened, 300 were enrolled, and 257 individuals (155 HIV-uninfected and 102 PLHIV) had > 1 swabbing visit (median 5 visits [range 2-21]). Median time to cessation of shedding was 13 days (interquartile range [IQR] 6-25) and did not differ significantly by HIV infection. Among a subset of 94 patients (41 PLHIV and 53 HIV-uninfected) with initial respiratory sample Ct-value < 30, median time of shedding at high SARS-CoV-2 viral load was 8 days (IQR 4-17). This was significantly longer in PLHIV with CD4 count < 200 cells/μL, compared to HIV-uninfected persons (median 27 days [IQR 8-43] vs 7 days [IQR 4-13]; adjusted hazard ratio [aHR] 0.14, 95% confidence interval [CI] .07-.28, P < .001), as well as in unsuppressed-HIV versus HIV-uninfected persons.

CONCLUSIONS

Although SARS-CoV-2 shedding duration did not differ significantly by HIV infection, among a subset with high initial SARS-CoV-2 viral loads, immunocompromised PLHIV shed SARS-CoV-2 at high viral loads for longer than HIV-uninfected persons. Better HIV control may potentially decrease transmission time of SARS-CoV-2.

DR WAASILA JASSAT

DR MICHELLE J GROOME



Trends in Cases, Hospitalization and Mortality Related to the Omicron BA.4/BA.5 Sub-Variants in South Africa

JASSAT W, ABDOOL KARIM SS, OZOUGWU L, WELCH R, MUDARA C, MASHA M, ROUSSEAU P, WOLMARANS M, SELIKOW A, GOVENDER N, WALAZA S, VON GOTTBERG A, WOLTER N, TERRENCE PISA P, SANNE I, GOVENDER S, BLUMBERG L, COHEN C, **GROOME MJ; FOR THE DATCOV AUTHOR GROUP**

Clinical Infectious Diseases IMPACT FACTOR: 20,999

BACKGROUND

In this study, we compared admission incidence risk and the risk of mortality in the Omicron BA.4/BA.5 wave to previous waves.

METHODS

Data from South Africa's SARS-CoV-2 case linelist, national COVID-19 hospital surveillance system, and Electronic Vaccine Data System were linked and analyzed. Wave periods were defined when the country passed a weekly incidence of 30 cases/100 000 population. In-hospital case fatality ratios (CFRs) during the Delta, Omicron BA.1/BA.2, and Omicron BA.4/BA.5 waves were compared using post-imputation random effect multivariable logistic regression models.

RESULTS

The CFR was 25.9% (N = 37 538 of 144 778), 10.9% (N = 6123 of 56 384), and 8.2% (N = 1212 of 14 879) in the Delta, Omicron BA.1/BA.2, and Omicron BA.4/BA.5 waves, respectively. After adjusting for age, sex, race, comorbidities, health sector, and province, compared with the Omicron BA.4/BA.5 wave, patients had higher risk of mortality in the Omicron BA.1/BA.2 wave (adjusted odds ratio [aOR], 1.3; 95% confidence interval [CI]: 1.2–1.4) and Delta wave (aOR, 3.0; 95% CI: 2.8–3.2). Being partially vaccinated (aOR, 0.9; 95% CI: .9–.9), fully vaccinated (aOR, 0.6; 95% CI: .6–.7), and boosted (aOR, 0.4; 95% CI: .4–.5) and having prior laboratory-confirmed infection (aOR, 0.4; 95% CI: .3–.4) were associated with reduced risks of mortality.

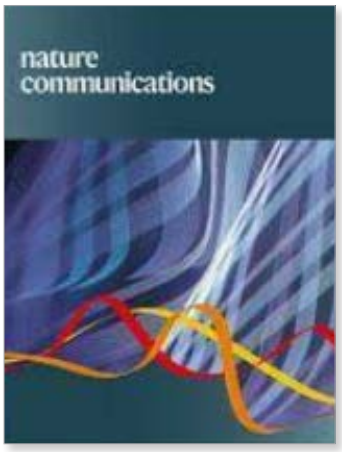
CONCLUSIONS

Overall, admission incidence risk and in-hospital mortality, which had increased progressively in South Africa's first 3 waves, decreased in the fourth Omicron BA.1/BA.2 wave and declined even further in the fifth Omicron BA.4/BA.5 wave. Mortality risk was lower in those with natural infection and vaccination, declining further as the number of vaccine doses increased.

Disclaimer: Impact factor scores contained in this publication were compiled in November/December 2022.

DR NICOLE WOLTER

PROF CHERYL COHEN



Clinical severity of SARS-CoV-2 Omicron BA.4 and BA.5 lineages compared to BA.1 and Delta in South Africa

NICOLE WOLTER , WAASILA JASSAT, SIBONGILE WALAZA, RICHARD WELCH, HARRY MOULTRIE, MICHELLE J GROOME, DANIEL GYAMFI AMOAKO, JOSIE EVERATT, JINAL N BHIMAN, CATHRINE SCHEEPERS, NAUME TEBEILA, NICOLA CHIWANDIRE, MIGNON DU PLESSIS , NEVASHAN GOVENDER , ARSHAD ISMAIL , ALLISON GLASS, KOLEKA MLISANA, WENDY STEVENS, FLORETTE K TREURNICHT, KATHLEEN SUBRAMONEY, ZINHLE MAKATINI, NEI-YUAN HSIAO, RAVEEN PARBOOSING, JEANNETTE WADULA, HANNAH HUSSEY, MARY-ANN DAVIES, ANDREW BOULLE, **CHERYL COHEN**

Nature Communications IMPACT FACTOR: 17,694

ABSTRACT

Omicron lineages BA.4 and BA.5 drove a fifth wave of COVID-19 cases in South Africa. Here, we use the presence/absence of the S-gene target as a proxy for SARS-CoV-2 variant/lineage for infections diagnosed using the TaqPath PCR assay between 1 October 2021 and 26 April 2022. We link national COVID-19 individual-level data including case, laboratory test and hospitalisation data. We assess severity using multivariable logistic regression comparing the risk of hospitalisation and risk of severe disease, once hospitalised, for Delta, BA.1, BA.2 and BA.4/BA.5 infections. After controlling for factors associated with hospitalisation and severe outcome respectively, BA.4/BA.5-infected individuals had a similar odds of hospitalisation (aOR 1.24, 95% CI 0.98–1.55) and severe outcome (aOR 0.72, 95% CI 0.41–1.26) compared to BA.1-infected individuals. Newly emerged Omicron lineages BA.4/BA.5 showed similar severity to the BA.1 lineage and continued to show reduced clinical severity compared to the Delta variant.

DR ANTHONY MARIUS SMITH

Multiplex PCR Assay for Clade Typing of *Salmonella* enterica Serovar Enteritidis

SARAH GALLICHAN, BLANCA M. PEREZ-SEPULVEDA, NICHOLAS A. FEASEY, JAY C.D. HINTON, JUNO THOMAS, **ANTHONY MARIUS SMITH**

American Society for Microbiology ("ASM") IMPACT FACTOR: 9,043

ABSTRACT

Salmonella Enteritidis is one of the most commonly reported serovars of non-typhoidal *Salmonella* causing human disease and is responsible for both gastroenteritis and invasive non-typhoidal *Salmonella* (iNTS) disease worldwide. Whole-genome sequence (WGS) comparison of *Salmonella* Enteritidis isolates from across the world have identified three distinct clades, named Global Epidemic, Central/East African and West African, all of which have been implicated in epidemics: the Global Epidemic clade was linked to poultry-associated gastroenteritis, while the two African clades were related to iNTS disease. However, the distribution and epidemiology of these clades across Africa is poorly understood because identification of these clades currently requires whole genome sequencing capacity. Here, we report a sensitive, time- and cost-effective real-time PCR assay capable of differentiating between the *Salmonella* Enteritidis clades to facilitate surveillance and to inform public health responses. The assay described here is limited to previously confirmed *S.* Enteritidis isolates.

IMPORTANCE

Challenges in the diagnosis and treatment of invasive *Salmonella* Enteritidis bloodstream infections in sub-Saharan Africa are responsible for a case fatality rate of approximately 15%. It is important to identify distinct clades of S. Enteritidis in diagnostic laboratories in the African setting to determine the different health outcomes associated with particular outbreaks. Here, we describe the development of a high-quality molecular classification assay for clade typing of S. Enteritidis that is ideal for use in public health laboratories in resource-limited settings.

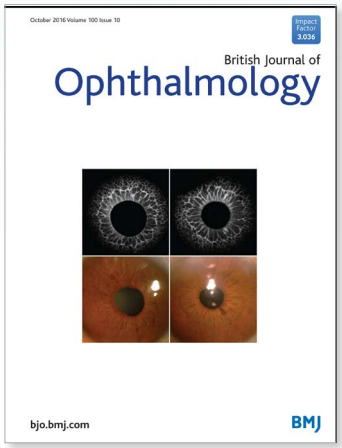
Disclaimer: Impact factor scores contained in this publication were compiled in November/December 2022.

DR MAZVITA SENGAYI-MUCHENGETI

Incidence and epidemiology of conjunctival squamous cell carcinoma in relation to the HIV epidemic in South Africa: a 25-year analysis of the National Cancer Registry (1994–2018)

STUART, KELSEY VERNON; SHEPHERD, DANIEL JOHN; LOMBARD, AMY; HOLLHUMER, ROLAND; **MUCHENGETI, MAZVITA**

British Journal of Ophthalmology IMPACT FACTOR: 5,907



AIMS

To describe the incidence and epidemiology of conjunctival squamous cell carcinoma (CSCC) in South Africa over a 25-year period (1994–2018), with particular reference to the HIV epidemic.

METHODS

Incident cases of histologically diagnosed CSCC were identified from the pathology-based South African National Cancer Registry. Crude and direct age-standardised incidence rates (ASIRs) per 100 000 persons (Segi World Standard Population) were calculated using national population statistics and compared by age, sex and ethnicity. Trends in the incidence and demographic features of CSCC were described and analysed. Incidence rates were compared with national HIV-related statistics for the same time period.

RESULTS

In total, there were 9016 reported CSCC cases (women: 56.6%, black: 86.8%, mean age: 41.5 years). The overall ASIR was 0.78 per 100 000. Two distinct epidemiological patterns were identified: (1) older white men, and (2) younger black women. There was a sixfold increase in CSCC incidence rates between 1994 and 2009 with a corresponding shift from the first to the second disease profile. Despite rising HIV seroprevalence, CSCC incidence rates have declined since 2009. A strong ecological correlation (r=0.96) between CSCC incidence and widespread antiretroviral therapy (ART) provision was identified.

CONCLUSION

This study highlights the evolving trends and disease burden of CSCC in South Africa. Widespread ART provision is ecologically correlated with declining CSCC rates over the last decade. These findings are in keeping with reported trends for other HIV-related cancers and have important implications for future incidence studies and public health policy.

MS THANDEKA MOYO-GWETE

Enhanced neutralization potency of an identical HIV neutralizing antibody expressed as different isotypes is achieved through genetically distinct mechanisms

MOYO-GWETE T, SCHEEPERS C, MAKHADO Z, KGAGUDI P, MZINDLE NB, ZIKI R, MADZORERA S, MANAMELA NP, FRANCES A, LAMBSON BE, RICHARDSON SI, MORRIS L, **MOORE PL**

Scientific Reports IMPACT FACTOR: 4,997

PROF PENNY MOORE

ABSTRACT

Antibodies with the same variable region can exist as multiple isotypes with varying neutralization potencies, though the mechanism for this is not fully defined. We previously isolated an HIV-directed IgA1 monoclonal antibody (mAb), CAP88-CH06, and showed that IgA1 and IgG3 isotypes of this antibody demonstrated enhanced neutralization compared to IgG1. To explore the mechanism behind this, hinge region and constant heavy chain (CH1) chimeras were constructed between the IgA1, IgG3 and IgG1 mAbs and assessed for neutralization activity, antibody-dependent cellular phagocytosis (ADCP) and antibody-dependent cellular cytotoxicity (ADCC). Hinge chimeras revealed that the increased neutralization potency and phagocytosis of the IgG3 isotype was attributed to its longer hinge region. In contrast, for IgA1, CH1 chimeras showed that this region was responsible both for enhanced neutralization potency and decreased ADCP, though ADCC was not affected. Overall, these data show that the enhanced neutralization potency of CAP88-CH06 IgG3 and IgA1, compared to IgG1, is achieved through distinct mechanisms. Understanding the influence of the hinge and CH1 regions on Fab domain function may provide insights into the engineering of therapeutic antibodies with increased neutralization potency.

DR NICOLETTE M DU PLESSIS

Hepatitis A virus seroprevalence among children and adolescents in a high-burden HIV setting in urban South Africa

NICOLETTE M. DU PLESSIS, AHMAD HAERI MAZANDERANI, NKENGAFAC VILLYEN MOTAZE, MAKHOSAZANE NGOBESE AND THEUNIS AVENANT

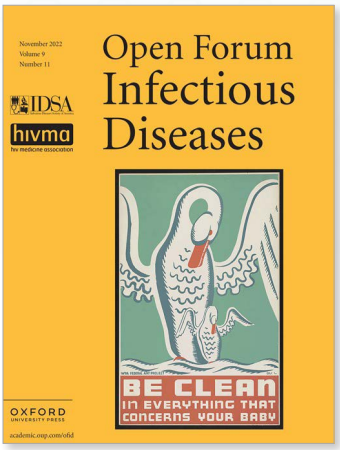
Nature Scientific Reports (Sci Rep) IMPACT FACTOR: 4,997

ABSTRACT

Hepatitis A virus (HAV) infection is one of the most important global causes of viral hepatitis. Recent reviews suggested that HAV endemicity in South Africa could shift from high to intermediate. A hospital-based HAV seroprevalence study was conducted between February 2018 and December 2019 in Pretoria, South Africa. Systematic sampling was performed on children and adolescents (1–15 years) who attended outpatient services. Participants with a known HIV status and valid HAV serology results were included. Of the 1220 participants, the median age was 7 years (IQR: 4–11), with 648 (53.11%) males and 572 (46.89%) females. Of 628 (51.48%) HIV-infected participants, most (329, 71.83%) were both immunologically and virologically controlled or had low-level viremia (74, 16.16%). Almost three-quarters (894, 73.28%) were living in formal dwellings, and just over half (688, 56.39%) had access to clean water sources inside the house. Increasing age was associated with testing HAV IgG-positive (OR 1.25; 95% CI 1.20–1.30, $p < 0.001$), with 19.8% of participants one year of age compared with 86.7% of participants 15 years of age. This study suggests that South Africa has an intermediate HAV seroprevalence, with rates < 90% by 10 years of age (68.6%). Increased age and informal dwellings are statistically associated with HAV seropositivity, while HIV status does not significantly influence HAV seropositivity.

Disclaimer: Impact factor scores contained in this publication were compiled in November/December 2022.

PROF CHERYL COHEN



Effectiveness of Influenza Vaccination of Pregnant Women for Prevention of Maternal and Early Infant Influenza-Associated Hospitalizations in South Africa: A Prospective Test-Negative Study

MARTA C NUNES, SIBONGILE WALAZA, SUSAN MEIRING, HEATHER J ZAR, GARY REUBENSON, MEREDITH MCMORROW, STEFANO TEMPIA, LIZA ROSSI, RAPHAELA ITZIKOWITZ, KATE BISHOP, AZWIFARWI MATHUNJWA, AMY WISE, FLORETTE K TREURNICHT, ORIENKA HELLFERSCEE, MATT LAUBSCHER, NATALI SERAFIN, CLARE L CUTLAND, SHABIR A MADHI, **CHERYL COHEN**

Open Forum Infectious Diseases IMPACT FACTOR: 4,433

BACKGROUND

Influenza vaccination during pregnancy reduces influenza-associated illness in the women and their infants, but effectiveness estimates against influenza-associated hospitalization are limited and lacking from settings with high human immunodeficiency virus (HIV) infection prevalence. We assessed the effect of maternal vaccination in HIV-uninfected women and women with HIV in preventing influenza-associated hospitalizations in infants and the women.

METHODS

During 2015–2018, influenza vaccination campaigns targeting pregnant women were augmented at selected antenatal clinics; these were coupled with prospective hospital-based surveillance for acute respiratory or febrile illness in infants aged <6 months and cardiorespiratory illness among pregnant or postpartum women. Vaccine effectiveness (VE) was assessed using a test-negative case-control study.

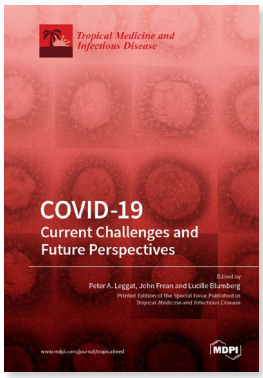
RESULTS

Overall, 71 influenza-positive and 371 influenza-negative infants were included in the analysis; mothers of 26.8% of influenza-positive infants were vaccinated during pregnancy compared with 35.6% of influenza-negative infants, corresponding to an adjusted VE (aVE) of 29.0% (95% confidence interval [CI], −33.6% to 62.3%). When limited to vaccine-matched strains, aVE was 65.2% (95% CI, 11.7%–86.3%). For maternal hospitalizations, 56 influenza-positive and 345 influenza-negative women were included in the analysis, with 28.6% of influenza-positive women being vaccinated compared with 38.3% of influenza-negatives, for an aVE of 46.9% (95% CI, −2.8% to 72.5%). Analysis restricted to HIV-uninfected women resulted in 82.8% (95% CI, 40.7%–95.0%) aVE. No significant aVE (−32.5% [95% CI, −208.7% to 43.1%]) was detected among women with HIV.

CONCLUSIONS

Influenza vaccination during pregnancy prevented influenza-associated hospitalizations among young infants when infected with vaccine strains and among HIV-uninfected women.

PROF GAYLE G. SHERMAN



Infant HIV Testing Amid the COVID-19 Pandemic and Evolving PMTCT Guidelines in Johannesburg, South Africa

COCEKA N. MNYANI, ANDOMEI SMIT AND **GAYLE G. SHERMAN**

Trop. Med. Infect. Dis IMPACT FACTOR: 3,711

BACKGROUND

The COVID-19 pandemic impacted HIV programmes with the diversion of resources and lockdown measures. We assessed the impact of COVID-19 on infant HIV diagnosis in the context of updated 2019 prevention of mother-to-child transmission of HIV (PMTCT) guidelines in Johannesburg, South Africa.

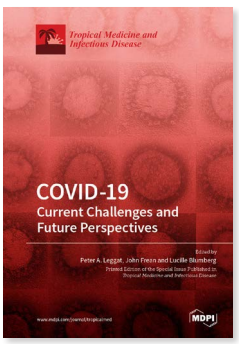
METHODS

HIV PCR data for children <2 years were extracted from the National Health Laboratory Service database from October 2018 to September 2021, inclusive. Trends in the total number of tests performed and the total number of children with HIV diagnosed, stratified by age, were determined to assess the effect of different COVID-19 lockdown levels and updated guidelines. Results: When comparing three 12-month periods ending September 2019–2021, respectively, the total number of HIV PCR tests performed increased (from 41 879 to 47 265 to 56 813), and the total number of children with HIV decreased (from 659 to 640 to 620), year-on-year. There was a substantial increase in 6-month testing in response to updated guidelines. Excluding 6-month testing, the year-on-year increase in total tests was maintained with birth and 10-week testing closely approximating total live births to women living with HIV. A decrease in the total number of children with HIV diagnosed was noted in Q2 2020, coinciding with the most restrictive lockdown, followed by a rebound in cases.

CONCLUSIONS

Despite the restrictions and diversion of resources associated with COVID-19, there was a successful implementation of PMTCT guideline updates and minimal disruption to infant HIV testing. However, much work remains in order to achieve the elimination of mother-to-child transmission of HIV.

PROF BASIL BROOKE



Malaria Vector Surveillance and Control in an Elimination Setting in South Africa

BASIL D. BROOKE, WITS RESEARCH INSTITUTE FOR MALARIA, FACULTY OF HEALTH SCIENCES, UNIVERSITY OF THE WITWATERSRAND, JOHANNESBURG 2050, SOUTH AFRICA

Tropical Medicine and Infectious Disease IMPACT FACTOR: 3,711

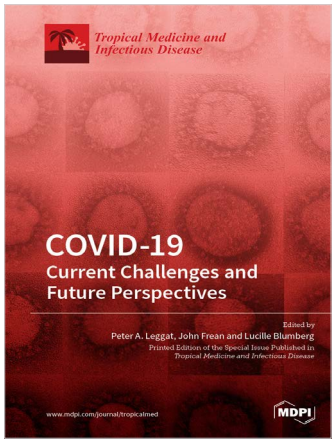
ABSTRACT

South Africa's malaria elimination plans are aligned to the World Health Organization's aim for a malaria-free world and include specific objectives within a specified time frame. These are proving difficult to achieve owing to the sporadic nature of locally acquired malaria in some affected districts, while other districts that were endemic for the disease are either malaria-free or very close to that goal. The WHO also specifies that continued measures to prevent the re-establishment of transmission are required in areas where elimination has been achieved. These measures include routine malaria vector surveillance in endemic districts that are free of malaria to assess receptivity and risk of reintroduction, which may prove difficult to justify in the face of competing public health priorities and limited resources. These issues are discussed here within the framework of vector surveillance and control and include recommendations on how they can be addressed going forward.

Disclaimer: Impact factor scores contained in this publication were compiled in November/December 2022.

MS RUTH MOGOKOTLENG

DR SABELLE JALLOW



A Retrospective Analysis of Culture-Confirmed Enterococci Bloodstream Infections in South Africa, 2016–2020: A Cross-Sectional Study

MOGOKOTLENG, R, ISMAIL, H, PEROVIC, O, **JALLOW, S**

Tropical Medicine and Infectious Disease IMPACT FACTOR: 3,711

BACKGROUND

The emergence of multidrug resistance enterococci is a major public health concern. This study aimed to determine the prevalence and antimicrobial resistance of enterococci isolated from blood cultures over a five-year period (2016–2020) at public hospitals in South Africa.

METHODS

A retrospective analysis of clinical enterococci isolated from bloodstream infection samples at the South African public hospitals was conducted. The ESKAPE dataset from January 2016 to December 2020 was obtained from the central data warehouse (CDW) at the National Health Laboratory Service (NHLS).

RESULTS

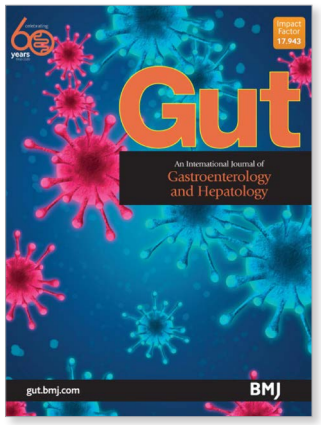
Following de-duplication, a total of 130,352/306,592 organisms isolated from blood cultures were identified as ESKAPE pathogens. In this study, K. pneumoniae (25%; 33,082/130,352), was the most frequently isolated pathogen from blood cultures, followed by S. aureus (23%; 29,922/130,352) and enterococci (16%; 21,339/130,352). Of the enterococci cases, about 43% (9132/21,339) of cases were from the infants aged (<1-year old) and 32% (6745/21,339) from the adult patients. No changes observed in vancomycin, teicoplanin, and linezolid susceptibility; however, E. faecium and E. faecalis blood culture isolates remained highly susceptible (>97%) to these antibiotics.

CONCLUSIONS

The current study revealed a significant increase of E. faecalis and E. faecium blood culture isolates as compared to the previous national ESKAPE data. Low vancomycin resistance was observed. Continuous monitoring of antimicrobial resistant Enterococcus species is warranted in South Africa.

MS SIOBHAN L JOHNSTONE

DR JUNO THOMAS



Diagnostic testing practices for diarrhoeal cases in South African public hospitals

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BMC Infect Dis IMPACT FACTOR: 3,669

BACKGROUND

Stool samples submitted for diagnostic testing represent a proportion of diarrhoeal cases seeking healthcare, and an even smaller proportion of diarrhoeal cases in the community. Despite this, surveillance relies heavily on these laboratory results. This study described diarrhoeal diagnostic practices and aetiological agents of diarrhoea in patients admitted to three South African public hospitals in order to understand biases in surveillance data, and inform guidelines, diagnostic and laboratory practices to improve clinical management.

METHODS

A doctors' survey was conducted to determine sample submission, diarrhoeal treatment and barriers to submitting samples for testing. Results for all samples submitted for routine diagnostics were obtained from the NHLS Central Data Warehouse. An enhanced surveillance study enrolled patients with acute diarrhoea at the same hospitals over the same period. Differences between routine culture results and molecular testing from the surveillance study were described.

RESULTS

Stool samples were seldom submitted for diagnostic testing (median of 10% of admitted cases). Current diagnostic guidelines were not useful, hence most doctors (75.1%) relied on their own clinical judgement or judgement of a senior clinician. Although most doctors (90.3%) agreed that diagnostics were helpful for clinical management, they reported patients being unwilling to provide samples and long laboratory turnaround times. Routine diagnostic data represent cases with chronic diarrhoea and dysentery since doctors are most likely to submit specimens for these cases. Pathogen yield (number of pathogens detected for samples tested for specific pathogens) was significantly higher in the surveillance study, which used molecular methods, than through routine diagnostic services (73.3% versus 8.2%, $p < 0.001$), including for viruses (48.9% versus 2.6%, $p < 0.001$), bacteria (40.1% versus 2.2%, $p < 0.001$) and parasites (16.2% versus 3.6%, $p < 0.001$). Despite viruses being commonly detected in the surveillance study, viral testing was seldom requested in routine diagnostic investigations.

CONCLUSIONS

Comprehensive diagnostic and treatment guidelines are required for diarrhoeal diseases. These guidelines should be informed by local epidemiological data, where diagnostic testing is reserved for cases most likely to benefit from specific treatment. Optimisation of current diagnostic processes and methods are required for these cases, specifically in terms of minimising turnaround times while maximising diagnostic acumen.

Disclaimer: Impact factor scores contained in this publication were compiled in November/December 2022.

DR JACQUELINE WEYER

Monkeypox: Is the 'vacated niche' being filled?

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AOSIS: African Journal of Laboratory Medicine IMPACT FACTOR: n/a

ABSTRACT

Could the monkeypox or cowpox virus emerge from its natural reservoir to become a fully human-adapted pathogen, occupying the ecological niche vacated by the eradication of smallpox? We cannot know the answer, but doubt about the possibility should be tempered by the realisation that smallpox itself must once have been a zoonosis. To read the full study please click on the following link: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC9772718/

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