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Division of the National Health Laboratory Service

SCIENCE FOCUS

A quarterly nexus of scientific insights

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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.

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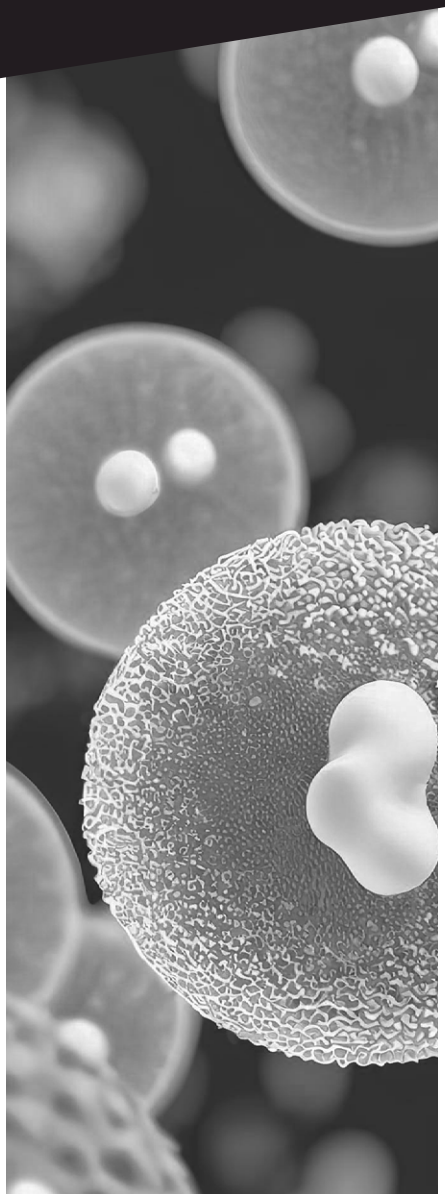
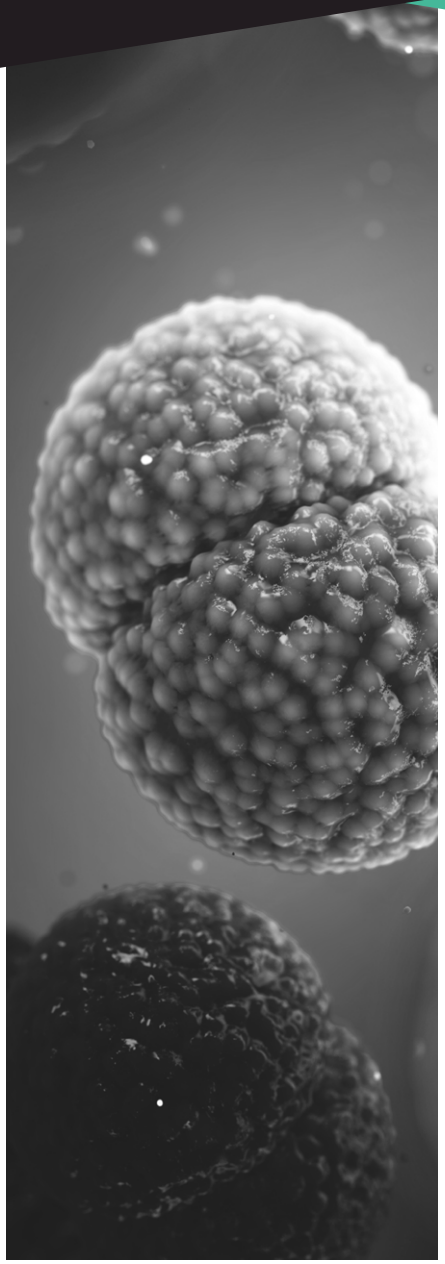
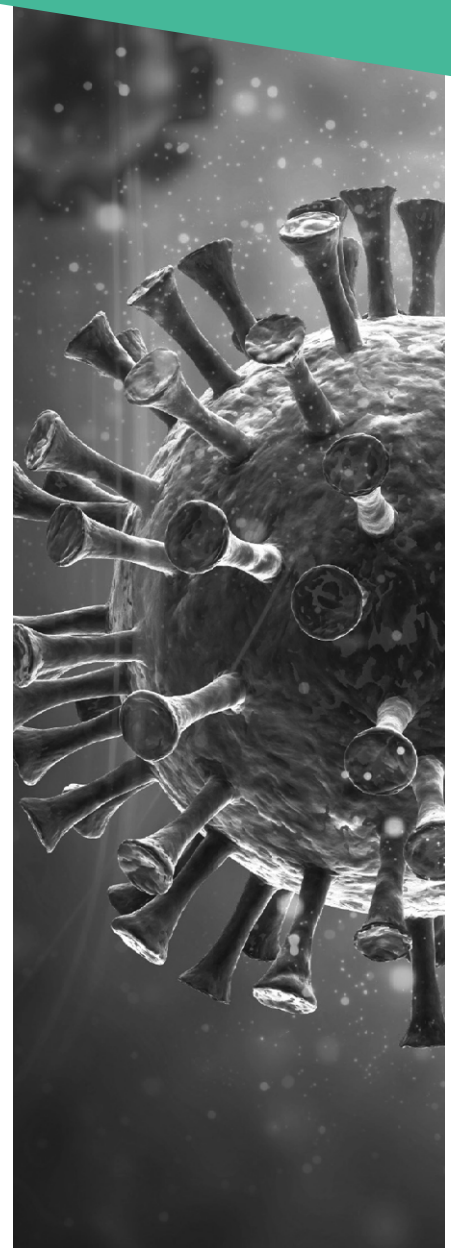






MS SINENHLANHLA JIMOH
SENIOR COMMUNICATIONS MANANGER

Forge Ahead In Excellence

As we close this calendar year with this captivating instalment of the Science Focus under my stewardship, I am deeply grateful to the Science Focus Team for their unwavering support and dedication throughout my time here. Together, we have made Science Focus a leading source of scientific information for the broader community.

This 27th edition embarks on an enlightening journey through the intricate world of infectious diseases, public health interventions, and the genetic blueprints that underpin public health. The studies presented in this issue, primarily conducted in South Africa, offer invaluable insights into the epidemiology, prevention, and treatment of a diverse array of ailments.

To our readers, I hope you enjoy immersing yourselves in the diverse research papers contained in this calendar year's final edition, which focuses on infectious disease control in sub-Saharan Africa, highlighting the epidemiology of diarrhoea in HIV patients, imported cholera cases, malaria control priorities, and rabies immunoglobulin neutralisation. The studies underscore the importance of collaborative research and evidence-based interventions to overcome these diseases.

"I am incredibly proud of the work the NICD Community has accomplished over the years, and I am confident that the Science Focus will continue to flourish in the years to come".

Forge ahead in excellence; from me, it's bon voyage.

With heartfelt gratitude,
Sinenhlanhla Jimoh
Senior Communications Manager

EXCEPTIONAL RESEARCH STATISTICS

Top Published Authors

1 PROF NELESH GOVENDER

2 PROF CHERYL COHEN

3 PROF ANNE VON GOTTBERG

4 DR NICOLE WOLTER

5 DR JINAL BHIMAN

Disclaimer: Impact factor scores contained in this publication were compiled in August /September 2023.

PROF NELESH GOVENDER

Impact of prior cryptococcal antigen screening on in-hospital mortality in cryptococcal meningitis or fungaemia among HIV-seropositive individuals in South Africa: a cross-sectional observational study

Olivier Paccoud, Liliwe Shuping, Rudzani Mashau, Greg Greene, Vanessa Quan, Susan Meiring, Nelesh P Govender; for GERMS-SA

Clin Microbiol Infect

IMPACT FACTOR: 14,2

https://doi.org/10.1016/j.cmi.2023.04.016

OBJECTIVES

We investigated whether patients with (CM) or fungaemia detected through South Africa's laboratory cryptococcal antigen (CrAg) screening programme had better outcomes than those presenting directly to the hospital.

METHODS

We compared 14-day in-hospital case-fatality ratios of HIV-seropositive individuals with CD4 counts below 100 cells/μL and laboratory-confirmed CM/fungaemia from 2017-2021, with or without evidence of a positive blood CrAg test within 14 days prior to diagnosis. We evaluated whether the impact of prior CrAg screening on mortality varied according to the study period (pre-COVID-19: before March 2020 vs. COVID-19: after March 2020).

RESULTS

Overall, 24.5% (830/3390) of patients had a prior positive CrAg test within 14 days of diagnosis. CrAg-screened patients were less likely to have an altered mental status at baseline than non-CrAg-screened patients (38.1% [296/776] vs. 42.6% [1010/2372], p = 0.03), and had a lower crude 14-day case-fatality ratio (24.7% [205/830] vs. 28.3% [724/2560]; OR, 0.83 [95% CI, 0.69-0.99]; p = 0.045). Previous CrAg screening was associated with a greater reduction in the crude 14-day mortality during the COVID-19 period (OR, 0.64 [0.47-0.87]; p = 0.005) compared with before (OR, 0.95 [0.76-1.19]; p = 0.68). After adjustment, previous CrAg screening within 14 days was associated with increased survival only during the COVID-19 period (adjusted OR, 0.70 [0.51-0.96]; p = 0.03).

DISCUSSION

Previous CrAg screening was associated with a survival benefit in patients hospitalized with CM/fungaemia during the COVID-19 period, with fewer patients having an altered mental status at baseline, suggesting that these patients may have been diagnosed with cryptococcosis earlier.

DR ANTHONY SMITH

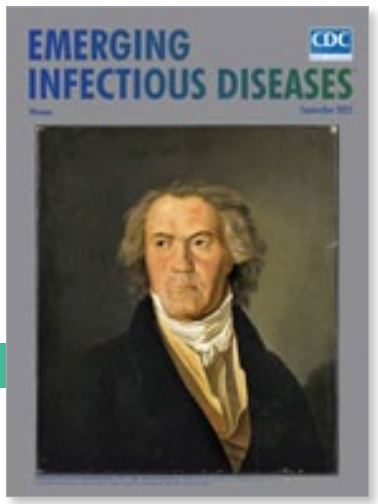
Imported cholera cases, South Africa, 2023

Smith AM, Sekwadi P, Erasmus LK, Lee CC, Stroika SG, Ndzabandzaba S, Alex V, Nel J, Njamkepo E, **Thomas J,** Weill F-X. 2023

Emerging Infectious Diseases

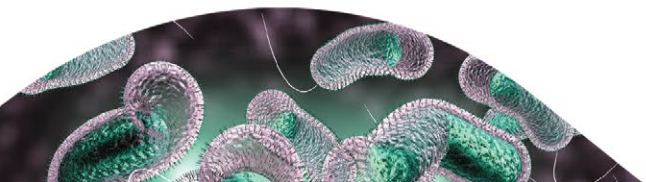
IMPACT FACTOR: 11,8

https://doi.org/10.3201/eid2908.230750



ABSTRACT

Since February 2022, Malawi has experienced a cholera outbreak of >54,000 cases. We investigated 6 cases in South Africa and found that isolates linked to the outbreak were Vibrio cholerae O1 serotype Ogawa from seventh pandemic El Tor sublineage AFR15, indicating a new introduction of cholera into Africa from south Asia.



MS LILIWE SHUPING

PROF NELESH GOVENDER

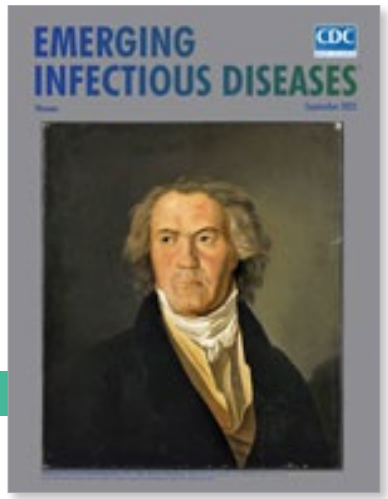
High prevalence of candida auris colonizationduring protracted neonatal unit outbreak, South Africa

Shuping L, Maphanga TG, Naicker SD, Mpembe R, Ngoma N, Velaphi S, Nakwa F, Wadula J, Jaglal P, **Govender NP.**

Emerg Infect Dis

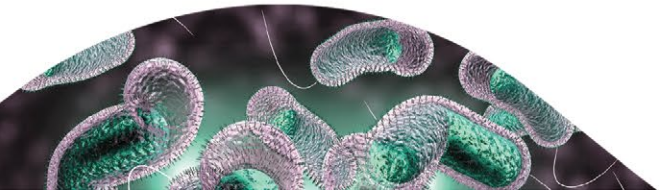
IMPACT FACTOR: 11,8

https://doi.org/10.3201/eid2909.230393



ABSTRACT

One third of patients were colonized by Candida auris during a point-prevalence survey in a neonatal unit during an outbreak in South Africa. The sensitivity of a direct PCR for rapid colonization detection was 44% compared with culture. The infection incidence rate decreased by 85% after the survey and implementation of isolation/cohorting.



MS DIKELEDI KEKANA

PROF NELESH GOVENDER

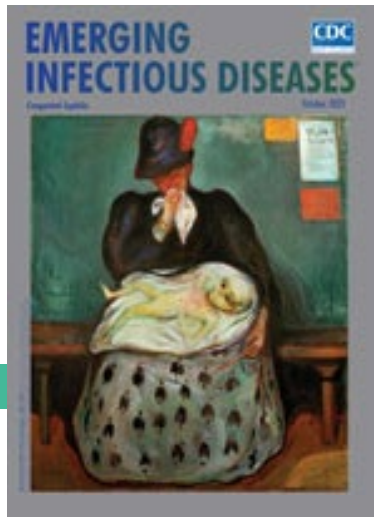
Candida auris clinical isolates associated with outbreak in neonatal unit of tertiary academic hospital, South Africa.

Kekana D, Naicker SD, Shuping L, Velaphi S, Nakwa FL, Wadula J, **Govender NP; for GERMS-SA1.**

Emerg Infect Dis

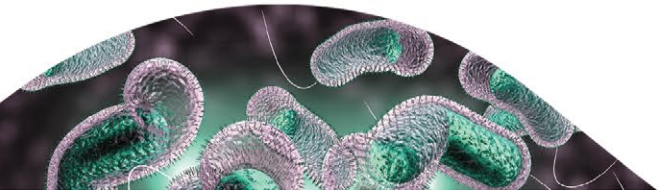
IMPACT FACTOR: 11,8

https://doi.org/10.3201/eid2910.230181



ABSTRACT

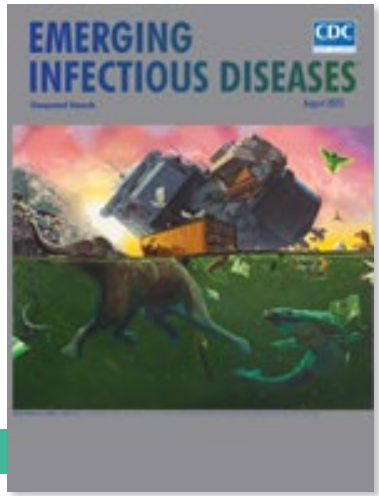
Candida auris was first detected at a university-affiliated hospital in Johannesburg, South Africa, in 2009. We used whole-genome sequencing to describe the molecular epidemiology of C. auris in the same hospital during 2016-2020; the neonatal unit had a persistent outbreak beginning in June 2019. Of 287 cases with culture-confirmed C. auris infection identified through laboratory surveillance, 207 (72%) had viable isolates and 188 (66%) were processed for whole-genome sequencing. Clade III (118/188, 63%) and IV (70/188, 37%) isolates co-circulated in the hospital. All 181/188 isolates that had a fluconazole MIC >32 µg/mL had ERG11 mutations; clade III isolates had VF125AL substitutions, and clade IV isolates had K177R/N335S/E343D substitutions. Dominated by clade III, the neonatal unit outbreak accounted for 32% (91/287) of all cases during the study period. The outbreak may have originated through transmission from infected or colonized patients, colonized healthcare workers, or contaminated equipment/environment.



PROF NELESH GOVENDER

Outbreak of NDM-1- and OXA-181-producing klebsiella pneumoniae bloodstream infections in a neonatal unit, South Africa

Magobo RE, **Ismail H,** Lowe M, Strasheim W, **Mogokotleng R, Perovic O,** Kwenda S, Ismail A, Makua M, Bore A, Phayane R, Naidoo H, Dennis T, Ngobese M, Wijnant W, **Govender NP; for Baby GERMS-SA1.**



Emerg Infect Dis

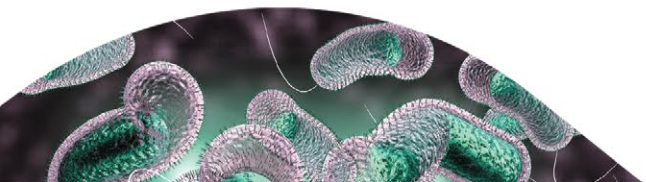
IMPACT FACTOR: 11,8

https://doi.org/10.3201/eid2908.230484

ABSTRACT

After an increase in carbapenem-resistant Klebsiella pneumoniae (CRKP) bloodstream infections and associated deaths in the neonatal unit of a South Africa hospital, we conducted an outbreak investigation during October 2019–February 2020 and cross-sectional follow-up during March 2020–May 2021. We used genomic and epidemiologic data to reconstruct transmission networks of outbreak-related clones. We documented 31 cases of culture-confirmed CRKP infection and 14 deaths. Two outbreak-related clones (blaNDM-1 sequence type [ST] 152 [n = 16] and blaOXA-181 ST307 [n = 6]) cocirculated.

The major clone blaNDM-1 ST152 accounted for 9/14 (64%) deaths. Transmission network analysis identified possible index cases of blaOXA-181 ST307 in October 2019 and blaNDM-1 ST152 in November 2019. During the follow-up period, 11 new cases of CRKP infection were diagnosed; we did not perform genomic analysis. Sustained infection prevention and control measures, adequate staffing, adhering to bed occupancy limits, and antimicrobial stewardship are key interventions to control such outbreaks.



DR WENLONG CARL CHEN

Genome-wide association study of esophageal squamous cell cancer identifies shared and distinct risk variants in African and Chinese populations

Chen WC, Brandenburg JT, Choudhury A, **Hayat M,** Sengupta D, Swiel Y, **Babb de Villiers C,** Ferndale F, Aldous C, Soo CS, Lee S, Curtis C, Newton R, Waterboer T, Sitas F, Bradshaw D, Abnet CC, Ramsay M, Parker MI, **Singh E,** Lewis CM, Mathew CG

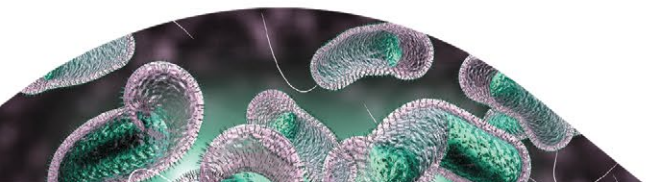
The American Journal of Human Genetics

IMPACT FACTOR: 11,04

https://doi.org/10.1016/j.ajhg.2023.08.007

ABSTRACT

Esophageal squamous cell carcinoma (ESCC) has a high disease burden in sub-Saharan Africa and has a very poor prognosis. Genome-wide association studies (GWASs) of ESCC in predominantly East Asian populations indicate a substantial genetic contribution to its etiology, but no genome-wide studies have been done in populations of African ancestry. Here, we report a GWAS in 1,686 African individuals with ESCC and 3,217 population-matched control individuals to investigate its genetic etiology. We identified a genome-wide-significant risk locus on chromosome 9 upstream of FAM120A (rs12379660, p = 4.58 × 10-8, odds ratio = 1.28, 95% confidence interval = 1.22-1.34), as well as a potential African-specific risk locus on chromosome 2 (rs142741123, p = 5.49 × 10-8) within MYO1B. FAM120A is a component of oxidative stress-induced survival signals, and the associated variants at the FAM120A locus co-localized with highly significant cis-eQTLs in FAM120AOS in both esophageal mucosa and esophageal muscularis tissue. A trans-ethnic meta-analysis was then performed with the African ESCC study and a Chinese ESCC study in a combined total of 3,699 ESCC-affected individuals and 5,918 control individuals, which identified three genome-wide-significant loci on chromosome 9 at FAM120A (rs12379660, pmeta = 9.36 × 10-10), chromosome 10 at PLCE1 (rs7099485, pmeta = 1.48 × 10-8), and chromosome 22 at CHEK2 (rs1033667, pmeta = 1.47 × 10-9). This indicates the existence of both shared and distinct genetic risk loci for ESCC in African and Asian populations. Our GWAS of ESCC conducted in a population of African ancestry indicates a substantial genetic contribution to ESCC risk in Africa.



MR SIZEKA MASHELE

Risk factors for breast cancer among women in Ekurhuleni Metropolitan Municipality, Gauteng province of South Africa, 2017–2020: a case-control study

Sizeka A Mashele, Thembekile B Zwane, Lazarus Kuonza, Mazvita M Muchengeti, Lactatia Motsuku

ecancermedicalscience

IMPACT FACTOR: 9,8

https://doi.org/10.3332/ecancer.2023.1593

INTRODUCTION

Breast cancer (BC) is the most common cancer among women in South Africa (SA), with an age-standardised incidence rate of 52.6 and an age-standardised mortality rate of 16.0 per 100,000 population. There is a paucity of evidence on the risk factors for BC among women of all races in SA. Given the rising prevalence of BC in SA, literature-based evidence is critical for the appropriate dissemination of preventative measures. This study aimed to identify the risk factors associated with the development of BC among women in Ekhuruleni Metropolitan Municipality.

METHODS

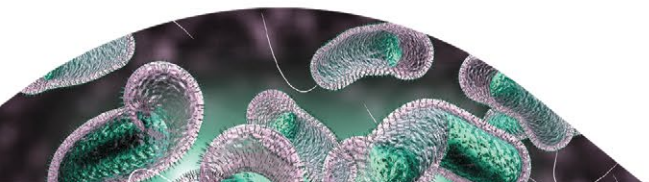
An unmatched case-control study was conducted from 1 January 2017 to 31 December 2020 using secondary data extracted from the Ekurhuleni Population-Based Cancer Registry. Unconditional multivariable logistic regression analysis was carried out using the adjusted odds ratio (aOR). The variables race, employment, human immunodeficiency virus (HIV), smoking and alcohol status were included in the multivariable logistic regression model while the model was adjusted for age.

RESULTS

A total of 2,217 cases and 851 controls were enrolled in the study. The mean age (±SD) in years was 55.7 (±15.2). The White population group, being self-employed and being HIV positive was significantly associated with reduced odds of BC development. HIV-positive women were 61% less likely to have BC than women who were HIV-negative (aOR 0.39; 95% confidence interval (CI): 0.27-0.57). White women were 65% less likely to have BC than women of other races (aOR 0.35; 95% CI: 0.29-0.43). Self-employed women were 59% less likely to have BC than women who were formally employed (aOR 0.41; 95% CI: 0.18-0.97). No evidence of association was observed between tobacco smoking and BC as well as alcohol consumption and BC.

CONCLUSION

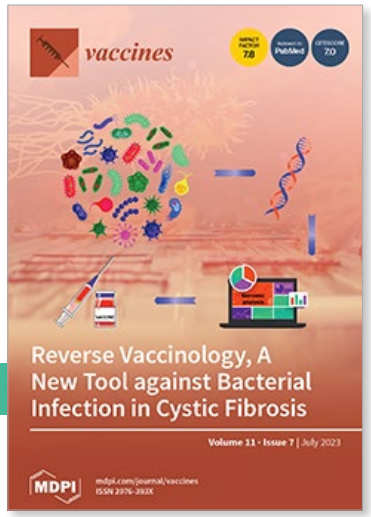
There was a 65% reduction in BC risk among White women compared to other races. HIV-positive women demonstrated a 61% lower likelihood of BC while self-employed women showed a 59% reduced risk of developing BC. These findings suggest that being White, self-employed or HIV-positive may provide some protection against BC. However, additional research is needed to validate these results and establish the underlying reasons behind these associations.



DR JESSICA COERTSE

Comparative neutralization activity of commercial rabies immunoglobulin against diverse lyssaviruses

Jessica Coertse, Natalie Viljoen, Jacqueline Weyer, Wanda Markotter



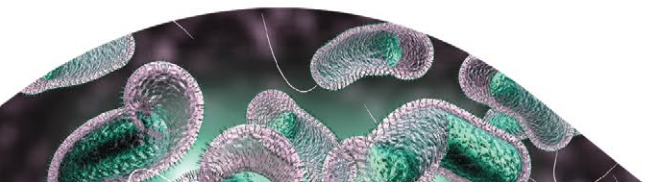
Vaccines

IMPACT FACTOR: 7,8

https://doi.org/10.3390/vaccines11071255

ABSTRACT

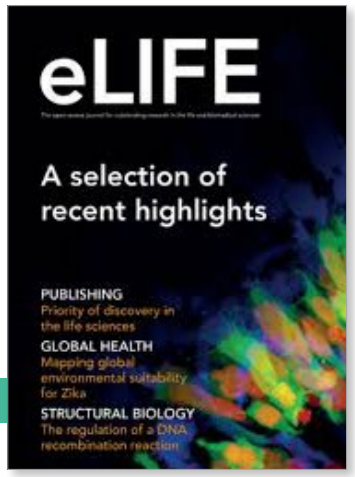
Novel lyssaviruses, the causative agents of rabies, continue to be described mostly due to increased surveillance in bat hosts. Biologicals for the prevention of rabies in humans have, however, remained largely unchanged for decades. This study aimed to determine if commercial rabies immunoglobulin (RIG) could neutralize diverse lyssaviruses. Two commercial preparations, of human or equine origin, were evaluated against a panel consisting of 13 lyssavirus species. Reduced neutralization was observed for the majority of lyssaviruses compared to rabies virus and was more evident for lyssaviruses outside of phylogroup I. Neutralization of more diverse lyssaviruses only occurred at very high doses, except for Ikoma lyssavirus, which could not be neutralized by the RIG evaluated in this study. The use of RIG is a crucial component of rabies post-exposure prophylaxis and the data generated here indicate that RIG, in its current form, will not protect against all lyssaviruses. In addition, higher doses of RIG may be required for neutralization as the genetic distance from vaccine strains increases. Given the limitations of current RIG preparations, alternative passive immunization options should be investigated.



DR JACKIE KLEYNHANS

Association of close-range contact patterns with SARS-CoV-2: a household transmission study

Jackie Kleynhans, Lorenzo Dall'Amico, Laetitia Gauvin, Michele Tizzoni, Lucia Maloma, **Sibongile Walaza,** Neil A Martinson, **Anne von Gottberg, Nicole Wolter, Mvuyo Makhasi, Cheryl Cohen,** Ciro Cattuto, **Stefano Tempia**; SA-S-HTS Group (SA-S-HTS Group: Amelia Buys, Daniel G Amoako, Dylan Toi, Jinal N Bhiman, Juanita Chewparsad, Kedibone Ndlangisa, Leisha Genade, Limakatso Lebina, Linda de Gouveia, Mzimasi Neti, Retshidisitswe Kotane)



eLife

IMPACT FACTOR: 7,7

https://doi.org/10.7554/elife.84753

BACKGROUND

Households are an important location for severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) transmission, especially during periods when travel and work was restricted to essential services. We aimed to assess the association of close-range contact patterns with SARS-CoV-2 transmission.

METHODS

We deployed proximity sensors for two weeks to measure face-to-face interactions between household members after SARS-CoV-2 was identified in the household, in South Africa, 2020-2021. We calculated the duration, frequency, and average duration of close-range proximity events with SARS-CoV-2 index cases. We assessed the association of contact parameters with SARS-CoV-2 transmission using mixed effects logistic regression accounting for index and household member characteristics.

RESULTS

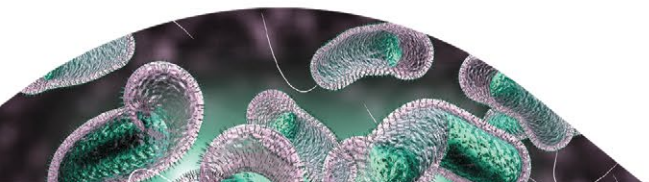
We included 340 individuals (88 SARS-CoV-2 index cases and 252 household members). On multivariable analysis, factors associated with SARS-CoV-2 acquisition were index cases with minimum Ct value <30 (aOR 16.8 95% CI 3.1-93.1) vs >35, and female contacts (aOR 2.5 95% CI 1.3-5.0). No contact parameters were associated with acquisition (aOR 1.0-1.1) for any of the duration, frequency, cumulative time in contact, or average duration parameters.

CONCLUSIONS

We did not find an association between close-range proximity events and SARS-CoV-2 household transmission. Our findings may be due to study limitations, that droplet-mediated transmission during close-proximity contacts plays a smaller role than airborne transmission of SARS-CoV-2 in the household, or due to high contact rates in households.

Funding: Wellcome Trust (Grant number 221003/Z/20/Z) in collaboration with the Foreign, Commonwealth, and Development Office, United Kingdom.

Keywords: SARS-CoV-2; contacts; epidemiology; global health; household; infectious disease; microbiology; transmission; viruses.



DR TAFADZWA DHOKOTERA

Gynaecologic and breast cancers in women living with HIV in South Africa: A record linkage study

Dhokotera TG, Muchengeti M, DavidoviÄ M, Rohner E, **Olago V,** Egger M, Bohlius J.

Int J Cancer

IMPACT FACTOR: 7,32

https://doi.org/10.1002/ijc.34712

ABSTRACT

Breast and gynaecologic cancers account for approximately half of all cancers diagnosed amongst women in South Africa, many of whom also live with HIV. We aimed to determine the incidence of and risk factors for developing breast and gynaecologic cancers in women living with HIV (WLHIV) in South Africa. This is a longitudinal analysis of the South African HIV Cancer Match study including women aged ≥15years with two or more HIV-related laboratory tests. We used Cox proportional hazard models to determine the association of Human Papilloma Virus (HPV)-related and hormone-related gynaecologic cancer with patient- and municipal-level characteristics. From 3447908 women and 10.5 million years of follow-up, we identified 11384 incident and 7612 prevalent gynaecologic and breast cancers. The overall crude incidence rate was 108/100000 person-years (pyears) (95% confidence interval [CI]: 106-110), with the highest incidence observed for cervical cancer (70/100000 pyears; 95% CI: 68.5-71.7). Low CD4 cell counts and high HIV RNA viral loads increased the risk of cervical and other HPV-related cancers. Age was associated with both HPV-related and hormone-related cancers. Women accessing health facilities in high socioeconomic position (SEP) municipalities were more likely to be diagnosed with HPV-related cancers and breast cancer than women accessing care in low SEP municipalities. It is important to improve the immunologic status of WLHIV as part of cancer prevention strategies in WLHIV. Cancer prevention and early detection programmes should be tailored to the needs of women ageing with HIV. In addition, SEP disparities in cancer diagnostic services have to be addressed.

MS BOITUMELO MOTSOENENG

DR SIMONE RICHARDSON

Despite delayed kinetics, people living with HIV achieve equivalent antibody function after SARS-CoV-2 infection or vaccination

Motsoeneng BM, Manamela NP, Kaldine H, Kgagudi P, Hermanus T, Ayres F, Makhado Z, Moyo-Gwete T, van der Mescht MA, Abdullah F, Boswell MT, Ueckermann V, Rossouw TM, Madhi SA, **Moore PL, Richardson SI.**

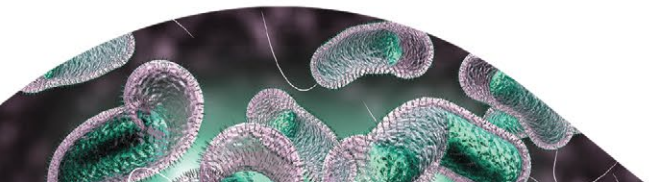
Frontiers in Immunology

IMPACT FACTOR: 7,3

https://doi.org/10.3389/fimmu.2023.1231276

ABSTRACT

The kinetics of Fc-mediated functions following SARS-CoV-2 infection or vaccination in people living with HIV (PLWH) are not known. We compared SARS-CoV-2 spike-specific Fc functions, binding, and neutralization in PLWH and people without HIV (PWOH) during acute infection (without prior vaccination) with either the D614G or Beta variants of SARS-CoV-2, or vaccination with ChAdOx1 nCoV-19. Antiretroviral treatment (ART)-naïve PLWH had significantly lower levels of IgG binding, neutralization, and antibody-dependent cellular phagocytosis (ADCP) compared with PLWH on ART. The magnitude of antibody-dependent cellular cytotoxicity (ADCC), complement deposition (ADCD), and cellular trogocytosis (ADCT) was differentially triggered by D614G and Beta. The kinetics of spike IgG-binding antibodies, ADCC, and ADCD were similar, irrespective of the infecting variant between PWOH and PLWH overall. However, compared with PWOH, PLWH infected with D614G had delayed neutralization and ADCP. Furthermore, Beta infection resulted in delayed ADCT, regardless of HIV status. Despite these delays, we observed improved coordination between binding and neutralizing responses and Fc functions in PLWH. In contrast to D614G infection, binding responses in PLWH following ChAdOx-1 nCoV-19 vaccination were delayed, while neutralization and ADCP had similar timing of onset, but lower magnitude, and ADCC was significantly higher than in PWOH. Overall, despite delayed and differential kinetics, PLWH on ART develop comparable responses to PWOH, supporting the prioritization of ART rollout and SARS-CoV-2 vaccination in PLWH.



PROF PENNY MOORE

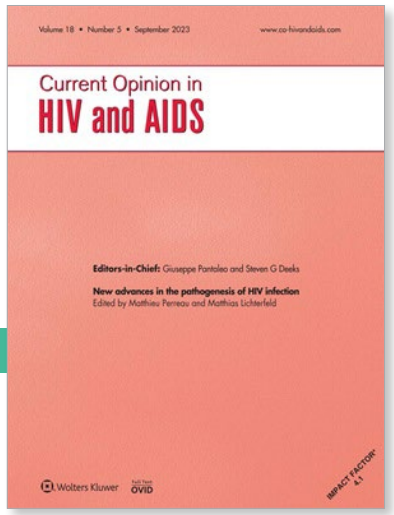
Anticipating viral escape–resistance to active and passive immunization

Williamson C, Lynch RM, **Moore PL**

Current Opinion in HIV & AIDS

IMPACT FACTOR: 4,1

https://doi.org/10.1097/COH.0000000000000816



PURPOSE

Active and passive immunization strategies are challenged by the extraordinary diversity of HIV, and the need for high titers of neutralizing antibodies to confer protective immunity. This review summarises recent studies and the barrier that these interventions will need to overcome to prevent viral resistance.

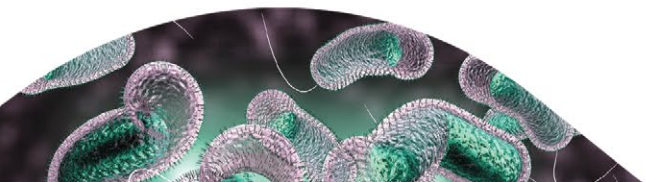
RECENT FINDINGS

Studies from the antibody mediated prevention trial identified a measure of protective titers, finding that higher titers than anticipated will be needed to prevent infection. This benchmark has advanced our ability to predict combinations of broadly neutralizing antibodies (bNAbs) that will provide optimal coverage. To limit escape, these combinations should ensure that the majority of viruses are bound by a minimum of two antibodies.

The characterization of currently circulating viruses has revealed increased resistance to some bNAbs over time, highlighting the need for continued surveillance, especially in under-studied populations and subtypes. Active vaccination will face similar challenges in combating diversity, although despite successes in germline targeting, this approach is not yet able to elicit bNAbs.

SUMMARY

Cumulatively these studies highlight the need to target multiple antibody epitopes for maximum coverage, but also to restrict escape pathways. Successful immunization strategies should anticipate viral escape and devise strategies to counteract this.



DR NICOLE WOLTER

PROF CHERYL COHEN

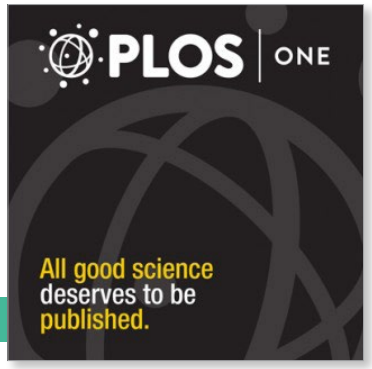
Healthcare utilization during the first two waves of the COVID-19 epidemic in South Africa: A cross-sectional household survey

Nicole Wolter, Stefano Tempia, **Anne von Gottberg, Jinal N. Bhiman, Sibongile Walaza, Jackie Kleynhans, Jocelyn Moyes,** Sue Aitken,Sarah Magni,Jessica Yun,Tamika Fellows,Tetelo Makamadi, Renay Weiner, Cherie Cawood,Neil Martinson, Limakatso Lebina, **Cheryl Cohen**

Plos one

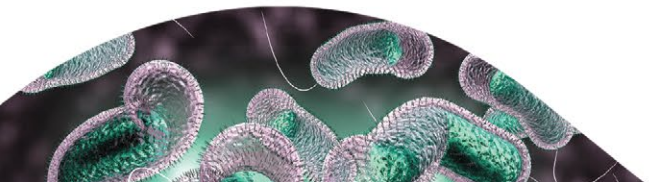
IMPACT FACTOR: 3,7

https://doi.org/10.1371/journal.pone.0290787



ABSTRACT

Healthcare utilization surveys contextualize facility-based surveillance data for burden estimates. We describe healthcare utilization in the catchment areas for sentinel site healthcare facilities during the first year of the COVID-19 pandemic. We conducted a cross-sectional healthcare utilization survey in households in three communities from three provinces (KwaZulu-Natal, Western Cape and North West). Field workers administered structured questionnaires electronically with the household members reporting influenza-like illness (ILI) in the past 30 days or severe respiratory illness (SRI) since March 2020. Multivariable logistic regression was used to identify factors associated with healthcare utilization among individuals that reported illness. From November 2020 through April 2021, we enrolled 5804 households and 23,003 individuals. Any respiratory illness was reported by 1.6% of individuals; 0.7% reported ILI only, 0.8% reported SRI only, and 0.1% reported both ILI and SRI. Any form of medical care was sought by 40.8% (95% CI 32.9% - 49.6%) and 71.3% (95% CI 63.2% - 78.6%) of individuals with ILI and SRI, respectively. On multivariable analysis, respiratory illness was more likely to be medically attended for individuals at the Pietermaritzburg site (aOR 3.2, 95% CI 1.1-9.5, compared to Klerksdorp), that were underweight (aOR 11.5, 95% CI 1.5-90.2, compared to normal weight), with underlying illness (aOR 3.2, 95%CI 1.2-8.5), that experienced severe illness (aOR 4.8, 95% CI 1.6-14.3) and those with symptom duration of ≥10 days (aOR 7.9, 95% CI 2.1-30.2, compared to <5 days). Less than half of ILI episodes and only 71% of SRI episodes were medically attended during the first two COVID-19 waves in South Africa. Facility-based data may underestimate disease burden during the COVID-19 pandemic.



DR AHMAD HAERI MAZANDERANI

PROF GAYLE SHERMAN

Eliminating vertical transmission of HIV in South Africa: establishing a baseline for the global alliance to end AIDS in children

Ahmad F. Haeri Mazanderani, Tanya Y. Murray, Leigh F. Johnson, Mathilda Ntloana, Tabisa Silere-Maqetseba 4, Sufang Guo 5 and **Gayle G. Sherman**

Diagnostics

IMPACT FACTOR: 3,6

https://doi.org/10.3390/diagnostics13152563

ABSTRACT

To gain a detailed overview of vertical transmission in South Africa, we describe insights from the triangulation of data sources used to monitor the national HIV program. HIV PCR results from the National Health Laboratory Service (NHLS) were analysed from the National Institute of Communicable Diseases (NICD) data warehouse to describe HIV testing coverage and positivity among children <2 years old from 2017–2021. NICD data were compared and triangulated with the District Health Information System (DHIS) and the Thembisa 4.6 model. For 2021, Thembisa estimates a third of children living with HIV go undiagnosed, with NICD and DHIS data indicating low HIV testing coverage at 6 months (49%) and 18 months (33%) of age, respectively. As immunisation coverage is reported at 84% and 66% at these time points, better integration of HIV testing services within the Expanded Programme for Immunization is likely to yield improved case findings. Thembisa projects a gradual decrease in vertical transmission to 450 cases per 100,000 live births by 2030. Unless major advances and strengthening of maternal and child health services, including HIV prevention, diagnosis, and care, can be achieved, the goal to end AIDS in children by 2030 in South Africa is unlikely to be realised.

DR SIOBHAN JOHNSTONE

PROF NICOLA PAGE

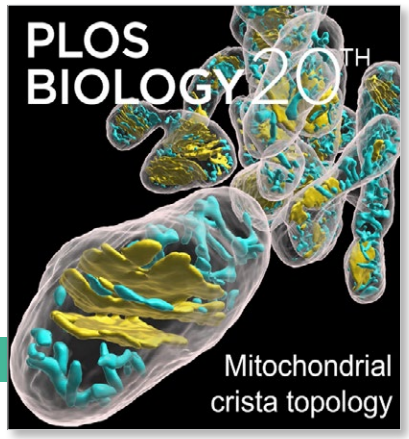
Epidemiology and aetiology of moderate to severe diarrhoea in hospitalised patients > 5 years old living with HIV in South Africa, 2018– 2021: A case-control analysis

Johnstone SL, Erasmus L, Thomas J, Groome MJ, du Plessis NM, Avenant T, de Villiers M, **Page NA**

PLOS: Global Public Health

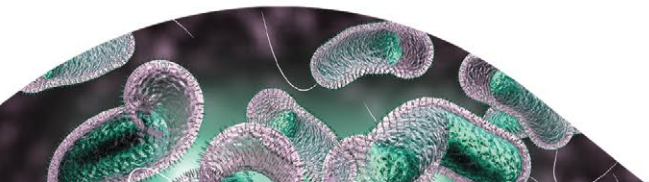
IMPACT FACTOR: 3,3

https://doi.org/10.1371/journal.pgph.0001718



ABSTRACT

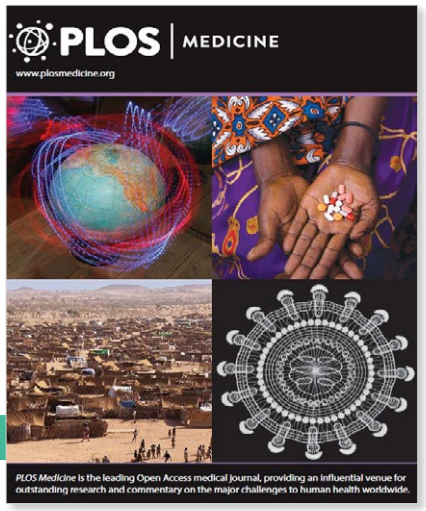
Diarrhoea is a recognised complication of HIV-infection, yet there are limited local aetiological data in this high-risk group. These data are important for informing public health interventions and updating diagnostic and treatment guidelines. This study aimed to determine the pathogenic causes of diarrhoeal admissions in people living with HIV (PLHIV) compared to hospital controls between July 2018 and November 2021. Admitted diarrhoeal cases (n = 243) and non-diarrhoeal hospital controls (n = 101) ≥5 years of age were enrolled at Kalafong, Mapulaneng and Matikwana hospitals. Stool specimens/rectal swabs were collected and pathogen screening was performed on multiple platforms. Differences in pathogen detections between cases and controls, stratified by HIV status, were investigated. The majority (n = 164, 67.5%) of enrolled diarrhoeal cases with known HIV status were HIV-infected. Pathogens could be detected in 66.3% (n = 228) of specimens, with significantly higher detection in cases compared to controls (72.8% versus 50.5%, p<0.001). Amongst PLHIV, prevalence of Cystoisospora spp. was significantly higher in cases than controls (17.7% versus 0.0%, p = 0.028), while Schistosoma was detected more often in controls than cases (17.4% versus 2.4%, p = 0.009). Amongst the HIV-uninfected participants, prevalence of Shigella spp., Salmonella spp. and Helicobacter pylori was significantly higher in cases compared to controls (36.7% versus 12.0%, p = 0.002; 11.4% versus 0.0%, p = 0.012; 10.1% versus 0.0%, p = 0.023). Diarrhoeal aetiology differed by HIV status, with Shigella spp. (36.7%) and Salmonella spp. (11.4%) having the highest prevalence amongst HIV-uninfected cases and Shigella spp. (18.3%), *Cystoisospora* (17.7%), and *Cryptosporidium* spp. (15.9%) having the highest prevalence in cases amongst PLHIV. These differences should be considered for the development of diagnostic and treatment guidelines.



PROF ADRIAN PUREN

Seroprevalence survey of anti-SARS-CoV-2 antibody and associated factors in South Africa: Findings of the 2020–2021 population based household survey

Moyo S, Simbayi L, Zuma K, Marinda E, Jooste S, **Fortuin M, Singh B,** Mabaso M, Reddy T, Parker W, Naidoo I, Manda S, Goga A, Ngandu N, Cawood C, **Morris L, Moore PL, Puren A & the NCAS Study Team**



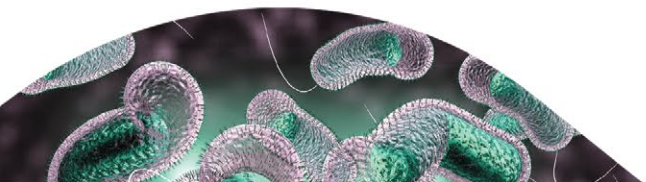
PLOS Global Public Health

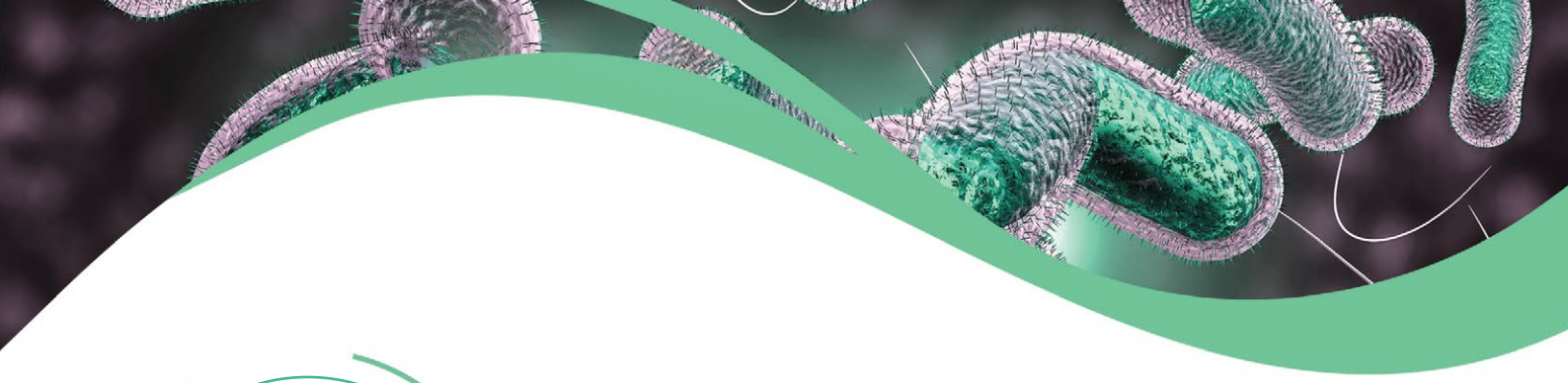
IMPACT FACTOR: 3,3

https://doi.org/10.1371/journal.pgph.0002358

ABSTRACT

Population-based serological testing is important to understand the epidemiology and estimate the true cumulative incidence of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) to inform public health interventions. This study reports findings of a national household population SARS-CoV-2 serosurvey in people 12 years and older in South Africa. This cross-sectional multi-stage random stratified cluster survey undertaken from November 2020 to June 2021 collected sociodemographic data, medical history, behavioural data, and blood samples from consenting participants. The samples were tested for SARS-CoV-2 antibodies using the Roche ElecsysAnti-SARS-CoV-2 chemiluminescence immunoassay (CLIA) Total Antibody Test. The survey data were weighted by age, race, sex, and province with final individual weights benchmarked against the 2020 mid-year population estimates and accounted for clustering. Descriptive statistics summarize the characteristics of participants and seroprevalence. Logistic regression analyses were used to identify factors associated with seropositivity. From 13290 survey participants (median age 33 years, interquartile range (IQR) 23–46 years), SARS-CoV-2 seroprevalence was 37.8% [95% Confidence Interval (CI) 35.4–40.4] and varied substantially across the country's nine provinces, and by sex, age and locality type. In the final adjusted model, the odds of seropositivity were higher in women than in men [aOR = 1.3 (95% CI: 1.0–1.6), p = 0.027], and those living with HIV (self-report) [aOR = 1.6 (95% CI: 1.0–2.4), p = 0.031]. The odds were lower among those 50 years and older compared to adolescents 12–19 years old [aOR = 0.6 (95% CI: 0.5–0.8), p<0.001] and in those who did not attend events or gatherings [aOR = 0.7 (95% CI: 0.6–1.0), p = 0.020]. The findings help us understand the epidemiology of SARS-CoV-2 within different regions in a low-middle-income country. The survey highlights the higher risk of infection in women in South Africa likely driven by their home and workplace roles and also highlighted a need to actively target and include younger people in the COVID-19 response.





MS SHELINA MOONSAMY

DR NISHI PRABDIAL-SING

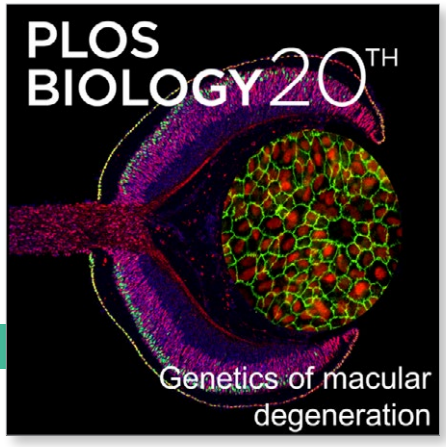
Hepatitis B infection status among South Africans attending public health facilities over a five-year period: 2015 to 2019

Moonsamy, S. Pillay, P. and **Prabdial-Sing, N**

PLOS Glob Public Health

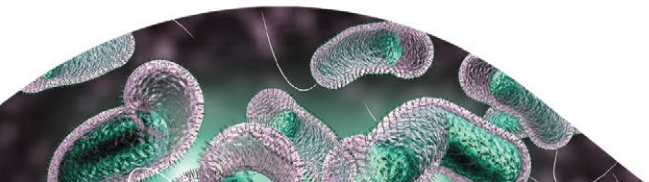
IMPACT FACTOR: 3,3

https://doi.org/10.1371/journal.pgph.0000992



ABSTRACT

Hepatitis B, a potentially life-threatening viral infection of the liver, remains a global public health concern despite the availability of effective vaccines for over three decades. The aim of our study was to provide national data on active hepatitis B infections in the public health sector of South Africa. We conducted retrospective analyses on national laboratory data over the period 2015 to 2019. We identified 176,530 cases who tested positive for HBsAg (active infection) with a test positivity rate of 9.02%. Of these active infections, 11,355 (6.43%) were found to be chronically infected. We linked 24,839 (14.07%) and 2,461 (21.67%) HBeAg positive results to all active HBV infections and identified chronic infections respectively. Clearance of HBsAg was observed in 5,569 cases, inclusive of clearance in 135 chronic cases. Active HBV infections were significantly higher in men than women over the five years ($p < 0.0001$). Among individuals who were vaccine-eligible as infants (0 to 19 years old), we observed 4,981 active HBV infections, including 1,131 infections under five years old, majority of which (65.78%) were under one year old. In the under five-year age group, the HBsAg population positivity rate was 0.02% and test positivity rate was 4.83%. Among all women with active HBV infections (78,935), 85.17% were of reproductive age and of these, 13.73% were HBeAg positive. Without a birth dose of the HBV vaccine, lack of routine HBsAg screening at antenatal care, and HBsAg and HBeAg prevalence among women of reproductive age, it is likely that the majority of cases under five years old were vertically infected. Optimal HBV vaccine coverage, inclusive of a birth dose, is key to eliminating horizontal and vertical transmission of HBV. Early identification of HBV chronicity through real time data analysis is fundamental in reducing the risk of liver cirrhosis and hepatocellular carcinoma.



DR JAISHREE RAMAN

Defining operational research priorities to improve malaria control and elimination in sub-Saharan Africa: results from country-driven research prioritization setting process

Roger Tine, Samatha Herrera, Mouhamed Ahmed Badji, Kyle Daniels, Pascal Ndiaye, Cara Smith Gueye, Fassiatou Tairou, Laurence Slutsker, Jimee Hwang, Evelyn Ansah, megan Littrell, **Jaishree Raman.**

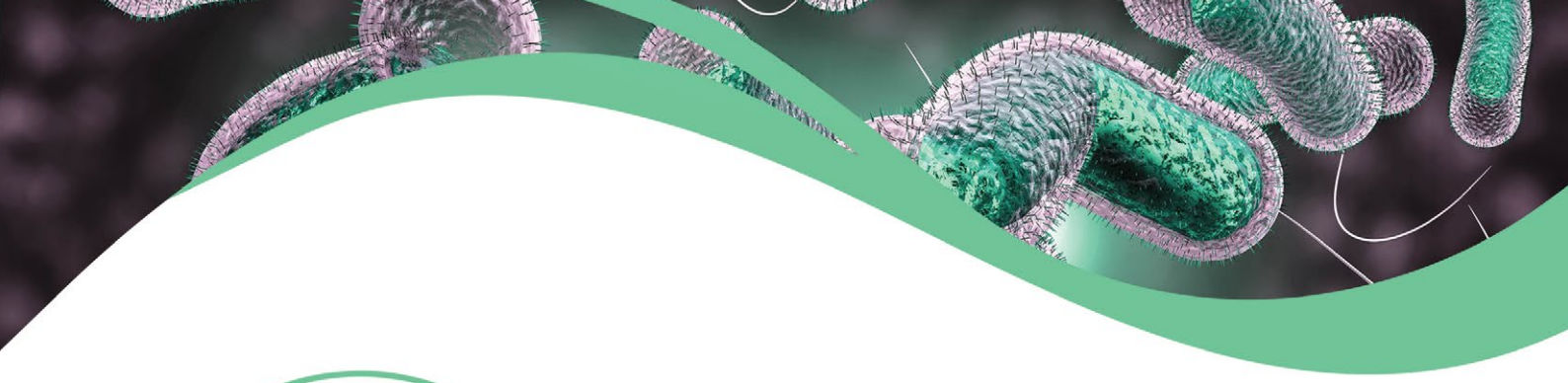
Malaria Journal

IMPACT FACTOR: 3,0

https://doi.org/10.1186/s12936-023-04654-8

ABSTRACT

In order to reignite gains and accelerate progress toward improved malaria control and elimination, policy, strategy, and operational decisions should be derived from high-quality evidence. The U.S. President's Malaria Initiative (PMI) Insights project together with the Université Cheikh Anta Diop of Dakar, Senegal, conducted a broad stakeholder consultation process to identify pressing evidence gaps in malaria control and elimination across sub-Saharan Africa (SSA), and developed a priority list of country-driven malaria operational research (OR) and programme evaluation (PE) topics to address these gaps. Methods Five key stakeholder groups were engaged in the process: national malaria programmes (NMPs), research institutions in SSA, World Health Organization (WHO) representatives in SSA, international funding agencies, and global technical partners who support malaria programme implementation and research. Stakeholders were engaged through individual or small group interviews and an online survey, and asked about key operational challenges faced by NMPs, pressing evidence gaps in current strategy and implementation guidance, and priority OR and PE questions to address the challenges and gaps. Results Altogether, 47 interviews were conducted with 82 individuals, and through the online survey, input was provided by 46 global technical partners. A total of 33 emergent OR and PE topics were identifed through the consultation process and were subsequently evaluated and prioritized by an external evaluation committee of experts from NMPs, research institutions, and the WHO. The resulting prioritized OR and PE topics predominantly focused on generating evidence needed to close gaps in intervention coverage, address persistent challenges faced by NMPs in the implementation of core strategic interventions, and inform the efective deployment of new tools.



DR MONICA BIRKHEAD

Ultrastructure for the diagnosis of primary ciliary dyskinesia in South Africa, a resource-limited setting

Monica Birkhead, Samuel Otido, Theodore Mabaso, Keketso Mopeli, Dorcas Tlhapi, Charl Verwey, Ziyaad Dangor

Frontiers in Pediatrics

IMPACT FACTOR: 2,6

https://doi.org/10.3389/fped.2023.1247638

INTRODUCTION

International guidelines recommend a multi-faceted approach for successful diagnoses of primary ciliary dyskinesia (PCD). In the absence of a gold standard test, a combination of genetic testing/microscopic analysis of structure and function/nasal nitric oxide measurement is used. In resource-limited settings, often none of the above tests are available, and in South Africa, only transmission electron microscopy (TEM) is available in central anatomical pathology departments. The aim of this study was to describe the clinical and ultrastructural findings of suspected PCD cases managed by pediatric pulmonologists at a tertiary-level state funded hospital in Johannesburg.

METHODS

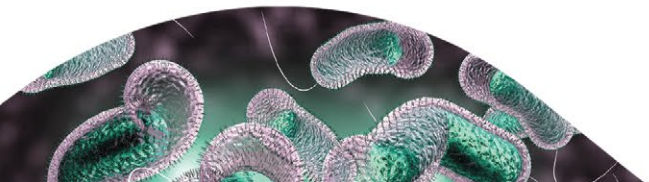
Nasal brushings were taken from 14 children with chronic respiratory symptoms in keeping with a PCD phenotype. Ultrastructural analysis in accordance with the international consensus guidelines for TEM-PCD diagnostic reporting was undertaken.

RESULTS

TEM observations confirmed 43% (6) of the clinically-suspected cases (hallmark ultrastructural defects in the dynein arms of the outer doublets), whilst 57% (8) required another PCD testing modality to support ultrastructural observations. Of these, 25% (2) had neither ultrastructural defects nor did they present with bronchiectasis. Of the remaining cases, 83% (5) had very few ciliated cells (all of which were sparsely ciliated), together with goblet cell hyperplasia. There was the apparent absence of ciliary rootlets in 17% (1) case.

DISCUSSION

In resource-limited settings in which TEM is the only available testing modality, confirmatory and probable diagnoses of PCD can be made to facilitate early initiation of treatment of children with chronic respiratory symptoms.



DR NICOLE WOLTER

Knowledge, attitudes, practices and intention to get vaccinated against COVID-19: results from a cross-sectional survey in three peri-urban communities in South Africa

Renay Weiner, Sarah Magni, Tetelo Maakamadi, Tamika Fellows, Susan Aitken, Jessica Yun, **Stefano Tempia, Anne von Gottberg, Jinal Bhiman, Sibongile Walaza, Jocelyn Moyes,** Cherie Cawood, Neil Martinson, Limakatso Lebina, **Cheryl Cohen, Nicole Wolter**

Pan African Medical Journal

IMPACT FACTOR: 1,2

DOI: 10.11604/pamj.2023.45.120.37210

INTRODUCTION

South Africa has the largest number of confirmed cases of COVID-19 in Africa. Data to inform public health strategies to mitigate the spread of new variants and severity of disease is needed, including information on knowledge, attitudes and practices (KAP) regarding COVID-19, factors associated with intention to get vaccinated, and viewpoints on reliable sources of data.

METHODS

We investigated these topics as part of the COVID-19 healthcare utilization and seroprevalence (HUTS) cross-sectional survey in three communities in South Africa: Mitchell´s Plain (Western Cape Province), Pietermaritzburg (KwaZulu-Natal Province) and Klerksdorp (North West Province) during and after the second wave of COVID-19 prior to vaccine availability.

Results

Primary caregivers from 5799 households participated in the study, 41.1% from Pietermaritzburg, 34.2% from Klerksdorp and 24.7% from Mitchells Plain. Two-thirds and 94.7% of respondents had correct knowledge on the cause and spread of COVID-19, respectively. Knowledge measures were significantly associated with age less than 65 years, the highest level of education and site (Mitchells Plain). Desired preventive behaviors were associated with higher socio-economic status. While 64.7% of people intended to get vaccinated, those over 64 years of age were more likely to intend to vaccinate (aOR: 1.25, 95% CI:1.06-1.47). Vaccine intention related to protection of self (58.4%) and family (40.0%). The most trusted source of COVID-19 information was television (59.3%) followed by radio (20.0%).

CONCLUSION

These data can be used to design targeted public health campaigns for the current COVID-19 and future epidemics, ensuring that socio-economic constraints and preference for trusted information are considered.

MS CARROLL TSHABANE

Estimation of shedding time in laboratory-confirmed COVID-19 cases in South Africa: a population-based record linkage study, March-December 2020

Carroll Tshabane, Lazarus Kuonza, Hetani Mdose, Alfred Musekiwa, Nkengafac Villyen Motaze

Pan African Medical Journal

IMPACT FACTOR: 1,2

https://doi.org/10.11604/pamj.2023.46.24.41047

INTRODUCTION

In South Africa, COVID-19 cases are notifiable and hospitalized cases are reported on a dedicated platform. It is crucial to estimate the duration of SARS-CoV-2 shedding to inform public health interventions. We aimed to estimate viral shedding time among laboratory-confirmed COVID-19 cases in South Africa.

METHODS

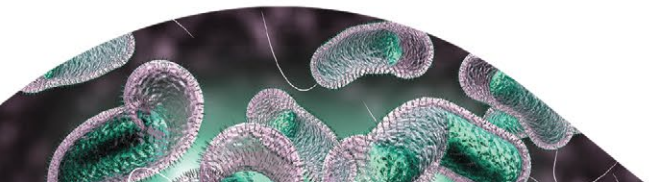
We analyzed COVID-19 PCR results from 5 March to 31 December 2020. We included cases with at least 2 consecutive positive PCR tests and a subsequent negative test. We performed multiple linear regression to determine the association between shedding time and predictor variables (age, sex, admission status and province). We included 2752 cases that met the inclusion criteria.

RESULTS

About 39.9% (1099/2752) of participants were inpatients and 60.1% (1653/2752) were outpatients. The median shedding time was 17 days (range: 1-128). There was no difference in shedding time between males and females and between hospitalized patients and outpatients. Individuals aged 0-4 years had the lowest shedding time (median: 14 days, range: 1-72). After adjusting for age, sex and province, shedding time was shorter for hospitalized patients compared to outpatients (co-efficient: -0.14, CI: -0.24 - -0.03, P-value: 0.014). Six provinces (KwaZulu-Natal, Gauteng, Limpopo, North West, Mpumalanga, and Western Cape) had a significant association with shedding time.

CONCLUSION

The duration of viral shedding within our population varies from 1-128 days. Although prolonged shedding might not necessarily indicate infectiousness, individual patient monitoring and management are needed for patients with prolonged shedding. Further studies are required to explore the association between comorbidities and SARS-CoV-2 shedding time.



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