



**NATIONAL INSTITUTE FOR  
COMMUNICABLE DISEASES**

Division of the National Health Laboratory Service

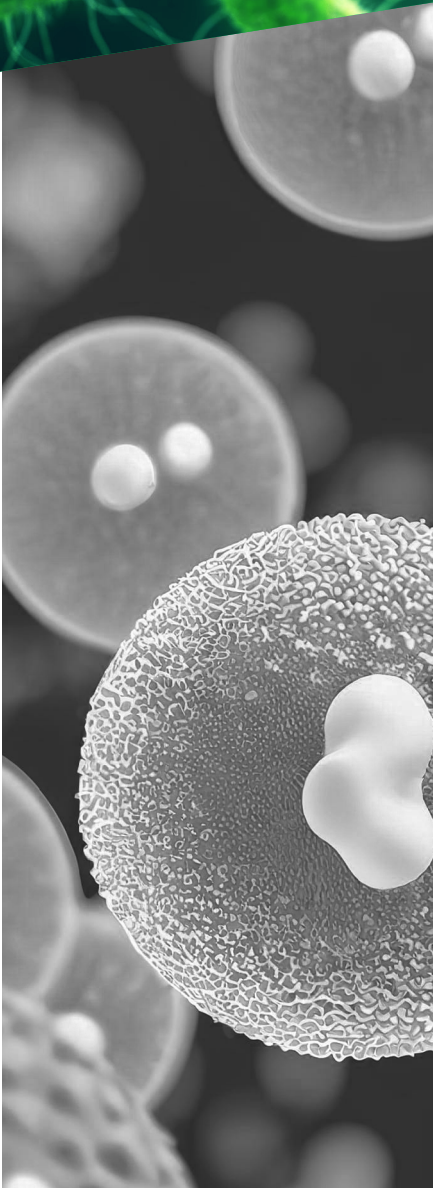
# SCIENCE FOCUS

A quarterly nexus of  
scientific insights

**ISSUE 28 | Q3 | 2023/2024**

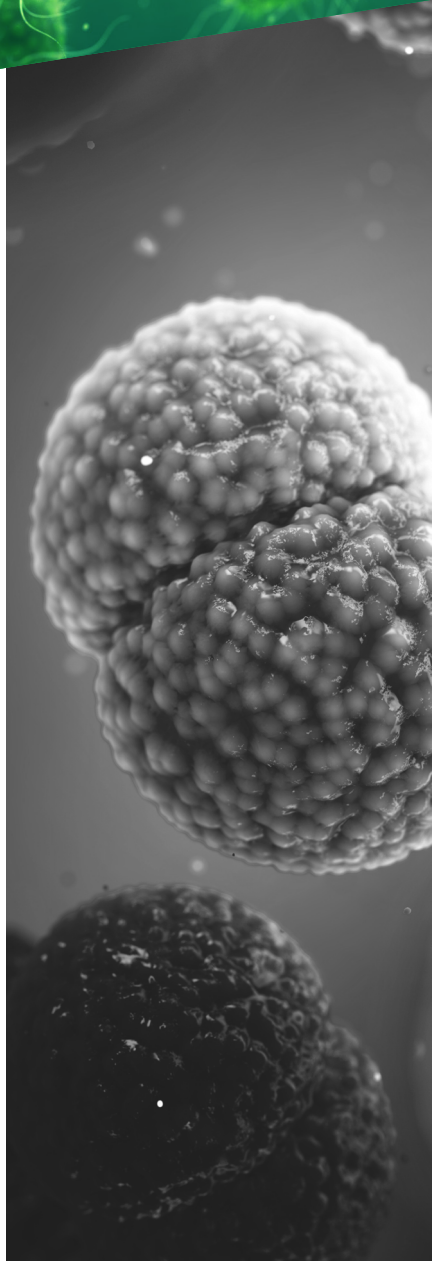
The Science Focus acknowledges NICD members of staff who have published in peer-reviewed journals. This publication is a compilation of scientific publications where an NICD staff member is either the first or last author.

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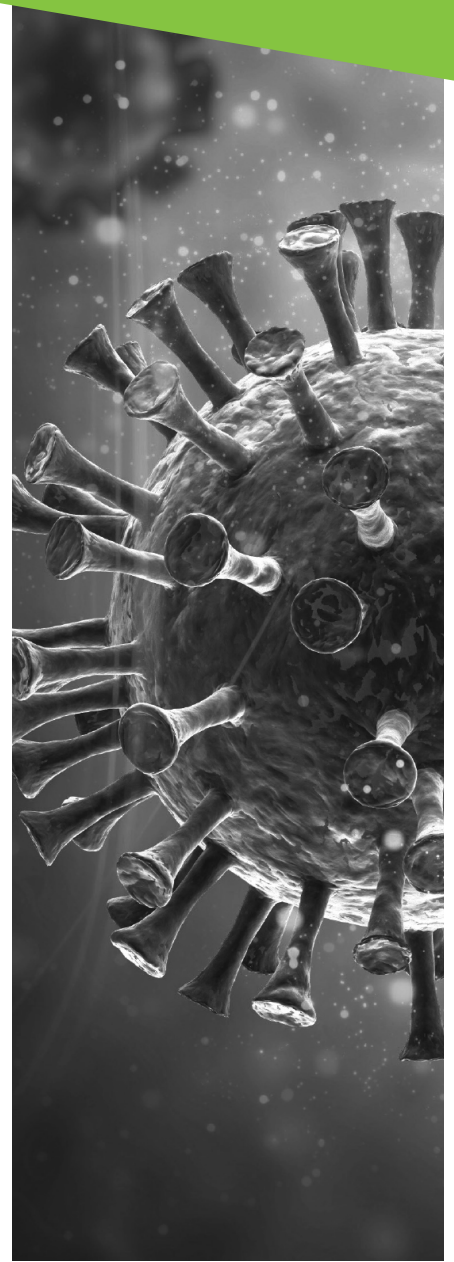
**EDITOR'S  
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**TOP PUBLISHED  
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AUTHOR PUBLISHED  
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**MR VUYO SABANI**  
(ACTING) SENIOR COMMUNICATIONS  
MANAGER

# Advancing NICD's Research with Resolve

We are pleased to present the 28th edition of Science Focus, a publication dedicated to highlighting and celebrating the remarkable research achievements of the National Institute for Communicable Diseases (NICD). Presented in this issue are collaborative research efforts of promising young researchers, established and internationally acclaimed researchers.

We commend and recognise all the authors whose contributions grace our pages in this issue, with special recognition for the top three authors: Prof Anne von Gottberg, Prof Cheryl Cohen, and Dr Nicole Walter. Their work exemplifies the calibre of research excellence that defines the NICD. This publication is rich with diverse scientific research content, offering valuable insights into disease surveillance and public health. We encourage you to explore all the studies and recommend that you make time to view the following studies which share light on some of the pressing challenges facing our nation:

- “SARS-CoV-2 genomic surveillance in wastewater as a model for monitoring the evolution of endemic viruses.” This study aimed to identify and characterise SARS-CoV-2 variants in wastewater samples collected from urban centres across South Africa (See page 7).

- “Vaccinating people with HIV (PWH) – a short-circuit to an effective HIV vaccine” (See page 6).
- “Diabetes mellitus mortality by major occupation category in South Africa, 2009-2016”. Published in our Public Health Bulletin, this article highlights the heightened risk of diabetes mellitus mortality across various occupational categories in South Africa, emphasising the need for targeted interventions.

We trust that you will find this issue both informative and enlightening, reflecting the dedication and expertise of our contributors.

Thank you for your continued support and engagement with Science Focus.

On behalf of the team

**Vuyo Sabani**

Acting Senior Communications Manager



# EXCEPTIONAL RESEARCH STATISTICS

# Top Published Authors



PROF ANNE VON GOTTBERG



PROF CHERYL COHEN



DR NICOLE WOLTER



PROF ARSHAD ISMAIL



DR KERRIGAN MCCARTHY



DR MIGNON DU PLESSIS



DR HARRY MOULTRIE



DR TENDESAYI KUFA-CHAKEZHA



PROF PENNY MOORE

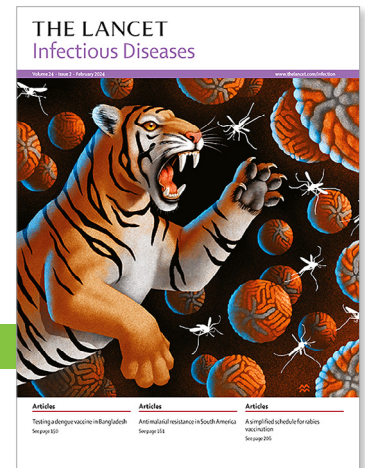
## Vaccinating people with HIV (PWH) – a short-circuit to an effective HIV vaccine

Trkola A, Moore PL.

Lancet Infectious Diseases

IMPACT FACTOR: 71,4

<https://www.sciencedirect.com/science/article/abs/pii/S1473309923004814>



### ABSTRACT

Globally, the number of new HIV infections remains unacceptably high, and urgent new approaches are needed to advance HIV vaccine science. However, the development of a preventive HIV vaccine has proven to be an intractable scientific challenge. Recent advances in HIV immunogen design have taken the field a step closer to triggering the rare precursors of broadly neutralising antibodies, which are widely assumed to be necessary for a vaccine. Nonetheless, these same studies and previous studies in people living with HIV have also highlighted the major hurdles that must be overcome to boost the cross-reactivity and potency of these responses to sufficient levels. Here, we describe an opportunity

for fast-tracking the evaluation of candidate preventive and therapeutic vaccines by immunising people with HIV who are antiretroviral therapy suppressed. We argue that such studies, unlike traditional studies of vaccines in participants not infected with HIV, will be faster and more informative and will allow the vaccine field to bypass multiple hurdles. This approach will accelerate the process of defining the capacity of immunogens to trigger relevant antibodies, currently an extremely slow and expensive pathway, and provide a quick path to creating an HIV vaccine.





DR MUKHLID YOUSIF



DR KERRIGAN MCCARTHY

## SARS-CoV-2 genomic surveillance in wastewater as a model for monitoring evolution of endemic viruses

Mukhlid Yousif, Said Rachida, Setshaba Taukobong, Nkosenhle Ndlovu, Chinwe Iwu-Jaja, Wayne Howard, Shelina Moonsamy, Nompilo Mhlambi, Siphso Gwala, Joshua I Levy, Kristian G Andersen, Cathrine Scheepers, Anne von Gottberg, Nicole Wolter, Jinal N Bhiman, Daniel Gyamfi Amoako, Arshad Ismail, Melinda Suchard, Kerrigan McCarthy

Nature Communications

IMPACT FACTOR: 17.69

<https://doi.org/10.1038/s41467-023-41369-5>



### ABSTRACT

As global SARS-CoV-2 burden and testing frequency have decreased, wastewater surveillance has emerged as a key tool to support clinical surveillance efforts. The aims of this study were to identify and characterize SARS-CoV-2 variants in wastewater samples collected from urban centers across South Africa. Here we show that wastewater sequencing analyses are temporally concordant with clinical genomic surveillance and reveal the presence of multiple lineages not detected by clinical surveillance. We show that wastewater genomics can support SARS-CoV-2

epidemiological investigations by reliably recovering the prevalence of local circulating variants, even when clinical samples are not available. Further, we find that analysis of mutations observed in wastewater can provide a signal of upcoming lineage transitions. Our study demonstrates the utility of wastewater genomics to monitor evolution and spread of endemic viruses.





PROF PENNY MOORE

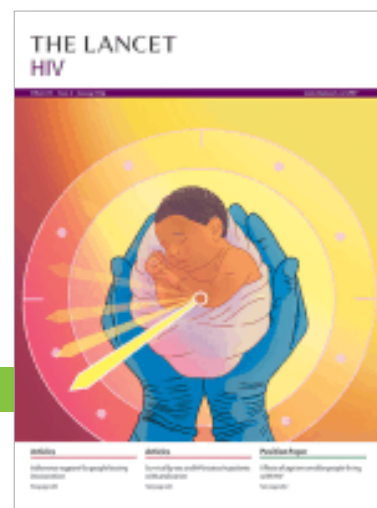
## Super early treatment for HIV acquired in utero

van de Perre P, Moore PL.

Lancet HIV

IMPACT FACTOR: 16.07

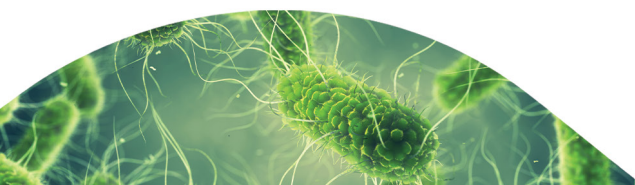
[https://www.thelancet.com/journals/lanhiv/article/PIIS2352-3018\(23\)00260-6/abstract](https://www.thelancet.com/journals/lanhiv/article/PIIS2352-3018(23)00260-6/abstract)



### ABSTRACT

Despite spectacular progress in the prevention of vertical transmission of HIV, UNAIDS estimates that the number of new paediatric HIV infections has plateaued over the past 8 years at 130 000–160 000 new infections per year, mostly in sub-Saharan

Africa. Although postnatal transmission through breastfeeding accounts for at least half of these new cases, the early diagnosis and care of infants infected in utero or during the intrapartum period remains a public health concern.





MS THANDEKA MOYO-GWETE



PROF PENNY MOORE

## Homologous Ad26.COVS.2 vaccination results in reduced boosting of humoral responses in hybrid immunity, but elicits antibodies of similar magnitude regardless of prior infection

**Moyo-Gwete T, Richardson SI, Keeton R, Hermanus T, Spencer H, Manamela NP, Ayres F, Makhado Z, Motlou T, Tincho MB, Benede N, Ngomti A, Baguma R, Chauke MV, Mennen M, Adriaanse M, Skelem S, Gogo A, Garrett N, Bekker L, Gray G, Ntusi NAB, Riou C, Burgers WA, Moore PL**

PLoS Pathogens

IMPACT FACTOR: 7.46

<https://doi.org/10.1371/journal.ppat.1011772>



### ABSTRACT

The impact of previous SARS-CoV-2 infection on the durability of Ad26.COVS.2 vaccine-elicited responses, and the effect of homologous boosting has not been well explored. We followed a cohort of healthcare workers for 6 months after receiving the Ad26.COVS.2 vaccine and a further one month after they received an Ad26.COVS.2 booster dose. We assessed longitudinal spike-specific antibody and T cell responses in individuals who had never had SARS-CoV-2 infection, compared to those who were infected with either the D614G or Beta variants prior to vaccination. Antibody and T cell responses elicited by the primary dose were durable against several variants of concern over the 6 month follow-up period, regardless of infection history. However, at 6 months after first vaccination, antibody binding, neutralization and ADCC were as much as 33-fold higher in individuals with hybrid immunity

compared to those with no prior infection. Antibody cross-reactivity profiles of the previously infected groups were similar at 6 months, unlike at earlier time points suggesting that the effect of immune imprinting diminishes by 6 months. Importantly, an Ad26.COVS.2 booster dose increased the magnitude of the antibody response in individuals with no prior infection to similar levels as those with previous infection. The magnitude of spike T cell responses and proportion of T cell responders remained stable after homologous boosting, concomitant with a significant increase in long-lived early differentiated CD4 memory T cells. Thus, these data highlight that multiple antigen exposures, whether through infection and vaccination or vaccination alone, result in similar boosts after Ad26.COVS.2 vaccination.







MS SILONDIWE NZIMANDE



DR TSIDISO MAPHANGA

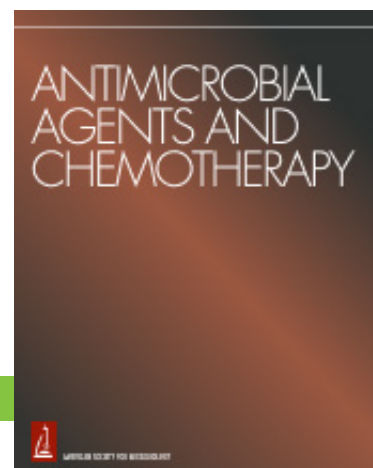
## ***In vitro* manogepix susceptibility testing of South African *Emergomyces africanus*, *Emergomyces pasteurianus*, and *Blastomyces emzantsi* clinical isolates.**

Nzimande SP, Govender NP, Maphanga TG.

Antimicrob Agents Chemother

IMPACT FACTOR: 5.938

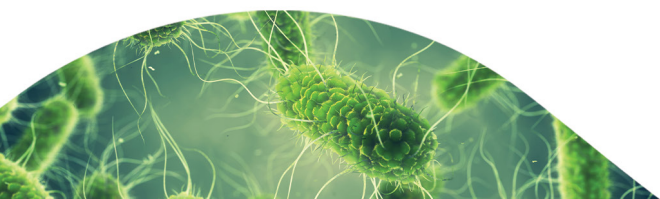
<https://journals.asm.org/doi/10.1128/aac.01104-23>



### **ABSTRACT**

We performed *in vitro* antifungal susceptibility testing of manogepix against the yeast phase of 78 *Emergomyces africanus*, 2 *Emergomyces pasteurianus*, and 5 *Blastomyces emzantsi* isolates using a reference broth microdilution method following Clinical and Laboratory Standards Institute recommendations. All three

pathogens had low minimum inhibitory concentrations ranging from <0.0005 to 0.008 mg/L. Manogepix should be investigated in animal models and potentially in future human clinical trials for endemic mycoses.





DR FAHIMA MOOSA



DR NICOLE WOLTER

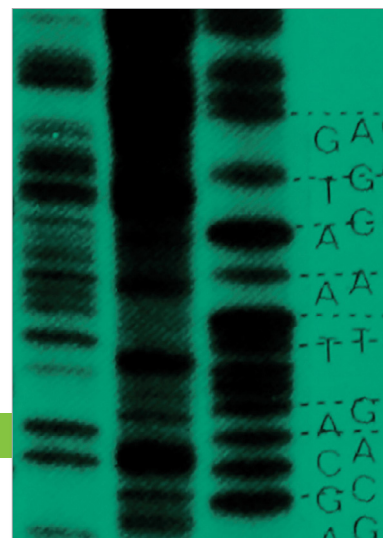
## Genomic characterization of *Bordetella pertussis* in South Africa, 2015-2019

Fahima Moosa, Mignon du Plessis, Michael R Weigand, Yanhui Peng, Dineo Mogale, Linda de Gouveia, Marta C Nunes, Shabir A Madhi, Heather J Zar, Gary Reubenson, Arshad Ismail, M Lucia Tondella, Cheryl Cohen, Sibongile Walaza, Anne von Gottberg, Nicole Wolter

### Microbial Genomics

IMPACT FACTOR: 4.86

<https://doi.org/10.1099/mgen.0.001162>



### ABSTRACT

Pertussis remains a public health concern in South Africa, with an increase in reported cases and outbreaks in recent years. Whole genome sequencing was performed on 32 *Bordetella pertussis* isolates sourced from three different surveillance programmes in South Africa between 2015 and 2019. Genome sequences were characterized using multilocus sequence typing, vaccine antigen genes (*ptxP*, *ptxA*, *ptxB*, *prn* and *fimH*) and overall genome structure. All isolates were sequence type 2 and harboured the pertussis toxin promoter allele *ptxP3*. The dominant genotype was *ptxP3-ptxA1-ptxB2-prn2-fimH2* (31/32, 96.9%), with no pertactin-deficient or other mutations in vaccine antigen genes identified. Amongst 21 isolates yielding closed genome assemblies, eight distinct genome structures were detected, with 61.9% (13/21)

of the isolates exhibiting three predominant structures. Increases in case numbers are probably not due to evolutionary changes in the genome but possibly due to other factors such as the cyclical nature of *B. pertussis* disease, waning immunity due to the use of acellular vaccines and/or population immunity gaps. Keywords: *B. pertussis*; Illumina sequencing; PacBio sequencing; genome structural characterization; vaccine antigen genes; whole genome sequencing.

### KEYWORDS

*B. pertussis*; Illumina sequencing; PacBio sequencing; genome structural characterization; vaccine antigen genes; whole genome sequencing."





DR NATALIE MAYET

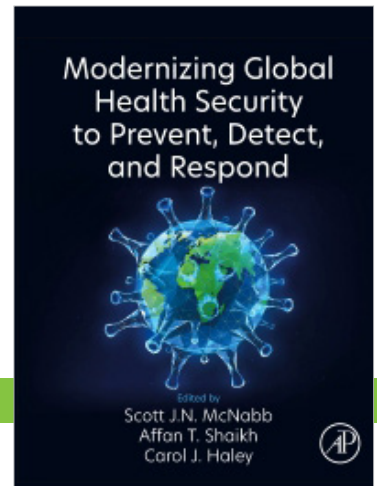
## Science and political leadership in global health security (Chapter 22 in Modernizing Global Health Security to Prevent, Detect, and Respond)

**Natalie Mayet**, Eliot England, Benjamin Djoudalbaye, Ebere Okereke and Wondimagegnehu Alemu

Science Direct

IMPACT FACTOR: 4.5

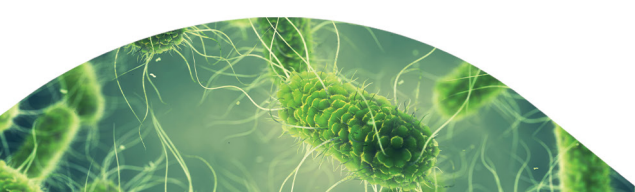
<https://elsevier-books-eproof.tnq.co.in/ECOMPS/00fc75b7383fcd79ffdb8d0a0af3f39f/?token=90a96dbfad078e9fc7edff52686f6b83>



### ABSTRACT

Health is a political choice. Politics is about access to and leveraging power to achieve a shared vision. Political leadership needs to appreciate the challenges and apply scientific knowledge in managing health emergencies including the COVID-19 pandemic. The scientific knowledge deployed to achieve global health security requires population-wide application and multidimensional response. The interdependency between science and political leadership offers opportunities for resolving conflicting priorities. Of particular concern is the risk of manipulating rapidly evolving scientific knowledge to address the needs of interest group.

In this chapter, we highlight the perspectives of scientific and political leaders by examining the interface between science and politics. We explore how these differences can affect the application of scientific solutions at the population level. Challenges in the application of evidence-based global health security instruments such as International Health Regulations include political expediency. We identify challenges and opportunities to improve alignment between scientific and political leadership and build collaborative partnerships in health emergency security measures is retained.





DR HALIMA SAID

## Determining the risk-factors for molecular clustering of drug-resistant tuberculosis in South Africa

Halima Said, Elizabeth Kachingwe, Yasmin Gardee, Zaheda Bhyat, John Ratabane, Linda Erasmus, Tiisetso Lebaka, Minty van der Meulen, Thabisile Gwala, Shaheed Omar, Farzana Ismail, Nazir Ismail

BMC Public Health

IMPACT FACTOR: 4.13

<https://bmcpublihealth.biomedcentral.com/articles/10.1186/s12889-023-17234-x>

### ABSTRACT

Drug-resistant tuberculosis (DR-TB) epidemic is driven mainly by the effect of ongoing transmission. In high-burden settings such as South Africa (SA), considerable demographic and geographic heterogeneity in DR-TB transmission exists. Thus, a better understanding of risk-factors for clustering can help to prioritise resources to specifically targeted high-risk groups as well as areas that contribute disproportionately to transmission.

### METHODS

The study analyzed potential risk-factors for recent transmission in SA, using data collected from a sentinel molecular surveillance of DR-TB, by comparing demographic, clinical and epidemiologic characteristics with clustering and cluster sizes. A genotypic cluster was defined as two or more patients having identical patterns by the two genotyping methods used. Clustering was used as a proxy for recent transmission. Descriptive statistics and multinomial logistic regression were used.

### RESULT

The study identified 277 clusters, with cluster size ranging between 2 and 259 cases. The majority (81.6%) of the clusters were small (2-5 cases) with few large (11-25 cases) and very large ( $\geq 26$  cases) clusters identified mainly in Western Cape (WC), Eastern Cape (EC) and Mpumalanga (MP). In a multivariable model, patients in clusters including 11-25 and  $\geq 26$  individuals were more likely to be infected by Beijing family, have XDR-TB, living in Nelson Mandela Metro in EC or Umgungunglovo in Kwa-Zulu

Natal (KZN) provinces, and having history of imprisonment. Individuals belonging in a small genotypic cluster were more likely to be infected with Rifampicin resistant TB (RR-TB) and more likely to reside in Frances Baard in Northern Cape (NC).

### CONCLUSION

Sociodemographic, clinical and bacterial risk-factors influenced rate of *Mycobacterium tuberculosis* (*M. tuberculosis*) genotypic clustering. Hence, high-risk groups and hotspot areas for clustering in EC, WC, KZN and MP should be prioritized for targeted intervention to prevent ongoing DR-TB transmission.

### KEYWORDS

Clustering; Drug resistant TB; Risk-factors; South Africa; Transmission. Background: Drug-resistant tuberculosis (DR-TB) epidemic is driven mainly by the effect of ongoing transmission. In high-burden settings such as South Africa (SA), considerable demographic and geographic heterogeneity in DR-TB transmission exists. Thus, a better understanding of risk-factors for clustering can help to prioritise resources to specifically targeted high-risk groups as well as areas that contribute disproportionately to transmission. in Kwa-Zulu Natal (KZN) provinces, and having history of imprisonment. Individuals belonging in a small genotypic cluster were more likely to be infected with Rifampicin resistant TB (RR-TB) and more likely to reside in Frances Baard in Northern Cape (NC).





DR NICOLE WOLTER



PROF CHERYL COHEN

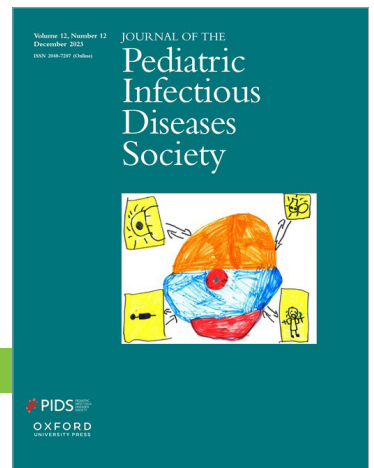
## Association of HIV Exposure and HIV Infection With In-hospital Mortality Among Hospitalized Infants <1 Year of Age, South Africa, 2016-2018

Nicole Wolter, Sibongile Walaza, Claire von Mollendorf, Anne von Gottberg, Stefano Tempia, Meredith L McMorrow, Jocelyn Moyes, Florette Treurnicht, Orienka Hellferscee, Malefu Moleleki, Mvuyo Makhasi, Neydis Baute, Cheryl Cohen

Journal of the Pediatric Infectious Diseases Society

IMPACT FACTOR: 3.80

<https://doi.org/10.1093/jpids/piad100>



### ABSTRACT

We enrolled 1323 hospitalized infants aged <1 year in 2016-2018, and examined the association between HIV status and in-hospital mortality. After controlling for confounders, HIV-exposed uninfected infants did not have an increased risk of mortality,

whereas infants living with HIV had 4 times greater risk compared with HIV-uninfected infants. Keywords: Africa; HIV exposure; HIV infection; infants; mortality.





DR ASIVE MYATAZA



DR ANTHONY SMITH

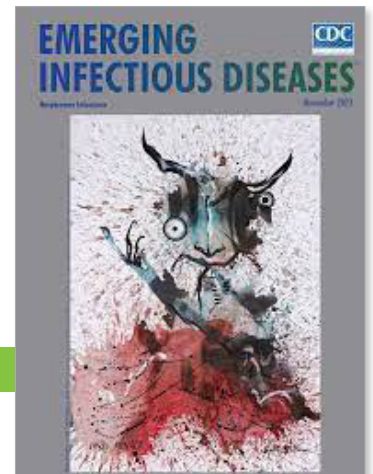
## Characterization of *Salmonella enterica* serovar Isangi from South Africa, 2020–2021

Asive Myataza, Juno Thomas, Anthony M. Smith

BMC Infectious Diseases

IMPACT FACTOR: 3.7

<https://doi.org/10.1186/s12879-023-08786-9>



### ABSTRACT

We describe the genotypic characteristics and antimicrobial resistance (AMR) determinants of *Salmonella enterica* serovar Isangi (*Salmonella* Isangi) clinical isolates in South Africa from 2020 through 2021.

### METHODS

During the years 2020 to 2021, the Centre for Enteric Diseases of the National Institute for Communicable Diseases, a national reference centre in South Africa for human infections resulting from enteric bacterial pathogens, investigated a total of 3549 clinical isolates of *Salmonella* species. Whole genome sequencing (WGS) was performed using Illumina NextSeq Technology. WGS data was analyzed using Centre for Genomic Epidemiology-based tools and EnteroBase web-based platform. Genotypic relatedness and cluster analysis was investigated based on coregenome multilocus sequence typing.

### RESULTS

Forty-nine isolates were confirmed to be *Salmonella* Isangi, with most submitted from Gauteng Province (24/49, 49%).

The most prevalent sequence type was ST335 (48/49, 98%), and the remaining 1 isolate was ST216. All ST335 isolates were genotypically multidrug-resistant (MDR), with resistance to fluoroquinolones, chloramphenicol, trimethoprim sulfamethoxazole and tetracycline; the ST216 isolate was resistant only to aminoglycosides. All ST335 isolates carried ESBL genes, the most common being blaCTX-M-15. Five clusters (consisting of isolates related within five allele differences) were detected, all being ST335.

### CONCLUSIONS

Most *Salmonella* Isangi isolates in South Africa are MDR and ESBL-positive. Ongoing monitoring of the epidemiology and AMR profile of this serovar is important for public health and treatment guidelines.

### KEYWORDS

*Salmonella enterica*, Serovar Isangi, Isangi, Africa, South Africa, ESBL





MR SUNNIEBOY LOT NJIKHO

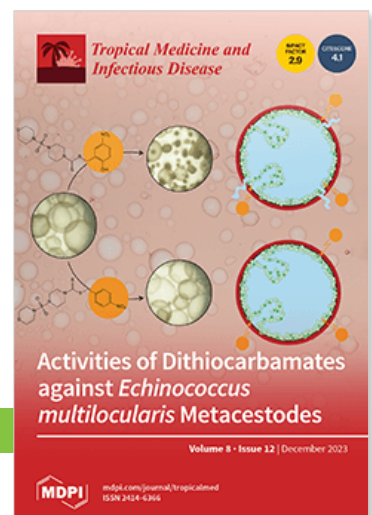
## Evaluating the Prevalence and Risk Factors of Schistosomiasis Amongst School-Aged Children in Low- and Middle-Income Communities: Ehlanzeni District Municipality, South Africa, 2015-2021

Sunnieboy Lot Njikho, Vanessa Cecilia Quan, Thokozani Patrick Mbonane, Renay Helouise Van Wyk

Tropical Medicine Infectious Disease

IMPACT FACTOR: 2.70

<https://www.mdpi.com/2414-6366/8/12/522>



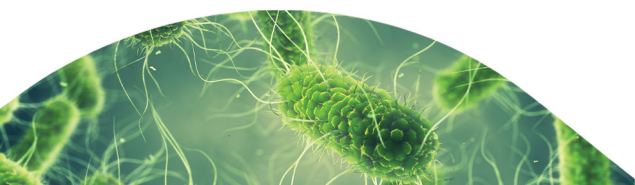
### ABSTRACT

This study aimed to assess the prevalence and identify risk factors of schistosomiasis among school-aged children in low- and middle-income communities. A retrospective cross-sectional study was conducted to review patient records of school-age children. Data on gender, age, sub-district, area residing in, patient status, history of bilharzia, presence of blood in the urine, and schistosomiasis diagnoses were collected. The data were analyzed using IBM Statistical Package for the Social Sciences (SPSS) version 27. Logistic regression was employed to determine the factors associated with schistosomiasis. The overall prevalence of schistosomiasis in the study population was 75%, with higher prevalence observed among male children (89%), children aged between 10 and 14 years (59%), urban areas (51%), and rural-dominated districts, particularly Bushbuckridge (42%) and City of Mbombela (51%). Age, especially 10-14 years old ( $p < 0.01$ ; 95%CI:

1.98-2.29), a history of bilharzia ( $p = 0.01$ ; 95%CI: 1.15-1.96), and the presence of blood in urine ( $p < 0.01$ ; 95%CI: 2.02-2.40) were significantly associated with schistosomiasis while being a female child was found to be a protective factor (AOR: 0.35; CI 0.35-0.41). This study underscores the importance of implementing robust screening procedures and the necessity for health education to mitigate the high prevalence of schistosomiasis and prevent its further spread.

### KEYWORDS

Disease; district municipality; environmental factors; low- and middle-income community; prevalence; risk factors; schistosomiasis.





DR BEVERLEY SINGH



PROF ADRIAN PUREN

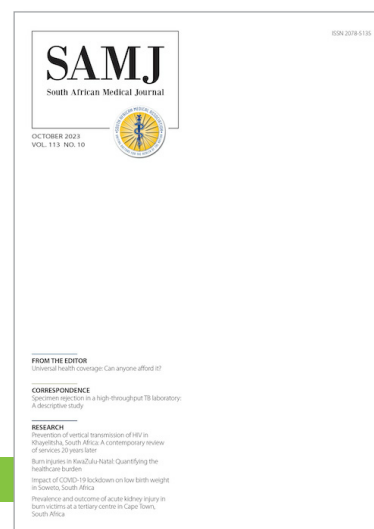
## Evaluation of the accuracy of the Asanté assay as a point-of-care rapid test for HIV-1 recent infections using serum bank specimens from blood donors in South Africa, July 2018 - August 2021

B Singh, J Mthombeni, G Olorunfemi, M Goosen, E Cutler, H Julius, Z Brukwe, A Puren

SAMJ Research

IMPACT FACTOR: 2.162

<https://doi.org/10.7196/SAMJ.2023.v113i10.678>



### ABSTRACT

Point-of-care (POC) rapid recency testing can be used as a cost-effective tool to identify recently infected individuals (i.e. infected within the last 12 months) in near-real time, support epidemic control and identify hotspots for transmission as part of recent infection surveillance.

### OBJECTIVE

To evaluate the performance of the Asanté (HIV-1) rapid recency assay as a POC rapid test among blood donors in South Africa (SA). Methods. The study was a cross-sectional and validity study of the Asanté HIV-1 Rapid Recency Assay performed on 715 consecutively archived plasma donor specimens from the SA National Blood Services to determine their recency and established HIV infection status. ELISA and rapid assays for HIV antibody detection were used as the reference-testing standard for confirming an infection, while the Maxim HIV-1 limiting antigen (LAg) avidity assay was used as a reference for comparing HIV recency status. Validity tests (sensitivity, specificity, negative and positive predictive values) and Cohen-Kappa tests of the agreement were conducted to compare the Asanté HIV-1 rapid recency assay results with the reference tests.

### RESULTS

Of the 715 studied blood samples, 63.1% (n=451/715) were confirmed to be HIV-positive based on the reference standard. The sensitivity and specificity of the Asanté HIV-1 rapid recency assay in diagnosing established HIV infection compared to the ELISA were 98.4% (95% CI 96.7 - 99.3) and 99.6% (95% CI 97.6 - 100), respectively. Compared with HIV rapid assay, the sensitivity and specificity of the Asanté HIV-1 rapid recency assay was 98.7% (95% CI 97.0 - 99.4) and 99.2% (95% CI 97.1 - 100), respectively. Of the 451 HIV-positive blood samples, 43% were confirmed as recent HIV infections by the Maxim HIV-1 LAg avidity assay. There was high agreement between the Asanté HIV-1 rapid recency assay and the Maxim HIV-1 LAg avidity assay (94.1%, k=0.879, p<0.0001). The sensitivity and specificity of the Asante HIV-1 assay was 89.4% (95% CI 84.0 - 93.0) and 97.7% (95% CI 94.8 - 99.0), respectively.

### CONCLUSION

The Asanté HIV-1 rapid recency assay test results demonstrated high accuracy (>90%) compared with the HIV ELISA and rapid assays for determining established infection and the Maxim HIV-1 LAg avidity assay for classifying recent HIV-1 infections. The assay's sensitivity for established infections was below the World Health Organization criteria (<99%) for POC devices. The Asanté HIV-1 rapid recency assay can be used to distinguish between recent and long-term infections, but may not be considered a POC test for determining HIV infection.





DR ETIENNE MÜLLER

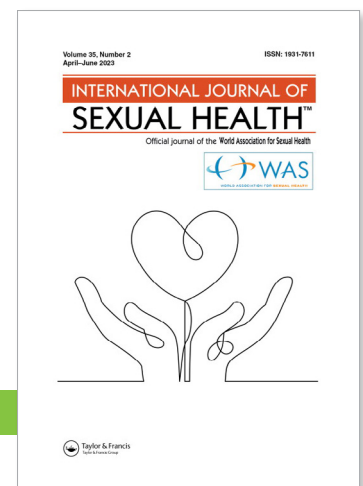
## Emergence of high-level azithromycin-resistant *Neisseria gonorrhoeae* causing male urethritis in Johannesburg, South Africa, 2021.

Müller EE, Gumede LYE, Maseko DV, Mahlangu MP, Venter JME, Da Costa Dias B, Nhlapho D, Kularatne RS.

### Sexual Health

IMPACT FACTOR: 1.6

<https://www.publish.csiro.au/SH/SH23143>



### ABSTRACT

In South Africa, *Neisseria gonorrhoeae*, which is the predominant cause of male urethritis, is treated syndromically using dual ceftriaxone and azithromycin therapy. We determined antimicrobial susceptibilities of *N. gonorrhoeae* isolates from urethral discharge specimens, and genetically characterised those with elevated minimum inhibitory concentrations (MICs) for first-line antimicrobials.

### METHODS

Routine antimicrobial susceptibility testing (AST) of *N. gonorrhoeae* isolates included E-test for ceftriaxone, cefixime and gentamicin and agar dilution for azithromycin and spectinomycin. *Neisseria gonorrhoeae* Sequence Typing for Antimicrobial Resistance (NG-STAR) was performed for isolates with elevated MICs to identify antimicrobial resistance (AMR) determinants, and *Neisseria gonorrhoeae* Multi-Antigen Sequence Typing (NG-MAST) was used to determine strain relatedness.

### RESULTS

*N. gonorrhoeae* was cultured from urethral discharge swab specimens obtained from 196 of 238 (82.4%) men presenting to a primary healthcare facility in Johannesburg in 2021. All viable isolates were susceptible to extended-spectrum cephalosporins. Four isolates had high azithromycin MICs ranging from 32 mg/L to >256 mg/L and grouped into two novel NG-MAST and NG-STAR groups. Two isolates from Group 1 (NG-MAST ST20366, NG-STAR ST4322) contained mutated *mtrR* (G45D) and 23S rRNA (A2059G) alleles, while the two isolates from Group 2 (NG-MAST ST20367, NG-STAR ST4323) had different mutations in *mtrR* (A39T) and 23S rRNA (C2611T).

### CONCLUSIONS

We report the first cases of high-level azithromycin resistance in *N. gonorrhoeae* from South Africa. Continued AMR surveillance is critical to detect increasing azithromycin resistance prevalence in *N. gonorrhoeae*, which may justify future modifications to the STI syndromic management guidelines.



DR TENDESAYI KUFA-CHAKEZHA

## Evaluating SA's Congenital Syphilis Notification Surveillance System

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<https://www.phbsa.ac.za/cs-surveillance-system/>



### ABSTRACT

Congenital syphilis (CS) is a public health problem in South Africa (SA) and is a category 2 notifiable medical condition (NMC). We conducted a cross-sectional evaluation of the CS notification system using qualitative and quantitative methods. The evaluation was guided by the United States Centers for Disease Control and Prevention (US-CDC) and the World Health Organization (WHO) surveillance guidelines for evaluating surveillance systems and their attributes.

For the quantitative analysis, we used the CS line list, including all nine provinces in SA. For the qualitative analysis, we used data collected from a REDCap online questionnaire of healthcare workers (HCWs) who had notified a CS case using the NMC system and from CS surveillance officers of NMC and the Centre for HIV/STI (CHIVSTI) of the National Institute for Communicable Diseases (NICD) in the preceding year. This evaluation found that CS surveillance was done through the notifiable medical conditions surveillance system (NMCSS) platform, where all HCWs must report a case within seven days of diagnosis. Congenital syphilis cases are notified by completing and sending a paper-based case notification form (CNF) through the electronic NMC App and a paper-based case investigation form (CIF) emailed or faxed to the programme.

The evaluation also showed that during 2020, there were 357 clinical CS cases in infants reported from 31 districts within the nine provinces in SA through the NMCSS. The mean age at diagnosis was 14 days (standard deviation = 49 days), with 184 (51.5%) males. 254 (71.15%) of the reported cases were notified within seven days or fewer from the date of diagnosis. KwaZulu-Natal Province reported more cases – 176 (49.30%) – than other

provinces. Qualitatively, the HCW's response rate was 28.6% (14/50), with many (57%) using the paper based reporting system to notify cases. Almost half of the HCWs 6/14 (43%) had good knowledge and understanding of the CS surveillance system.

Data quality was compromised due to missing or incomplete data, and no CIF was attached to the CNF in many cases. All the key informants and HCWs accepted and were willing to report CS cases through the NMCSS. Most HCWs found the CS case definition challenging, although the NMC surveillance officers found the system simple to extract data from. It is therefore concluded that the CS surveillance system in SA is useful, acceptable, and timely. The notifying system is simple to understand and use, but the case definition is not easy to use.

It is recommended that:

- The NMC/CHIVSTI and the National Department of Health (NDoH) educate HCWs on screening and diagnosing infants with CS.
- The government's sexual and reproductive programmes and maternal healthcare centres continue to implement comprehensive syphilis screening, testing, and treatment for pregnant women and their partners to reduce the recurrence of infection.
- The NDoH, policymakers, and the NMCSS continuously communicate the urgency of eliminating CS by 2030.
- HCWs be provided with better resources, such as electronic devices and internet connectivity, to enable use of the NMC App.



MS ASHLEY CHITAKA

## Diabetes mellitus mortality by major occupation category in South Africa, 2009—2016

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<https://www.phbsa.ac.za/wp-content/uploads/2023/10/Diabetes-mellitus-in-South-Africa-2009-2016-Naicker.pdf>



### ABSTRACT

In South Africa, diabetes mellitus (DM) is an escalating non communicable disease (NCD) and a leading cause of death. Certain occupational groups have an increased risk of diabetes. This study aimed to identify occupations associated with increased risk of DM mortality. We conducted a cross-sectional study using Statistics South Africa (StatsSA) mortality data. Participants aged 16—70 years, whose underlying cause of death was DM and whose occupations were provided, were included in the study. We used multivariable logistic regression to assess the association between DM mortality and occupation. Deaths from diabetes accounted for 184 080 (4.44%) of 4 147 326 total deaths for the period 2009—2016. In the unadjusted analysis, mortality odds ratios (MORs) increased significantly between 2009 and 2016. The adjusted MORs indicated that all major occupation groups had a higher risk of DM associated mortality compared to the reference major occupation (skilled agricultural and fishery workers). We conclude that workers in all occupations are at comparatively high risk of diabetes mellitus mortality in South Africa. Specific risk factors include diet, sedentary work and lifestyle, and the causes of stress and reduced mental health. Diabetes mellitus morbidity likely affects productivity leading to adverse impacts on individuals,

businesses and other entities, and the economy in general. Interventions and preventative measures (policies and awareness) are therefore indicated in all workplaces irrespective of the occupational group.

We recommend that workplaces provide:

- Access to, and education on, healthy food options that reduce the risk of DM;
- Support programmes and awareness campaigns regarding stress management and mental health;
- Awareness programmes and specific policies to prevent workplace violence and harassment;
- Policies and practices to alleviate long hours of sedentary work by encouraging periodic physical activity within a safe working environment.



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