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

SCIENCE FOCUS

A quarterly nexus of scientific insights

ISSUE 38 | Q1 | 2026/2027

The Science Focus publication acknowledges NICD staff members who have published articles in peer-reviewed journals.

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MR VUYO SABANI
SENIOR COMMUNICATIONS MANAGER

NICD scientific research provides key insights into disease management

As someone who once lost a puppy to tick bite fever, a disease I was not familiar with until that unfortunate experience, the article titled "Tick bite fever in Southern Africa" resonated with me. Even though we took the puppy to the veterinarian as soon as it showed signs of illness, it sadly died two days later while still undergoing treatment.

According to the article, tick bite fever has been a persistent feature of the South African medical landscape since it was first described in the 1930s. The authors lament that despite this long history and the accumulated medical and scientific knowledge about the disease, "it is an unfortunate fact that even in South Africa, a few patients die from severe tick bite fever every year due to missed diagnosis and delayed or inappropriate treatment."

This article is one of 40 featured in this issue, showcasing the National Institute for Communicable Diseases' (NICD) peer-reviewed research output for the first quarter of the current financial year. The publication includes peer-reviewed articles published in various journals in which NICD staff members are co-authors. The first section highlights articles in which NICD researchers are lead authors (first or last authors), while the second features articles in which NICD staff are contributing co-authors.

Another study featured in this issue, "Effects of chilling, fluorescent dust marking, and X-ray irradiation on the quality of male Anopheles arabiensis for sterile insect technique applications," led by Dr Thabo Mashatola and Dr Givemore Munhenga from the NICD's Centre for Emerging Zoonotic and Parasitic Diseases. The researchers assessed the effects of chilling, fluorescent dust marking, and X-ray irradiation on the quality of laboratory-reared male *Anopheles arabiensis*.

Research of this nature is particularly important at a time when gains in malaria control in Africa are being reversed. In 2024 alone, malaria claimed approximately 600,000 lives, with challenges including growing insecticide resistance, mosquitoes adapting to biting and resting outdoors, and a limited vector-control toolbox underscoring the need for innovative approaches to prevention and control. The article on the hantavirus outbreak that drew global attention in May makes for an interesting read.

Enjoy these and many other insightful articles in this issue. And as for the story of losing my puppy to tick bite fever, I am glad to share that its mother survived. This year, she turned 11, a good innings for a Boerboel.

On behalf of the team,

Vuyo Sabani
Senior Communications Manager

DR JACQUELINE WEYER

Andes Hantavirus outbreak on a cruise ship, 2026

Leonidas Alexakis, Anna Agoritsa Baka, Tamas Bakonyi, Freddy Banza-Mutoka, Marie Roseline Belizare, Renu Bindra, **Lucille Blumberg,** Annelies Brilman, Colin Brown, Orlando Cenciarelli, Meera Chand, Menno De Jong, Sacha de Stoppelaar, Mathew Dryden, Shenaaz El-Halabi, **Nevashan Govender**, Esther Hamblion, William Hardy, Andreas Hoefer, Thomas Hofmann, Ana Hoxha, Chikwe Ihekweazu, Thomas Inns, **Nazir Ahmed Ismail**, Kuban Iyer, Hilary Kirkbride, **Vuyiswa Kumalo**, Favelle Lamb, Olivier le Polain de Waroux, Tjalling Leenstra, Anais Legand, Abdi Rahman Mahamud, Terry Marshall, Grazina Mirinaviciute, Chanelle Moore, Jeremy Nel, John Otshudiema, Boris I Pavlin, Richard Pebody, Ihor Perehinets, David Peres, Richard Puleston, Otim Patrick Ramadan, Chantal Reusken, Adriana Romani Vidal, Wilhelmina L. M. Ruijs, Esther Schadd, Dubravka Selenic Minet, Ettore Severi, Evan Shoul, **Lerato Sikhosana**, Fernando Simón, Gianfranco Spiteri, Lorenzo Subissi, Margreet te Wierik, Sherine Thomas, Annemiek A. Van der Eijk, Maria Van Kerkhove, Michele van Vugt, Thijs Veenstra, Veronique Verhoeven, Albert Vollaard, Joseph Francis Wamala, William Welfare, **Jacqueline Weyer**

The New England Journal of Medicine

IMPACT FACTOR: 84.5

https://doi.org/10.1056/nejmc2606496

ABSTRACT

On April 27, 2026, a man (later classified as Patient 3 in the outbreak) was medically evacuated to Ascension Island from the Dutch-flagged expedition cruise ship MV Hondius; he had severe acute respiratory infection (SARI) and reported shortness of breath and fever that had begun on April 21. He had signs of pneumonia, although findings on chest radiography were unremarkable. While he was on Ascension Island, his condition worsened, and he was transferred to Johannesburg, South Africa, for ventilator support and intensive care.1 He was in shock and had acute respiratory distress syndrome; findings on chest radiography were consistent with atypical pneumonia. The differential diagnosis in this clinical context is very broad and includes atypical pneumonias, bacterial or fungal sepsis, and vectorborne diseases such as malaria or dengue. The diagnostic evaluation, including respiratory pathogen panels, malaria smear and antigen, fungal biomarkers, blood cultures, and legionella urinary antigen, was unrevealing. Further details are provided in the Supplementary Appendix, available with the full text of this letter at NEJM.org.

MR PLEASURE MALOPE

DR SHAHEED VALLY OMAR

Bedaquiline resistance-associated genetic mutations and minimum inhibitory concentrations in drug-resistant tuberculosis clinical isolates from Limpopo province, South Africa

Pleasure Malope, Molebogeng Ruth Lekalakala-Mokaba, **Dumisani Cyril Ngcamu, Halima Said**, Ivy Rukasha, **Shaheed Vally Omar**

Frontiers in Microbiology

IMPACT FACTOR: 5.8

https://doi.org/10.3389/fmicb.2026.1803115

Background: Bedaquiline (BDQ) resistance is a significant threat to tuberculosis (TB) control efforts, particularly in areas with a high burden of multidrug-resistant (MDR) and extensively drug-resistant (XDR) tuberculosis, such as South Africa. Determining the minimum inhibitory concentration (MIC) of BDQ and identifying the associated resistance-conferring mutations are critical for understanding resistance patterns and guiding therapeutic decisions. This study investigated BDQ resistance in *Mycobacterium tuberculosis* isolates across five districts in Limpopo, South Africa, by analyzing the relationship between minimum inhibitory concentrations (MICs) and resistance-conferring mutations.

Method: This study is a cross-sectional study including 147 drug-resistant (DR-TB) isolates obtained from the Polokwane laboratory, Limpopo province, South Africa. The study used phenotypic MIC drug susceptibility testing and whole-genome sequencing (WGS) to investigate BDQ susceptibility patterns. MIC determination and genetic analysis were performed on all isolates with an MIC of >1 µg/mL and a subset of those with an MIC of <1 µg/mL as a control for sequencing.

Results: Of the 147 DR-TB isolates included, 128 (87.1%) had an MIC of ≤1 µg/mL (susceptible), while 19 (12.9%) had an MIC of >1 µg/mL (resistant). Whole-genome sequencing revealed that mutations in Rv0678 (89.1%), including frameshift and codon substitution variants, were mainly associated with drug resistance, while mutations in the atpE (5.1%) and Rv1979c (5.1%) were also identified. Of the BDQ-R strains, the Euro-American (L4) lineage was dominant, accounting for 62.5%.

Conclusion: In this study, BDQ resistance was primarily driven by Rv0678 mutations. As BDQ is one of the few potent drugs available for treating DR-TB, there is a critical need for early detection and continuous surveillance to prevent the spread of resistance.

PROF. PENNY MOORE

How vaccinating people living with HIV may guide bNAb-based vaccines

Penny L. Moore, Leonidas Stamatatos, Alexandra Trkola

Journal of the International AIDS Society

IMPACT FACTOR: 5.2

https://doi.org/10.1002/jia2.70119

ABSTRACT

The HIV pandemic continues to pose a major global public health challenge. Despite the success of antiretroviral therapy (ART), access to lifelong treatment for all people living with HIV (PLWH) worldwide is not universal or affordable, and is compromised by recent changes in the funding landscape, highlighting the need for preventative vaccines. Two large efficacy trials of a single broadly neutralizing antibody (bNAb), VRC01, provided evidence that bNAbs can block acquisition by antibody-sensitive HIV strains, corroborating previous studies in non-human primates. These trials provided proof-of-principle for antibody-mediated protection, and generated essential biological insights that strengthened HIV vaccine development1.

Recent years have seen extraordinary advances in HIV immunogen design. Early phase trials of "germline-targeting" immunogens (aimed at activating the extremely rare precursors of bNAbs) in HIV-naive participants have shown engagement of these naive B-cell receptors, and early maturation towards their broadly neutralizing forms2-4. However, the vaccination schema needed to go from this early stage of B-cell activation to complete bnAb maturation remains to be established, and will require extensive Phase I testing and validation in Phase II/III efficacy trials. Trials of bNAb-inducing vaccines have historically been tested in HIV-naive participants, the target population for a preventative vaccine. However, given that providing state-of-the-art prevention, including ART, to HIV-naive individuals participating in vaccine trials is an undeniable ethical necessity, the logistical challenges of conducting vaccine trials in populations with low rates of HIV transmission are immense. In this era of highly effective ART, only extremely large-scale trials have the statistical power to establish vaccine efficacy5. This provides an additional hurdle to vaccine development.

First and last authors published reviews

DR THABO MASHATOLA

Effects of chilling, fluorescent dust marking, and X-ray irradiation on the quality of male *Anopheles arabiensis* for sterile insect technique applications

Thabo Mashatola, Givemore Munhenga, Wadaka Mamai, Thomas Wallner, Simran Singh Kotla, Chantel J. de Beer & Hanano Yamada

Scientific Reports

IMPACT FACTOR: 4.9

https://doi.org/10.1038/s41598-026-52467-x

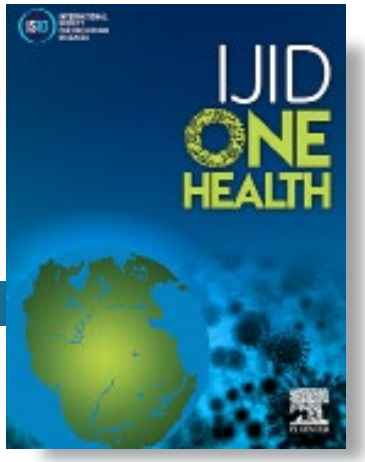
ABSTRACT

Malaria remains a major public health challenge in sub-Saharan Africa, with *Anopheles arabiensis* an important vector in several regions. Increasing insecticide resistance and flexible vector behavior limit the effectiveness of conventional control measures. The sterile insect technique (SIT) offers a complementary approach through the release of sterile males, with program success dependent on male quality. This study assessed the effects of chilling, fluorescent dust marking, and X-ray irradiation on the quality of laboratory-reared male *An. arabiensis*. Adult males were assigned to six treatment groups combining chilling, irradiation, and marking in different sequences. Male quality was evaluated through recovery, escape rates, reproductive performance, and longevity under standard insectary conditions. Recovery rates one-hour post-treatment were high across all groups (93.5–96.6%) and did not differ from controls. Escape rate was temporarily reduced at two hours but largely recovered by 24 h, with only chilled and marked males showing persistent impairment. Fecundity and female insemination rates were unaffected by treatment. Fertility remained high in non-irradiated groups and was reduced to < 0.2% following irradiation. Longevity was not significantly affected. These results indicate that male *An. arabiensis* are resilient to routine SIT handling procedures. Brief chilling followed by irradiation and marking preserves key quality traits, supporting optimized operational protocols for SIT-based malaria vector control.

PROF. JOHN FREAN

Tick bite fever in southern Africa

John Frean, Jeremy Nel, **Lucille Blumberg**, Jantjie Taljaard



International Journal of Infectious Diseases

IMPACT FACTOR: 4.6

https://doi.org/10.1016/j.ijidoh.2026.100130

ABSTRACT

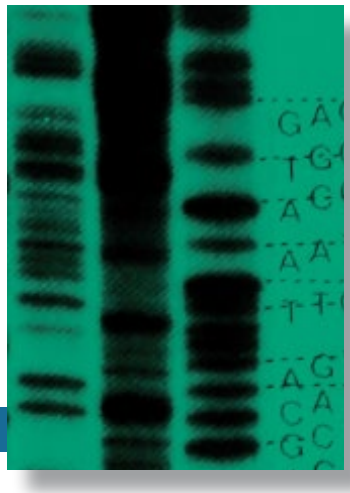
Tick bite fever (TBF) is a well-known zoonotic disease in southern Africa, caused by ixodid tick-transmitted rickettsial pathogens of the spotted fever group, which target endothelial cells, producing widespread vasculitis. Two epidemiologic and clinical forms of the condition can be distinguished, namely, African TBF and Mediterranean spotted fever–like infection. TBF is generally a mild illness, but delayed diagnosis and inappropriate treatment may lead to severe, potentially fatal, disease resembling bacterial sepsis, viral hemorrhagic fever, malaria, or other serious infections. Along with compatible epidemiologic history, common clinical diagnostic features at initial presentation are fever, headache, rash, myalgia and eschar; tender regional lymphadenopathy is common. Clinical diagnosis is sufficient to warrant treatment because serological response is slow to develop; although polymerase chain reaction of eschar material is an additional or alternative diagnostic option, this method may not be readily available. The treatment of choice is doxycycline, with macrolides as second-line antibiotics. Personal prevention revolves around awareness of risks and measures to limit exposure to ticks. As a zoonosis with a wide range of reservoir hosts, the disease cannot be eliminated but risk can be reduced by application of One Health principles.

First and last authors published reviews

MS CEBILE LEKHULENI

DR MIGNON DU PLESSIS

Clonal expansion of global pneumococcal sequence cluster 3 within serotype 8 after 13-valent pneumococcal conjugate vaccine introduction, South Africa



Cebile Lekhuleni, Kedibone Ndlangisa, Ana D Sanches Ferreira, Hsueh-Chien R Cheng, Oliver Lorenz, Jackie Kleynhans, **Linda de Gouveia, Happy Skosana, Vanessa Quan,** Amelieke J H Cremers, Paulina A Hawkins, Sopio Chochua, Lesley McGee, Stephen D Bentley, **Susan Meiring, Cheryl Cohen,** Stephanie W Lo, **Anne von Gottberg, Mignon du Plessis**

Microbial Genomics

IMPACT FACTOR: 4.5

https://doi.org/10.1099/mgen.0.001737

Background: Serotype 8 has emerged as a common non-vaccine serotype causing invasive pneumococcal disease (IPD) in children and adults globally after the introduction of pneumococcal conjugate vaccines (PCV). We aimed to determine serotype 8 incidence and genomic epidemiology in South Africa.

Methods: From national, laboratory-based surveillance for IPD in South Africa, we calculated the incidence of serotype 8 and global pneumococcal sequence cluster 3 (GPSC3) before and after PCV introduction. We performed phylodynamic analysis of genomes from clonal complex (CC) 53 and described South African isolates in the context of a global collection of serotype 8 and GPSC3 genomes.

Results: Compared to the pre-PCV period, serotype 8 incidence increased in the late-PCV13 period among children <5 years [incidence rate ratio (IRR) 2.3, 95% confidence interval (CI) 1.3-4.1] and adults >64 years (2.8, 1.1-8.3). Similarly, GPSC3 rates increased among children <5 years (IRR 2.4, 95% CI 1.4-4.3) and individuals of all ages (1.7, 1.3-2.1). Serotype 8 CC53 population dynamics predicted at least five clonal expansions since the most recent common ancestor in 1929 (credible interval 1919-1937), with future predictions showing increases in the effective population size despite remaining largely susceptible to first-line treatment. Serotype 8 CC53 isolates from South Africa had a clonal structure when contextualized within a global collection of serotype 8 and GPSC3 genomes.

Conclusions: Serotype 8 invasive disease incidence increased in South Africa after PCV introduction. Predictions showed sustained increases over time. Since South Africa switched to a lower-valency PCV10 (Pneumosil, Serum Institute of India) that does not include serotype 8 in 2024, continued surveillance will be crucial to inform PCV policy-making.

DR WENLONG CARL CHEN

Lifestyle and environmental risk factors for esophageal squamous cell carcinoma: evidence from the Johannesburg cancer study

Wenlong Carl Chen, Debbie Bradshaw, Thendo Ramaliba, Chantal Babb de Villiers, Rob Newton, Tim Waterboer, Christopher G. Mathew, **Mazvita Muchengeti,** Freddy Sitas

JCO Global Oncology

IMPACT FACTOR: 3.8

https://doi.org/10.1200/GO-25-00669

Background: Esophageal squamous cell carcinoma (ESCC) remains a major cause of cancer mortality in South Africa. Understanding locally relevant and modifiable risk factors is crucial for prevention. This study clarifies the syndemic role of lifestyle and environmental factors, such as alcohol, tobacco, socioeconomic indicators (rurality and education), and fuel use, in ESCC.

Methods: We analyzed 939 histologically confirmed ESCC cases and 3,089 cancer controls from the Johannesburg Cancer Study. Multivariable logistic regression estimated adjusted odds ratios (aORs), with interaction terms for alcohol, tobacco, and sex. Population attributable fractions were calculated using both study-control and national prevalence estimates.

Results: Very high alcohol intake (≥840 g ethanol/wk) showed a modest independent association with ESCC (aOR, 1.56 [95% CI, 1.14 to 2.12]). Smoking was a strong risk factor, with aOR = 2.82 (95% CI, 2.20 to 3.62) for ex-smokers and 6.71 (95% CI, 5.15 to 8.76) for current smokers. Among never-smokers, alcohol showed little dose response. Among smokers, risks were high across all alcohol levels, with no consistent increase at higher intakes. Additional risks included rural origin or residence (aOR approximately equal to 1.22-2.38), lower educational attainment (aOR approximately equal to 1.45-1.69), and use of biomass or other fuels (aOR, 1.50 [95% CI, 1.21 to 1.87]).

Conclusions: In this high-burden setting, tobacco remains the principal modifiable driver of ESCC. Alcohol showed only a modest independent effect, limited to very high intake, and did not increase the risk among smokers beyond the high risk from smoking. Socioeconomic and environmental disadvantages cluster with behavioral risks, underscoring a syndemic context. These findings, consistent with prior Johannesburg Cancer Study reports yet offering greater exposure granularity, support targeted prevention strategies focused on smoking cessation, mitigation of hazardous drinking patterns, and reduction of household environmental exposures.

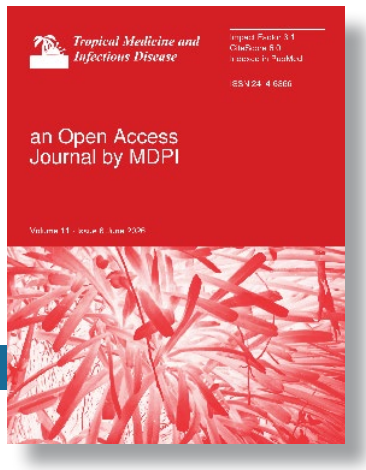
First and last authors published reviews

DR CHARLOTTE SRIRUTTAN-NEL

DR VEERLE DERMAUX-MSIMANG

Persistent burden of schistosomiasis in South Africa: a national laboratory-based analysis, 2019-2024

Charlotte Sriruttan-Nel, Bhavani Moodley, John Frean, Dumisani Mlotshwa, Veerle Msimang



Tropical Medicine and Infectious Disease

IMPACT FACTOR: 3.1

https://doi.org/10.3390/tropicalmed11060154

ABSTRACT

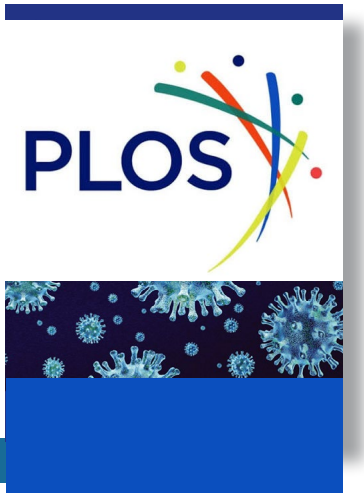
Schistosomiasis remains the second leading cause of death among parasitic diseases globally, contributing substantially to chronic morbidity and disability. South Africa (SA) is endemic for schistosomiasis, with ongoing efforts to expand mass drug administration. In the absence of true prevalence data, this study retrospectively analysed public sector laboratory-confirmed schistosomiasis cases from 2019 to 2024. Over this period, 73,680 cases were microscopically diagnosed, with Schistosoma haematobium accounting for 99.9% of infections. The test positivity rate of 20 per 100,000 population is lower than previously reported, with the burden concentrated among boys aged 5-19 years, particularly in the KwaZulu-Natal, Limpopo, and Mpumalanga provinces. These findings highlight a persistent burden within defined demographic groups and geographic areas, while also suggesting possible early signs of improvement that are potentially linked to public health interventions. The results provide valuable evidence to inform the scale-up of national schistosomiasis control programmes and the prioritisation of interventions towards the most affected populations.

DR ETIENNE MÜLLER

DR BIANCA DA COSTA DIAS

Sexually transmitted infection prevalence and *Neisseria gonorrhoeae* antimicrobial resistance patterns in men who have sex with men with or without urethral discharge syndrome in Johannesburg, South Africa, 2024

Etienne E. Müller, Mpumelelo Sibanda, Mahlape P. Mahlangu, Johanna M. E. Venter, Lindy Y.E. Gumede, Duduzile Valashiya, Dumisile V. Maseko, Frans Radebe, Thabitha Mathega, Portia Baloyi, Nelisiwe Swana, Tendesayi Kufa, Maurice Greeves, Joseph Adams, Magnus Unemo, Ismail Maatouk, **Bianca Da Costa Dias**



PLoS Global Public Health

IMPACT FACTOR: 2.8

https://doi.org/10.1371/journal.pgph.0006256

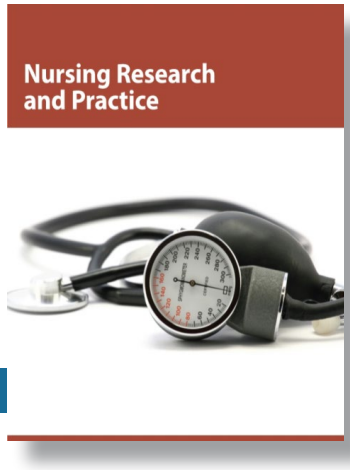
ABSTRACT

We conducted a cross-sectional study to estimate the prevalence of urogenital and extragenital sexually transmitted infections (STIs) among men who have sex with men (MSM) with and without urethral discharge syndrome, to assess infections missed by syndromic management, and to describe phenotypic antimicrobial susceptibility patterns of *Neisseria gonorrhoeae*. The study included 189 MSM attending the Engage Men's Health Clinic in Johannesburg, South Africa, in 2024. Urethral, rectal and oropharyngeal swabs were tested by multiplex PCR for *Neisseria gonorrhoeae* (NG), *Chlamydia trachomatis* (CT), *Mycoplasma genitalium* (MG) and *Trichomonas vaginalis* (TV). Genital ulcer swabs were tested for HSV-1/2, lymphogranuloma venereum (LGV), *Haemophilus ducreyi* (HD) and *Treponema pallidum* (TP). Serological diagnostic testing for HIV, hepatitis B virus (HBV) and syphilis was performed. NG isolates underwent culture and antimicrobial susceptibility testing. Among MSM with urethritis, NG was most prevalent (urethra: 80.3%, rectum: 41.7%), followed by CT (urethra: 14.8%, rectum: 11.7%). Pharyngeal NG was more common among MSM with urethritis than those without (18.0% vs 3.1%, p = 0.001). Among MSM without urethritis, rectal NG and CT prevalence were 13.5% and 9.5%; rectal LGV was detected in three cases. Among 22 participants with genital ulcers, an aetiology was identified in eight: HSV-2 (n = 3), TP (n = 4) and LGV (n = 1). All NG isolates were susceptible to ceftriaxone, cefixime, and azithromycin, and had low MICs of gentamicin. HIV, HBsAg and treponemal antibody seroprevalence were 31.4%, 3.2% and 50.8%. Active syphilis (RPR titres ≥1:32) was more frequent among MSM without urethral symptoms. Among MSM with urethritis, CT infection was less likely in those reporting recent insertive oro-anal sex and HIV pre-exposure prophylaxis (PrEP) use. Among MSM without urethritis, any discharge STI was associated with homosexual orientation, HIV positivity and lack of circumcision, NG with HIV positivity and being uncircumcised and CT with HIV positivity. Extragenital and asymptomatic STIs remain common among MSM in Johannesburg, stressing the need for routine multi-site molecular screening and inclusion of rapid serological syphilis testing in national STI guidelines for key populations.

DR MOSHIBUDI PONCHO PHAFANE

Predictors of long COVID-19 syndrome and hospital admissions among COVID-19-diagnosed adult patients who self-isolated at home in KwaZulu-Natal province, South Africa

Moshibudi Poncho Phafane, Alone Isabirye, Poovendhree Reddy



Nursing Research and Practice

IMPACT FACTOR: 2.5

https://doi.org/10.1155/nrp/9317685

ABSTRACT

Long COVID-19 (LC) syndrome is a complex systemic illness that is currently recognised to have a high morbidity rate and hospitalisations. The study analysed factors linked to LC in adults self-isolated during COVID-19 infection in KwaZulu-Natal Province, South Africa, focusing on two densely populated districts (uMgungundlovu and eThekwini Metro Municipality). We employed a cross-sectional study among individuals aged 18 years and above who self-isolated at home. Demographic data, COVID-19 vaccination status, and post-COVID-19 health symptoms were collected using a standardised questionnaire. The National Health and Nutrition Survey's Physical Functioning Questionnaire was adapted to evaluate health and functional outcomes six months after a COVID-19 diagnosis, addressing both physical and psychosocial symptoms during that timeframe. A modified Poisson regression model was used to determine the predictors of LC and hospitalisation. Of the 280 participants, 46% (n = 130) reported having at least one health-related symptom, while 36% (n = 47) had ≥ five symptoms. Approximately half of the participants (50%, n = 139) had at least one hospital admission following infection due to persistent symptoms. Older age (aIRR 1.5; 95% CI: 1.2–3.2; p = 0.021), reinfection (aIRR 2.0; 95% CI: 1.3–3.0; p = 0.001), having positive household contacts (aIRR 2.1; 95% CI: 1.4–3.2; p < 0.001) and hospitalisation (aIRR 7.7; 95% CI: 3.8–15.6; p < 0.001) increased the risk of developing LC. Post-infection hospitalisation was significantly associated with symptoms such as anxiety (aIRR 1.4; 95% CI: 1.1–1.7; p = 0.009), depression (aIRR 1.9; 95% CI: 1.6–2.3; p < 0.001), sore throat (aIRR 1.5; 95% CI: 1.7–2.0; p = 0.002) and weight loss (aIRR 1.8; 95% CI: 1.4–2.4; p < 0.001). A considerable percentage of participants with post-SARS-CoV-2 infections presented with long-term complications and required medical intervention. Postpandemic healthcare planning and resource allocation need to be considered since increased morbidities associated with LC place a burden on the already inadequately funded healthcare system.

DR VANESSA QUAN

PROF. NELESH P. GOVENDER

Maternal-infant characteristics of preterm and term neonates with bloodstream infections in lower-tier hospitals in South Africa: a cross-sectional Study

Vanessa Quan, Susan Meiring, Rudzani Mashau, Olga Perovic, Rindidzani Magobo, Marshagne Smith, Ruth Mpembe, Anne von Gottberg, Linda de Gouveia, Sibongile Walaza, Cheryl Cohen, Constance Kapongo, Cheryl Mackay, Mphekwa Thomas Mailula, Omphile Mekgoe, Lerato Motjale, Rose Phayane, Angela Dramowski, **Nelesh P Govender; for Baby GERMS-SA**

The Pediatric Infectious Disease Journal

IMPACT FACTOR: 2.3

https://doi.org/10.1097/inf.0000000000005127

Background: Bloodstream infections (BSI) are an important cause of neonatal deaths in low- and middle-income countries.

Methods: We conducted a cross-sectional study of culture-confirmed BSI in neonates aged <28 days at 6 lower-tier South African hospitals (October 2019 to September 2020), comparing maternal-infant characteristics between preterm and term babies.

Results: Of 907 BSI episodes, clinical data were available for 676 neonates. Median gestational age was 33 weeks [interquartile ranges (IQR), 29-37 weeks], with 70% (472/676) of neonates born preterm. Preterm neonates had longer median hospital stays than term neonates [19 days (IQR, 9-36) vs. 11 days (IQR, 6-17), P < 0.001], more BSI episodes during days 3-27 of life [72% (343/472) vs. 57% (119/204); P < 0.001] and higher maternal HIV prevalence [38% (177/463) vs. 24% (49/200); P = 0.001]. Fewer mothers of preterm versus term neonates attended antenatal clinic appointments [86% (367/426) vs. 94% (166/176); P = 0.004]. Crude mortality was higher among preterm versus term neonates [31% (146/472) vs. 8.3% (17/204); P < 0.001], with a higher BSI-attributable mortality (defined as death within 3 days of a BSI) [21% (97/472) vs. 5.4% (11/204); P < 0.001]. Preterm neonates had 3.7 times higher adjusted odds of death (1·71-8·14; P = 0.001) than term neonates.

Conclusion: Preterm neonates with a BSI were more likely to die than those who were term. Neonatal units should implement interventions to prevent horizontal transmission of infections among these small, sick neonates. Targeted antenatal and intrapartum interventions are needed to prevent preterm births as a root cause.

DR WENLONG CARL CHEN

External validation of a prognostic score for oesophageal cancer (PSOC) for patients treated with palliative intent in a resource-limited setting

Ferndale L, Bhadree S, **Wenlong Carl Chen**

South African Medical Journal

IMPACT FACTOR: 1.4

https://doi.org/10.7196/SAMJ.2026.v116i6.4209

Background: Oesophageal cancer (OC) is common in South Africa (SA), where late presentation limits curative treatment. In resource- constrained settings, staging may not benefit patients with a poor prognosis. The prognostic score for oesophageal cancer (PSOC), based on Eastern Cooperative Oncology Group performance status scale, body mass index and serum albumin, was previously developed to predict short-term survival.

Objectives: To externally validate PSOC in an independent cohort.

Methods: We performed a retrospective validation study using prospectively collected data from two public sector hospitals in KwaZulu- Natal Province, SA. Eligible patients had histologically confirmed OC and complete PSOC data, and were treated with palliative intent. The primary endpoint was survival ≥3 months. Logistic regression assessed associations between PSOC and survival. Discrimination was quantified using the area under the receiver operating characteristic curve (AUROC), calibration with the Hosmer-Lemeshow test and accuracy with the Brier score. Secondary analyses evaluated overall survival (OS) with Kaplan-Meier and Cox models.

Results: We included 465 patients (mean age 61 years; male:female ratio 1:1), 97% with squamous cell carcinoma. Higher PSOC scores predicted improved survival (score 4 v. 0: odds ratio 11.87, 95% confidence interval (CI) 4.87 - 28.91; p<0.001). AUROC was 0.681 (95% CI 0.630 - 0.732) with good calibration (Hosmer-Lemeshow p=0.920). Median OS was 4.8 months, with significant survival differences across score groups (log-rank p<0.001). The Brier score was 0.190, indicating good predictive accuracy.

Conclusion: PSOC is a simple, validated tool for predicting short-term survival in OC, and may guide decisions on staging v. palliation in high-incidence, resource-limited settings.

MS NOTHEMBELANI JONGISA

Factors associated with tuberculosis lost to follow-up among individuals in Buffalo City Metro, Eastern Cape province, South Africa, 2019 - 2022 (a retrospective cohort study)

Nothembelani Jongisa, Nqobile Ngoma, **Ruvimbo Chingonzoh**, **Hetani Mdose**, Thomas Dlamini, Alfred Musekiwa, Namhla Linda Mdingi-Buqa, Zonwabele Merile, Singilizwe Tinkili Moko

Pan African Medical Journal

IMPACT FACTOR: 0.9

https://www.panafrican-med-journal.com//content/article/54/42/full

Background: Tuberculosis (TB) is a treatable infection caused by *Mycobacterium tuberculosis*, an airborne bacterium spreading from person to person. Tuberculosis remains a major global health concern, and South Africa has the highest incidence. Tuberculosis control is hampered by loss to follow-up and low adherence to treatment. Tuberculosis lost to follow-up has never been described in Buffalo City Metro (BCM), Eastern Cape, South Africa. The aim of this study was to estimate the proportion of lost to follow-up and identify associated risk factors.

Methods: The retrospective cohort study was conducted using the secondary data from the Tier.Net system. Descriptive statistics were used to report epidemiological findings. The Poisson regression model was used to determine risk factors for lost to follow-up.

Results: During the study period there were 14,182 records of tuberculosis case patients in Buffalo City Metro. Of these, 1,969 (14.8%) were lost to follow-up. The median age was 40, Interquartile Range (IQR): 31-47 years, and the majority were male (1,432/1969, 72.7%), (1,801/1969, 91.4%) had pulmonary tuberculosis. Antiretroviral therapy (Adjusted Incidence Rate Ratio (aIRR) 0.80, 95% confidence interval (CI): 0.72-0.89; P<0.001), age 30-44 years (aIRR 0.88, 95% CI: 0.79-0.99; P=0.04) were associated with lower probability, and new tuberculosis case (aIRR 2.96, 95% CI: 2.28-3.83; P<0.001) was associated with higher probability of tuberculosis lost to follow-up.

Conclusion: Our study demonstrated that being on antiretroviral therapy and newly diagnosed with tuberculosis were independently and significantly associated with a lower risk of loss to follow-up. This demonstrates the importance of early initiation of antiretroviral therapy and tuberculosis treatment, age-appropriate tailored support, and enhanced retention to care is integral in continuity of care. Addressing these programmatic factors can improve lost to follow-up (LTFU) and improve linkage to care. Therefore, improve clinical TB outcomes in similar high-burden settings.

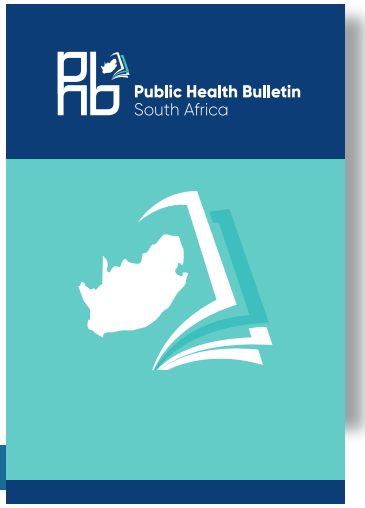
First and last authors published reviews

MR NEO LEGARE

DR SUSAN MEIRING

Provincial epidemiology of invasive pneumococcal disease in South Africa, 2019–2024: findings from laboratory-based surveillance in the Eastern, Northern, and Western Cape provinces

Neo Legare, Kate Bishop, Ghowa Booley, Sipho Dlamini, Angela Dramowski, Brian Eley, **Nondumiso Khoza**, Denise Kyazze, Siyazi Mda, Loyiso Mnqokoyi, Uafulufhedzea Ndou, Arifa Parker, Elizabeth Prentice, Kessendri Reddy, Anthea Ryan, Hafsah Tootla, **Linda de Gouveia, Sibongile Walaza, Cheryl Cohen, Anne von Gottberg, Vanessa Quan, Susan Meiring, for GERMS-SA.**



Public Health Bulletin South Africa

IMPACT FACTOR:N/A

https://www.phbsa.ac.za/provincial-epidemiology-invasive-pneumococcal-disease-south-africa-2019-2024/

Introduction: Invasive pneumococcal disease (IPD), caused by *Streptococcus pneumoniae*, remains a significant public health concern in South Africa, particularly among infants, older adults, and individuals with underlying conditions. While the introduction of pneumococcal conjugate vaccines (PCVs) into the Expanded Programme on Immunisation in 2009 led to substantial declines in disease incidence, IPD has not been eliminated. Ongoing transmission, alongside evolving serotype patterns, continues to shape the burden of disease across populations. National surveillance systems provide critical insight into overall IPD trends, but they can mask important differences at provincial level. Variations in population structure, healthcare access, HIV prevalence, and local health system capacity influence both disease incidence and clinical outcomes. These differences became more pronounced during and after the COVID-19 pandemic, when non-pharmaceutical interventions temporarily reduced transmission before incidence rebounded toward pre-pandemic levels. Laboratory-based surveillance offers a robust approach to monitoring IPD by capturing confirmed cases and enabling detailed analysis of incidence, serotype distribution, and patient characteristics. In this report, we describe the epidemiology of IPD in the Eastern Cape, Northern Cape, and Western Cape provinces from 2019 to 2024, using laboratory-confirmed cases reported through national surveillance.

Methods: Data were prospectively collected through GERMS-SA, a national infectious disease surveillance platform conducting laboratory-based, population-based, and enhanced surveillance. For this study, we selected three geographically adjacent provinces in SA (EC, NC, and WC) to provide detailed provincial-level analyses, with data from other provinces reported separately. From 2019 through 2024, all laboratory-confirmed cases of IPD in these provinces were included.

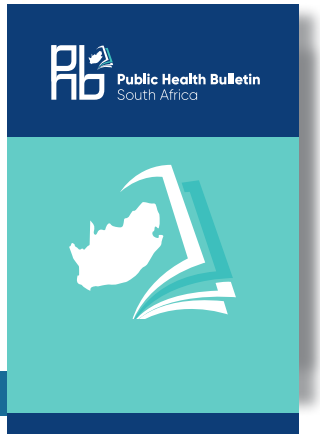
Results: Between January 2019 through to December 2024, 5 108 laboratory-confirmed IPD cases were reported to the GERMS-SA surveillance programme in the three provinces overall; 71% (3 647/5 108) of cases were confirmed on blood culture, ranging from 55% in the EC to 78% in the WC.

First and last authors published reviews

DR VANESSA QUAN

DR SUSAN MEIRING

2024 GERMS-SA: Annual surveillance review – Key findings



Vanessa Quan, Jackie Kleynhans, **Anne von Gottberg, Keeren Lutchminarain, Phuti Sekwadi, Charlotte Sriruttan-Nel, Bhavani Moodley, Tiisetso Lebaka, Pinky N Manana, Vindana Chibabhai, Susan Meiring**

Public Health Bulletin South Africa

IMPACT FACTOR: N/A

https://www.phbsa.ac.za/2024-germs-sa-annual-surveillance-review-key-findings/

Introduction: Infectious diseases caused by bacterial, fungal, and parasitic pathogens remain a major public health concern. Surveillance systems that rely on laboratory-confirmed cases provide critical insights into disease burden and epidemiology, but can be affected by disruptions in diagnostic and reporting capacity. GERMS-SA is a national, population-based laboratory surveillance programme led by the National Institute for Communicable Diseases, monitoring bacterial, fungal, and parasitic infections across South Africa through a network of laboratories and sentinel hospital sites. In 2024, marking over two decades of surveillance, findings showed that opportunistic infections, particularly cryptococcosis, remained major contributors to severe disease and mortality, while vaccine-preventable diseases continued to present a persistent burden with evolving epidemiology. Additionally, the programme was also expanded surveillance to include neglected tropical diseases, specifically schistosomiasis and soil-transmitted helminth infections in Limpopo and Mpumalanga. The following review summarises key findings from the GERMS-SA 2024 Annual Surveillance Review, highlighting trends across major infectious disease categories and reflecting on the role of long-standing surveillance systems in informing public health policy, vaccine strategies, and outbreak response in South Africa.

Methods: In essence, public and private microbiology laboratories nationally submit culture-positive isolates on Dorset transport media, in line with GERMS-SA case definitions, to the NICD, where reference laboratories confirm the organism, perform antimicrobial susceptibility testing, and conduct serogrouping/serotyping on viable isolates (or on PCR-confirmed, culture-negative specimens), as well as molecular characterisation. Laboratories also submit case reports to the NICD using standardised case definitions and laboratory case report forms containing patient demographics, specimen type, and laboratory test results.

Results: A total of 12 657 surveillance cases were detected in 2024 (including audit cases). Opportunistic infections, particularly cryptococcosis, remained major contributors to severe disease and mortality across all age groups. Vaccine-preventable and epidemic-prone diseases showed ongoing burden and shifting epidemiology, including increased meningococcal disease and persistent pneumococcal and enteric fever patterns. Neglected tropical disease surveillance in Limpopo and Mpumalanga showed high confirmation rates but highlighted under-submission of specimens and provincial variability.

First and last authors published reviews

MS TIISETSO LEBAKA

DR VANESSA QUAN

Epidemiology of cryptococcal disease in the Eastern, Northern, and Western Cape provinces of South Africa, 2022–2024

Tiisetso Lebaka, Susan Meiring, Mokupi Manaka, Vindana Chibabhai, Caroline Maluleka, Amanda Shilubane, Liliwe Shuping, Rudzani Mashau, Denise Kyazze, Loyiso Mnqokoy, Elizabeth Prentice, Uafulufhedzea Ndou, Kessendri Reddy, Sipho Dlamini, Arifa Parker, **Nelesh P. Govender, Vanessa Quan for GERMS-SA**

Public Health Bulletin South Africa

IMPACT FACTOR: N/A

https://www.phbsa.ac.za/epidemiology-of-cryptococcal-disease-in-the-eastern-northern-and-western-cape-provinces-of-south-africa-2022-2024/

Introduction: Cryptococcal disease is a serious fungal infection caused by *Cryptococcus* species, most commonly affecting people with weakened immune systems. In individuals living with HIV, particularly those with advanced disease, the infection can spread to the brain and cause cryptococcal meningitis, a life-threatening condition if not diagnosed and treated early. In South Africa, cryptococcal disease remains a major public health concern despite expanded access to antiretroviral therapy (ART). Late HIV diagnosis, interruptions in treatment, and challenges in linking patients to care continue to result in many individuals presenting with advanced immunosuppression, where the risk of severe opportunistic infections is highest. While routine surveillance provides national estimates of disease burden, it often does not capture detailed information on how patients present, the treatments they receive, and their outcomes. Laboratory-based surveillance, such as the GERMS-SA surveillance programme, addresses this gap by linking confirmed cases to clinical and treatment data, offering a clearer picture of disease patterns and care across provinces. The objective of this study was to describe the epidemiology, including clinical characteristics, antifungal treatment, and outcomes, of laboratory-confirmed cryptococcal disease reported through the GERMS-SA surveillance programme in the Eastern, Northern, and Western Cape provinces of South Africa between 01 January 2022 and 31 December 2024.

Methods: This was a descriptive study using data from the GERMS-SA national laboratory-based surveillance programme, which monitors laboratory-confirmed cases of cryptococcosis reported by both public and private clinical microbiology laboratories across South Africa. The study population comprised all individuals with confirmed cryptococcal disease diagnosed in the three provinces during the study period. Inclusion criteria for an incident case of cryptococcosis were defined by a positive cerebrospinal fluid (CSF) India ink test, a positive CSF CrAg test or culture of *Cryptococcus* species from any specimen. Duplicate episodes, defined as any positive laboratory sample within 30 days, were excluded. Cases of isolated cryptococcal antigenaemia (the presence of CrAg in the blood) were not included.

Results: Between 01 January 2022 and 31 December 2024, GERMS-SA detected 3 656 laboratory-confirmed cases of cryptococcal disease across the EC, NC, and WC provinces. Of these, 664 (18%) cases were identified at ESS, where clinical information is routinely collected, while the remaining 2 992 (82%) cases were reported from non-ESS facilities where no clinical data is available.

Other publications highlighting NICD staff contributions

Disclaimer: Impact factor scores contained in this publication were compiled in April - June 2026.

Other publications highlighting NICD staff contributions

PROF. NICOLA PAGE

Redefining diarrheal disease surveillance: long term nucleic acids stability with simple, low-cost stool preservation

Debes AK, Baumgartner ET, Safir AJ, Luo W, Williams C, Guenou E, Houpt ER, Ateudjieu J, Sack DA, **Page Nicola**, Liu J, Perin J

International Journal of Infectious Diseases
https://doi.org/10.1016/j.ijid.2026.108535

Influence of the broadly neutralizing antibody VRC01 on HIV breakthrough virus populations in antibody-mediated prevention trials

DR NONHLANHLA N. MKHIZE

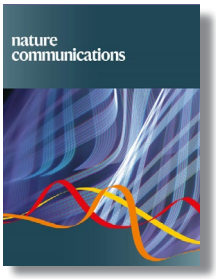
DR BRONWEN LAMBSON

MS HAAJIRA KALDINE

MS SINETHEMBA BHEBHE

PROF. PENNY L. MOORE

Carolyn Williamson, Chivonne Moodley, Craig A. Magaret, Elena E. Giorgi, Morgane Rolland, Dylan H. Westfall, Anna Yssel, Wenjie Deng, Raabya Rossenkhan, **Nonhlanhla N. Mkhize**, Lennie Chen, Hong Zhao, Tanmoy Bhattacharya, Alec Pankow, Ben Murrell, Talita York, Asanda Gwashu-Nyangiwe, Nonkululeko Ndabambi, Ruwayhida Thebus, Paula Cohen, **Bronwen Lambson, Haajira Kaldine, Sinethemba Bhebhe**, Michal Juraska, Hongjun Bai, Allan C. deCamp, Maurine D. Miner, James Ludwig, Cindy Molitor, Nicolas Beaume, David Matten, Yunda Huang, Lily Zhang, Daniel B. Reeves, Bryan Mayer, Shelly T. Karuna, John A. Hural, Lynn Morris, David Montefiori, Roger E. Bumgarner, **Penny L. Moore**, Paul T. Edlefsen, Srilatha Edupuganti, Nyaradzo Mgodi, M. Juliana McElrath, Myron S. Cohen, Lawrence Corey, Peter B. Gilbert, James I. Mullins



Nature Communications
https://doi.org/10.1038/s41467-026-70888-0

Role of casual contact in drug-resistant tuberculosis transmission: a molecular epidemiology study

DR KEEREN LUTCHMINARAIN

DR SHAHEED V. OMAR

MS THABISILE GWALA

MS LAVANIA JOSEPH

MS HERMINA M. VAN DER MEULEN

Neel R Gandhi, Kogieleum Naidoo, **Keeren Lutchminarain, Shaheed V Omar**, Hikari Yoshii, Fay Willis, Resha Boodhram, **Thabisile Gwala**, Angela Campbell, Megan M Coe, A Nichole Evans, Linrui Tang, Melanie H Chitwood, Senzo R Hlathi, Patience N Mbatha, **Lavania Joseph, Hermina Minty Van Der Meulen,** Koleka Mlisana, Samuel M Jenness, Mark N Lurie, Barry N Kreiswirth, Joshua L Warren, Kristin N Nelson Sara C Auld, James C M Brust, Ted Cohen, Barun Mathema, N Sarita Shah

American Journal of Respiratory and Critical Care Medicine
https://doi.org/10.1093/ajrccm/aamag140

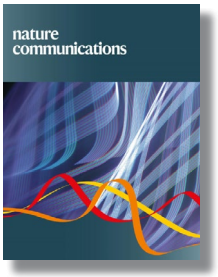
Disclaimer: Impact factor scores contained in this publication were compiled in April - June 2026.

Other publications highlighting NICD staff contributions


DR SHAHEED V. OMAR


PROF. NAZIR ISMAIL

Convolutional neural networks quantify antibiotic resistance in *Mycobacterium tuberculosis* with diagnostic grade accuracy and predict treatment response



Sanjana G Kulkarni, Anna G Green, Brendon C Mann, Samantha Malatesta, Suchitra Kulkarni-Goodwin, Nina Cesare, Shandukani Mulaudzi, Noorjahn Rawoot, Robin M. Warren, Karen R. Jacobson, Maha R. Farhat; **MIC-ML Consortium: Shaheed Vally Omar**, Hafid Soualhine, **Nazir Ismail**, Barun Mathema, Neel Gandhi, Helen McIlleron, Satoshi Mitarai, Kyungjong Kim, Helen Cox, Stuart Meier, Robin M. Warren, Elizabeth Streicher, Sacha Laurent, Timothy Rodwell, Carl-Michael Nathanson, Barry Kreiswirth, Elise DeVos, Daniela Cirillo, Vincent E. Escuyer, Elena Martinez, Vitali Sintchenko, Anzaan Dippenaar, Tim Heupink, Annelies Van Rie & James C. M. Brust

Nature Communications
https://doi.org/10.1038/s41467-026-72225-x

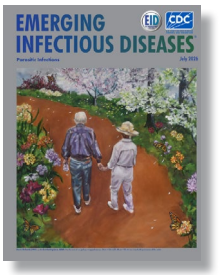
Public health response to toxigenic respiratory diphtheria outbreaks at correctional facility, South Africa, 2023-2025


DR JOCELYN MOYES


PROF. ANNE VON GOTTBERG


DR MIGNON DU PLESSIS


MS JANINE BEZUIDENHOUT



Maria Jose, Nectarios Papavarnavas, Arifa Parker, Charlene Lawrence, **Janine Bezuidenhout**, Levani Naidoo, Yolanda Cottee, Kathryn Grammer, Wentzel Dowling, **Jocelyn Moyes, Anne von Gottberg, Mignon du Plessis**, Hassan Mahomed

Emerging Infectious Diseases
https://doi.org/10.3201/eid3206.251957


DR JAISHREE RAMAN

The MARC SE-Africa dashboard: joining forces to counteract emerging antimalarial resistance in South and East Africa

Stephanie van Wyk, Ishen Seocharan, Eulambius M. Mlugu, Dhol S. Ayuen, Donnie Mategula, Tikhala Makhaza, James Kiarie, Victor Asua, Jimmy Opigo, Aimable Mbituyumuremyi, Kibor Kipkemoi Keitany, Emmah Mongina Nyandigisi, Pierre Sinarinzi, Peter Aguek Kon Baak, Tommy Nseka Manbul, Samwel Lazaro Nhiga, Sijenunu Aron Mwaikambo, Maulid Kassim, Sija Joseph Sija, Abdikarin Hussein Hassan, Michael Katende, **Jaishree Raman**, Karen I. Barnes

Plos Digital Health
https://doi.org/10.1371/journal.pdig.0000743

Disclaimer: Impact factor scores contained in this publication were compiled in April - June 2026.

Other publications highlighting NICD staff contributions

PROF. ANNE VON GOTTBERG

Oropouche virus: transmission, epidemiology, genetic diversity, and public health implications

Lorenzo Subissi, James R Otieno, Christopher Ruis, Ingrid Rabe, Anurag Agrawal, Laith Jamal Abu-Raddad, Esam I Azhar, Martin Beer, Haroldo Bezerra, Leon Caly, Meera Chand, Ariamys Companioni, Tulio de Oliveira, Isabelle Dietrich, Christian Drosten, Pablo Duran, Nuno R Faria, Adeola Fowotade, Lionel Gresh, Baoying Huang, Jason Kindrachuk, Marion P G Koopmans, Bette Korber, Yee-Sin Leo, Placide Mbala-Kingebeni, Martina McMenamin, Nada M Melhem, Vincent J Munster, Bruno T D Nunes, Bas B Oude Munnink, Felipe G Naveca, Malik Peiris, Gustavo Palacios, Paola Resende, Angel Rodriguez, Senjuti Saha, Tadaki Suzuki, Andrea Vicari, **Anne von Gottberg**, Pragya Yadav, Jairo Mendez-Rico, Maria D Van Kerkhove, Diana P Rojas

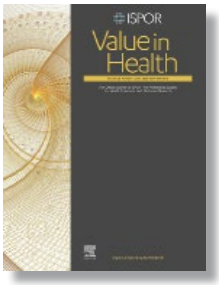
EClinicalMedicine
https://doi.org/10.1016/j.eclinm.2026.103871

Cost-effectiveness of conditional cash transfers with pre- and post-test tuberculosis counselling in South Africa: a modelling analysis

DR JUDITH MWANSA-KAMBAFWILE

DR SHAHEED V. OMAR

PROF. NAZIR ISMAIL

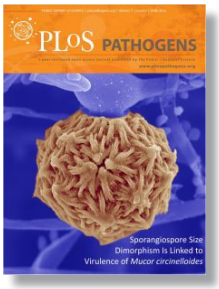


Lara Goscé, Elena Venero Garcia, Kasim Allel, **Judith Mwansa-Kambafwile**, Shabir A Madhi, **Shaheed Vally Omar**, Harry Moultrie, **Nazir Ahmed Ismail**, Rein Mgj Houben, Ibrahim Abubakar; LSHTM TB modelling group; UCL Institute for Global Health group

Value in Health
https://doi.org/10.1016/j.jval.2026.05.004

PROF. PENNY L. MOORE

Cell-free RNA reveals host and microbial correlates of broadly neutralizing antibody development against HIV



Mark Kowarsky, Mercedes Dalman, Mira N Moufarrej, Jennifer Okamoto, Yike Xie, Norma F Neff, Salim S Abdool Karim, Nigel Garrett, **Penny L Moore**, Joan Camunas-Soler, Stephen R Quake

PLoS Pathogens
https://doi.org/10.1371/journal.ppat.1014066

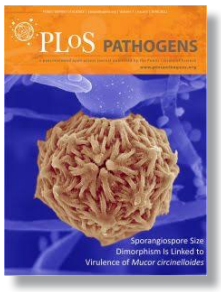
Disclaimer: Impact factor scores contained in this publication were compiled in April - June 2026.

Other publications highlighting NICD staff contributions


PROF. PENNY L. MOORE


DR NONHLANHLA N. MKHIZE

Contemporary HIV-1 envelope pseudovirus panels for detecting and assessing B cell lineages with broadly neutralizing antibody potential



Bette Korber, Michael S. Seaman, **Nonhlanhla N. Mkhize**, Kelli Greene, Hongmei Gao, Xiaoying Shen, Elizabeth Domin, Haili Tang, James Theiler, Kshitij Wagh, **Penny L Moore**, Carolyn Williamson, James I. Mullins, Nicole A. Doria-Rose, David Montefiori, Elena E. Giorgi

PLoS Pathogens
https://doi.org/10.1371/journal.ppat.1013739

Preclinical assessment of broadly neutralizing HIV-1 antibody BNT351 with optimized pharmacokinetics and potent antiviral activity


MS SINETHEMBA BHEBHE


DR NONHLANHLA N. MKHIZE


PROF. PENNY L. MOORE

Sven Kratochvil, Maximilian Kullmann, Henning Gruell, Sophie Sayettat, Chia-Hung Tsai, Natasa Vukovic, Christine Janaitis, Claudia Lindemann, Sandra Praßl, Ricarda Stumpf, Jacqueline Knüfer, Felix Tolksdorf, Uğur Şahin, Johannes Nelke, Alexandra Malz, Philipp Schommers, **Sinethemba Bhebhe, Nonhlanhla Mkhize, Penny Moore**, Michael S. Seaman, Florian Klein, Valentin Le Douce

iScience
https://doi.org/10.1016/j.isci.2026.116022


DR VICTOR MABASA

Seasonal and spatial variability of PMMoV in tropical urban wastewater-based surveillance: implications for accurate SARS-CoV-2 monitoring in Kampala, Uganda

Andrew Nsawotebba, Valeria Nakintu, Innocent Morunyanga, Jonathan Kabazzi,Jordan Magala, Samuel Jefferson Mutyaba, Noah C. Hull, **Victor Mabasa**, Denis Smith Akejo, Fatim Cham & Susan Nabadda

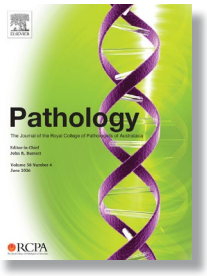
BMC Public Health
https://doi.org/10.1186/s12889-026-27515-w

Disclaimer: Impact factor scores contained in this publication were compiled in April - June 2026.

Other publications highlighting NICD staff contributions

PROF. NICOLA PAGE

Evaluation of the EntericBio multiplex polymerase chain reaction system as a routine method for the detection of stool pathogens and screening of carbapenemase-producing Enterobacterales

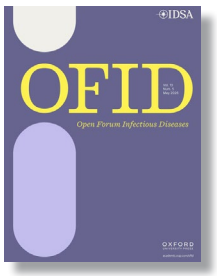


Safiyyah Khan, Lutfiyya Shaikjee-Moti, **Nicola Page**, Lebogang Busisiwe Skosana, Mohamed Said

Pathology
https://doi.org/10.1016/j.pathol.2026.02.008

PROF. NICOLA PAGE

Kinetics of enteric pathogen quantity during acute diarrhea in children in resource-limited settings



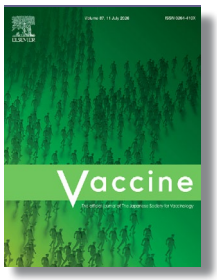
William J Lain , Sarah E Elwood, Jie Liu, Elizabeth T Rogawski McQuade, Gagandeep Kang, Margaret N Kosek, Aldo A M Lima, Pascal O Bessong, Amidou Samie, Rashidul Haque, Estomih R Mduma, Jose Paulo Leite, Ladaporn Bodhidatta, Najeeha T Iqbal, **Nicola Page**, Ireen Kiwelu, Zulfiqar A Bhutta, Tahmeed Ahmed, Eric R Houpt, James A Platts-Mills

Open Forum Infectious Diseases
https://doi.org/10.1093/ofid/ofag309

DR SIBONGILE WALAZA

PROF. CHERYL COHEN

Effectiveness of BNT162b2 and Ad26.COV2.S vaccines against COVID-19-related hospitalisation amongst adult members of a private health insurance plan in South Africa during the Delta and Omicron periods: A test-negative case-control study



Siobhan L Johnstone, Daniel Shapiro, Nicola Chiwandire, Lundi Matoti, Carmen Whyte, Jolene Bultinck-Human, Selaelo Mametja, Craig Getz, Boldwin Moyo, Mabatlo Semenya, **Sibongile Walaza, Cheryl Cohen**, Michelle J Groome

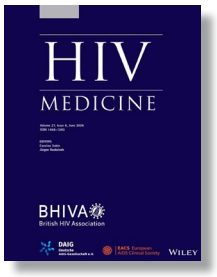
Vaccine
https://doi.org/10.1016/j.vaccine.2025.127068

Disclaimer: Impact factor scores contained in this publication were compiled in April - June 2026.

Other publications highlighting NICD staff contributions

DR AHMAD H. MAZANDERANI

Prevalence of low-level viremia and its association with virological failure among adolescents living with HIV in Eastern Cape, South Africa



Zea Leon, Olanrewaju Edun, Siyanai Zhou, Janke Tolmay, Lucie Cluver, Gayle Sherman, **Ahmad H. Mazanderani**, Elona Toska

HIV Medicine
https://doi.org/10.1111/hiv.70228

DR WENLONG C. CHEN

Disease characteristics, treatment, and overall survival outcomes of patients with locally advanced cervical cancer referred for radiation therapy in Johannesburg, South Africa: a 2-year retrospective study

Oluwatosin A. Ayeni, Daniel Mmereki, Himal Mistry, Okechinyere Achilonu, Megan Kassick, Sydnie Swanson, **Wenlong Carl Chen**, Maureen Joffe, Mpho Ratshikana, Katharine Rendle, Surbhi Grover & Duvern Ramiah

BMC Women's Health
https://doi.org/10.1186/s12905-026-04611-y

Evaluation and estimation of epidemic trajectories for SARS-CoV-2 from clinical and wastewater data in Gauteng province, South Africa

MS FIONA ELS

MR SIPHO GWALA

DR VICTOR MABASA

MS NATASHA SINGH

MR EMMANUEL PHALANE

MS MOKGAETJI MACHEKE

Zinhle E Mthombothi, Adrian Lison, **Fiona Els**, Cari van Schalkwyk, Leon Danon, Gillian Maree, Jeremy L Bingham, **Sipho Gwala, Victor Mabasa, Natasha Singh, Emmanuel Phalane, Mokgaetji Macheke**, Said Rachida, **Nkosenhle Ndlovu**, Chenoa Sankar, **Sibonginkosi Maposa, Mukhlid Yousif, Kerrigan McCarthy**, Kathleen M O'Reilly

PLOS Global Public Health
https://doi.org/10.1371/journal.pgph.0006424

Disclaimer: Impact factor scores contained in this publication were compiled in April - June 2026.

Other publications highlighting NICD staff contributions

DR JAISHREE RAMAN

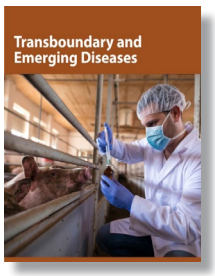
Target product profile of laboratory and data analytical frameworks for genotyping to monitor antimalarial efficacy

Mateusz M. Plucinski, Amy Wesolowski, Inna Gerlovina, Aimee R. Taylor, Jessica Briggs, Andrés Aranda-Díaz, Monica Golumbeanu, Marko Bajic, Jeffrey A. Bailey, Joel L. N. Barratt, Caroline Buckee, Awa B. Deme, Ingrid Felger, Anita Ghansah, Ian Hastings, Johanna Helena Kattenberg, Alfredo Mayor, Didier Menard, Leah F. Moriarty, Daniel Neafsey, Lucy Okell, Isabella Oyier, **Jaishree Raman**, Philip J. Rosenthal, Anna Rosanas-Urgell, Robert Verity, Sarah K. Volkman, Christian Nsanzabana Bryan Greenhouse

Plos Global Public Health
https://doi.org/10.1371/journal.pgph.0006500

DR JACQUELINE WEYER

Geospatial tracking of a rabies outbreak in the Eastern Cape province, South Africa, using molecular data



Mmantshuruge J Miyen, Antoinette Van Schalkwyk, Matthijs F Ravensberg, Jared Strydom, **Jacqueline Weyer**, Antoinette Grobbelaar, Veronique V Dermauw, Bas B Oude Munnink, Carmen W E Embregts, Corine H GeurtsvanKessel, Resoketswe C Moropeng , Claude T Sabeta

Transboundary and Emerging Diseases
https://doi.org/10.1155/tbed/2795613

Microbial networks and pathogen detection: insights from ticks and patients with acute febrile illness

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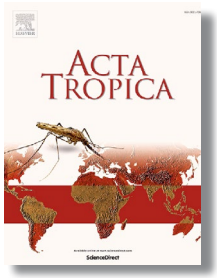
PROF. JOHN FREAN



Rebecca E. Ackermann, Kelly A. Brayton, Marinda C. Oosthuizen, Conrad A. Matthee, S. Marcus Makgabo, Harry Ngoveni, Dina M. Fagir, Ilana van Wyk, **Vanessa Quan**, Jennifer Rossouw, **Jacqueline Weyer**, **Lucille H. Blumberg**, **John Frean**, Nicola E. Collins

Acta Tropica
https://doi.org/10.1016/j.actatropica.2026.108138

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Other publications highlighting NICD staff contributions

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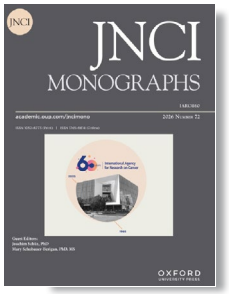
The continuing importance of the IARC's international remit in cancer research



Valerie McCormack, Hannah Simba, Christian C Abnet, Goeffrey Buckle, Daniel R S Middleton, Diana Menya, **Mazvita Muchengeti**, Eva J Kantelhardt, Adamu Addissie, Blandina T Mmbaga, Valery Lemmens, Orla Sheils, Pauline Boucheron, Joanne Kim, Joachim Schüz

Journal of the National Cancer Institute Monographs
https://doi.org/10.1093/jncimonographs/lgaf042

The need to strengthen laboratory leadership, systems, and networks to enhance outbreak detection and resilience in Africa: proceedings of a regional workshop

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BMC Proceedings
https://doi.org/10.1186/s12919-026-00382-4

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Kinetics of anti-SARS-CoV-2 IgG in saliva and serum post infection, and subsequent vaccination in South Africa

Maemu P. Gededzha, Mixo Sibiya, Celine Pellaton, Kubashni Woeber, Duduzile Nsibande, Nobuhle Mchunu, Brodie Daniels, Terusha Chetty, Reshmi Dassaye, Khanya Mohlabi, Shameem Jaumdally, Keertan Dheda, Ruth Lekalakala, Shabir A. Madhi, Elizabeth Mayne, Glenda Gray, Yves Levy, Craig Fenwick, Song Ding, **Penny L. Moore**, Ameena Goga

African Journal of Laboratory Medicine
https://doi.org/10.4102/ajlm.v15i1.3052

Disclaimer: Impact factor scores contained in this publication were compiled in April - June 2026.

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