

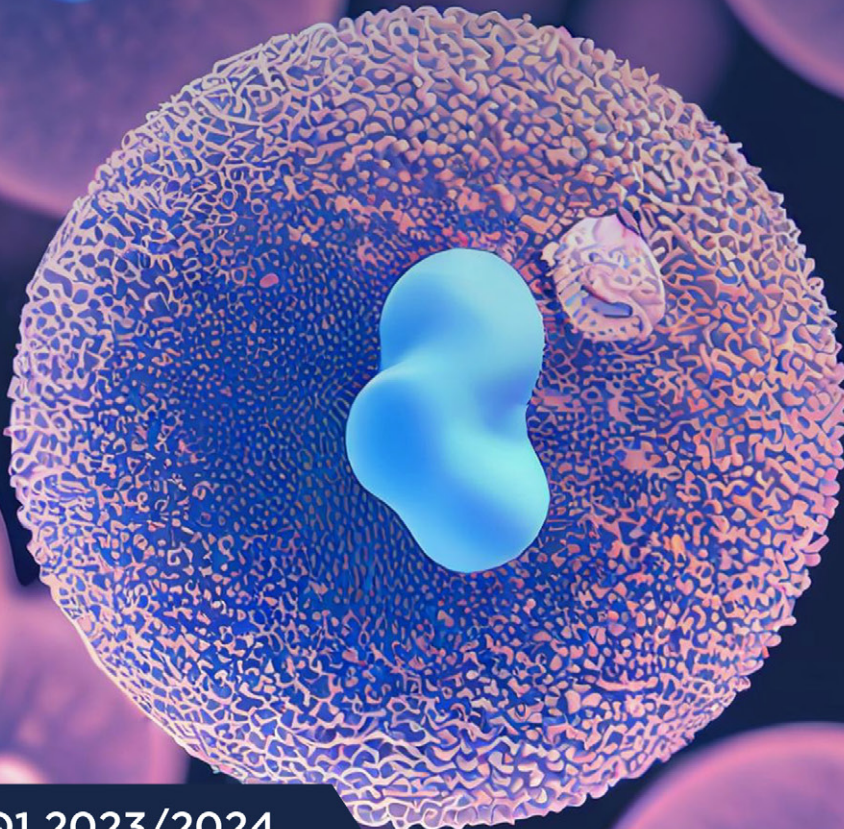


NATIONAL INSTITUTE FOR
COMMUNICABLE DISEASES

Division of the National Health Laboratory Service

Science Focus

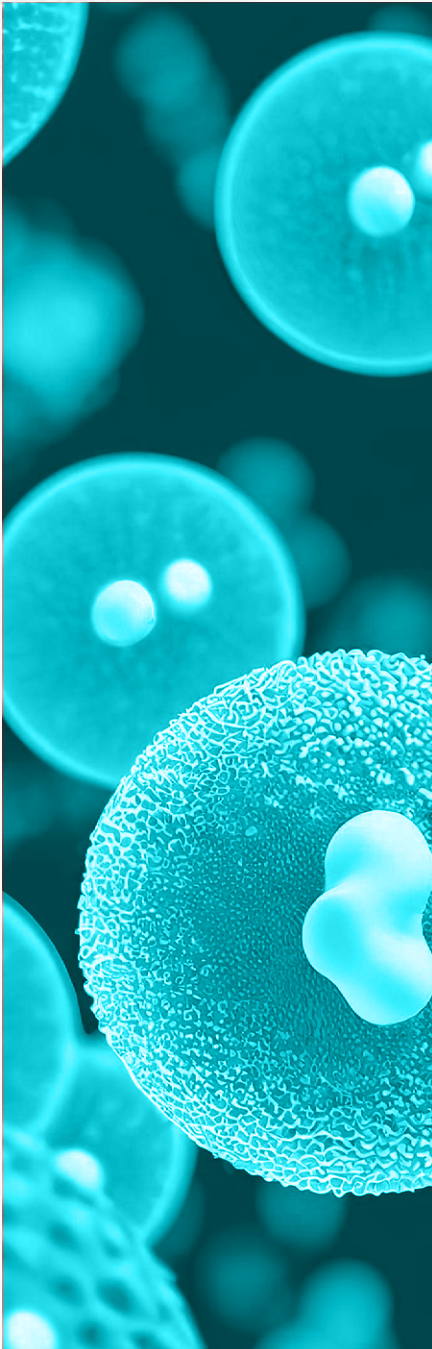
A quarterly nexus of
scientific insights



ISSUE 26 | Q1 2023/2024

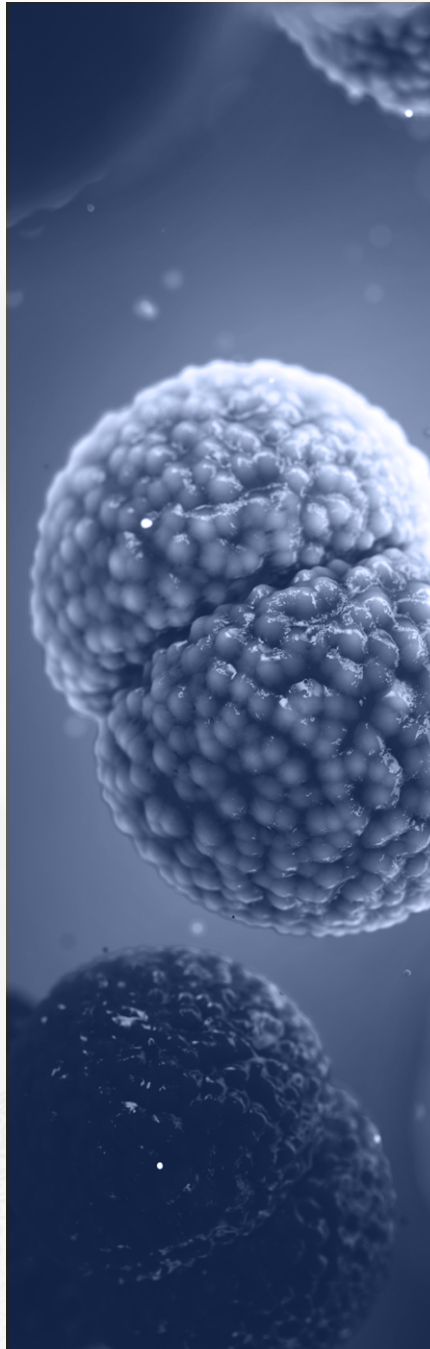
The Science Focus acknowledges NICD members of staff who have published in peer-reviewed journals. This publication is a compilation of scientific publications where an NICD staff member is either the first or last author.

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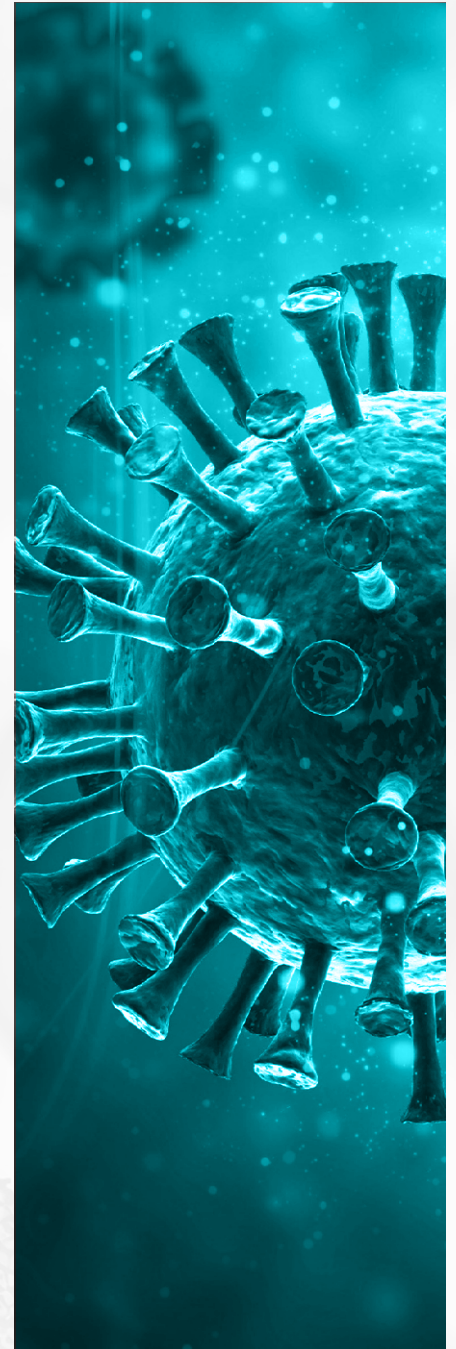
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NOTE**

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**TOP PUBLISHED
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“

**Look forward to
the new dawn of
the Science Focus**

”

MS SINENHLANHLA JIMOH
SENIOR COMMUNICATIONS MANAGER

Be part of this evolution, as we usher in a new phase aimed at enhancing the publications accessibility for all

Welcome to the 26th issue of Science Focus, a publication that has been dedicated to showcasing scientific research from NICD for over 6 years.

As we reach this milestone we can't help but reflect on the scientific gains of the institute and whether this publication still serves as useful in highlighting our collective output.

As such, we are in the process of identifying criteria that extends beyond the current inclusion criteria. This approach embraces inclusivity, ensuring that significant articles are not overlooked due to the restriction of considering solely the first and/or last author. We invite you to be part of this evolution, as we usher in a new phase aimed at enhancing the publications accessibility for all by sending us your suggestions via email: sinenhlanhla@nicd.ac.za

While we look forward to the new dawn of the Science Focus, in this issue, we highlight a variety of studies that are making significant contributions to our understanding of the world around us.

Prof Cheryl Cohen is our top publisher for this quarter. In this issue, one of her co-authored studies on the prevention of respiratory syncytial virus (RSV) in economically striving lands is featured. RSV is a major cause of death among children under five in low- and middle-income countries.

Dr Carole Metekoua and Dr Mazvita Muchengeti and colleagues are studying the decline in conjunctival squamous cell carcinoma (SCCC) incidence in HIV-affected South Africa. Their work suggests that immunodeficiency and ultraviolet rays are the leading causes of SCCC.

Prof Puren and Dr Kufa-Chakezha are leading experts on syphilis, and their study on the screening and positivity rates among HIV-treated pregnant women in South Africa is a valuable contribution to the field.

Dr Cortsee, Dr Weyer and peers made a breakthrough in the use of SYBR Green qPCR for bat-centric biosurveillance. This technique has the potential to improve our understanding of the spread of viruses and other pathogens.

We hope you enjoy reading these and other research outputs contained in this issue. Thank you for your support!

On behalf of the team,

Sinenhlanhla Jimoh

Senior Communications Manager



EXCEPTIONAL RESEARCH STATISTICS

Top Published Authors





PROF CHERYL COHEN

Prioritising respiratory syncytial virus prevention in low-income and middle-income countries.

Xavier Carbonell-Estrany , Eric Af Simões , Louis J Bont , Bosco A Paes, **Cheryl Cohen part of RSV Prevention Collaborators**

Lancet Global Health

IMPACT FACTOR: 34,3

2023 May;11(5):e655-e657. PMID: 37061306



ABSTRACT

Respiratory syncytial virus is a major cause of lower respiratory tract infection morbidity and mortality in children globally, causing 3·2–3·6 million hospitalisations and more than 100 000 deaths annually in children younger than 5 years, 99% of which occur in low-income and middle-income countries (LMICs).¹ Despite being identified 65 years ago, at the same time as poliovirus, there is no widely available and affordable preventive strategy for respiratory syncytial virus.



PROF PENNY MOORE

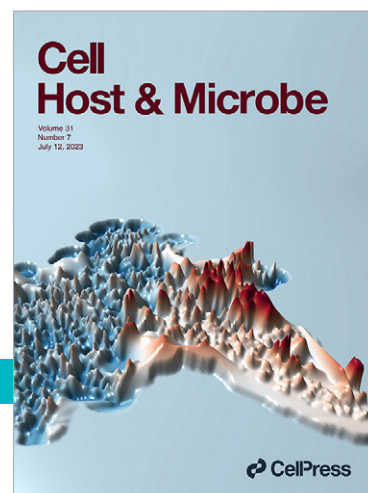
COVID-19 as a catalyst for vaccine manufacturing: a South African experience

Moore PL, Gray G.

Cell Host & Microbe

IMPACT FACTOR: 31,316

10.1016/j.chom.2023.05.015



ABSTRACT

COVID-19 highlighted inequitable vaccine distribution and the urgent need for vaccine manufacturing capacity on the African continent. This resulted in a burst of scientific engagement and international funding to augment capacity on the continent. However, short-term investment needs to be reinforced by a robust, strategic long-term plan to ensure sustainability.



PROF NELESH GOVENDER

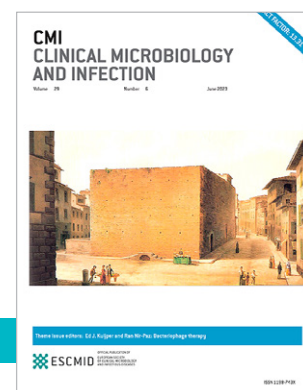
Impact of prior cryptococcal antigen screening on in-hospital mortality in cryptococcal meningitis or fungaemia among HIV-seropositive individuals in South Africa: a cross-sectional observational study

Paccoud O, Shuping L, Mashau R, Greene G, Quan V, Meiring S, Govender NP; for GERMS-SA

Clin Microbiol Infect

IMPACT FACTOR: 14,2

Clin Microbiol Infect. 2023 Apr 21:S1198-743X(23)00189-1. doi: 10.1016/j.cmi.2023.04.016.



ABSTRACT

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

METHODS

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

RESULTS

Overall, 24.5% (830/3390) of patients had a prior positive CrAg test within 14 days of diagnosis. CrAg-screened patients were

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

DISCUSSION

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



DR MONICA BIRKHEAD



DR JACQUILINE WEYERS

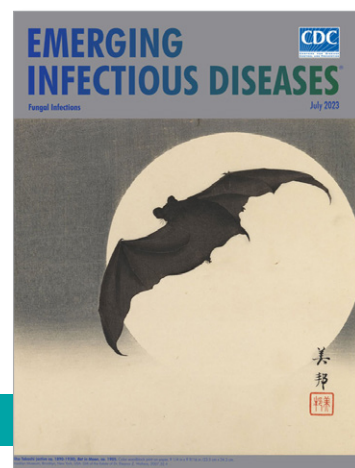
Tanapox, South Africa, 2022

Monica Birkhead, Wayne Grayson Antoinette Grobbelaar, Veerle Msimang, Naazneen Moolla, Angela Mathee, Lucille Blumberg, Terry Marshall, Daniel Morobadi, Marijana Popara, Jacqueline Weyer.

Emerging Infectious Diseases

IMPACT FACTOR: 11,8

DOI: <https://doi.org/10.3201/eid2906.230326>



ABSTRACT

Tanapox is a rarely diagnosed zoonosis known to be endemic to equatorial Africa. All previously reported human cases were acquired within 10° north or south of the Equator, most recently 19 years ago. We describe a human case of tanapox in South Africa (24° south of the Equator). Expanded surveillance for this pathogen is warranted.



DR CAROLE METEKOUA



DR MAZVITA MUCHENGETI

Decreasing Incidence of Conjunctival Squamous Cell Carcinoma in People with HIV in South Africa.

Metekoua C, Ruffieux Y, **Olago V**, **Dhokotera T**, Egger M, Bohlius J, Rohner E, **Muchengeti M**.

J Natl Cancer Inst

IMPACT FACTOR: 10,3

10.1093/jnci/djad119



ABSTRACT

The main risk factors for squamous cell carcinoma of the conjunctiva (SCCC) are immunodeficiency and exposure to ultraviolet radiation. Little is known about the SCCC epidemiology among people with HIV (PWH) in South Africa.



DR JOCELYN MOYES



PROF CHERYL COHEN

The burden of RSV-associated illness in children aged < 5 years, South Africa, 2011 to 2016

Jocelyn Moyes , Stefano Tempia , **Sibongile Walaza** , Meredith L McMorrow , Florette Treurnicht , **Nicole Wolter** , **Anne von Gottberg** , Kathleen Kahn , Adam L Cohen , Halima Dawood , Ebrahim Variava , **Cheryl Cohen**

BMC Medicine

IMPACT FACTOR: 9,3

2023 Apr 11;21(1):139. doi: 10.1186/s12916-023-02853-3 PMID: 37038125 PMCID: PMC10088270



ABSTRACT

Vaccines and monoclonal antibodies to protect the very young infant against the respiratory syncytial virus (RSV)-associated illness are effective for limited time periods. We aimed to estimate age-specific burden to guide implementation strategies and cost-effectiveness analyses.



DR JOCELYN MOYES



PROF CHERYL COHEN

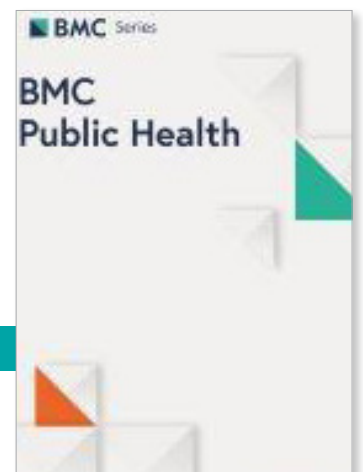
The economic burden of RSV-associated illness in children aged <5 years, South Africa 2011-2016.

Jocelyn Moyes , Stefano Tempia , **Sibongile Walaza** , Meredith L McMorro , Florette Treurnicht , **Nicole Wolter** , **Anne von Gottberg** , Kathleen Kahn , Adam L Cohen , Halima Dawood , Ebrahim Variava , **Cheryl Cohen**

BMC Medicine

IMPACT FACTOR: 9,3

2023 Apr 13;21(1):146. PMID: 37055799 PMCID: PMC10099882



ABSTRACT

Data on the economic burden of RSV-associated illness will inform decisions on the programmatic implementation of maternal vaccines and monoclonal antibodies. We estimated the cost of RSV-associated illness in fine age bands to allow more accurate cost-effectiveness models to account for a limited duration of protection conferred by short- or long-acting interventions.



DR JOCELYN MOYES



PROF CHERYL COHEN

The attributable fraction of respiratory syncytial virus among patients of different ages with influenza-like illness and severe acute respiratory illness in a high HIV prevalence setting, South Africa, 2012-2016.

Jocelyn Moyes , Stefano Tempia , **Sibongile Walaza** , Meredith L McMorrow , Adam L Cohen , Florette Treurnicht , Orienka Hellferscee , **Nicole Wolter** , **Anne Von Gottberg** , Halima Dawood , Ebrahim Variava , Kathleen Kahn , Shabir A Madhi , **Cheryl Cohen**

International Journal of Infectious Disease

IMPACT FACTOR: 8,4

2023 May 20;134:71-77. doi: 10.1016/j.ijid.2023.05.009. PMID: 37211271

ABSTRACT

The detection of respiratory syncytial virus (RSV) in upper airway samples does not necessarily infer causality of illness. We aimed to calculate the attributable fraction (AF) of RSV in clinical syndromes across age groups.





DR HUNT GILLIAN

Resistance is common in paediatric patients failing ART in South Africa.

Hunt GM, Yousif M, Levin L, Ledwaba J, Steegen K, Kufa T, Zwane H, Kalimashe M, Kana V, Aynalem G, Perlman J.

Journal of Antimicrobial Chemotherapy

IMPACT FACTOR: 5,2

<https://doi.org/10.1093/jac/dkac443>



ABSTRACT

Minimal data exist on HIV drug resistance patterns and prevalence among paediatric patients failing ART in resource-limited settings. We assessed levels of HIV drug resistance in children with virological failure.



DR JESSICA COERTSE



DR JACQUELINE WEYER

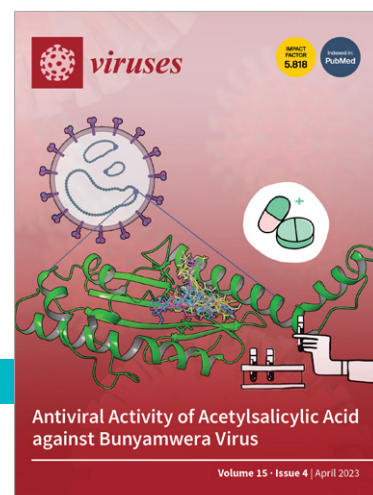
Development of a Pan-Filoviridae SYBR Green qPCR Assay for Biosurveillance Studies in Bats.

Jessica Coertse, Marinda Mortlock, **Antoinette Grbbelaar**, **Naazneen Moolla**, Wanda Markotter, **Jacqueline Weyer**.

Viruses

IMPACT FACTOR: 4,7

doi.org/10.3390/v15040987



ABSTRACT

Recent studies have indicated that bats are hosts to diverse filoviruses. Currently, no pan-filovirus molecular assays are available that have been evaluated for the detection of all mammalian filoviruses. In this study, a two-step pan-filovirus SYBR Green real-time PCR assay targeting the nucleoprotein gene was developed for filovirus surveillance in bats. Synthetic constructs were designed as representatives of nine filovirus species and used to evaluate the assay. This assay detected all synthetic constructs included with an analytical sensitivity

of 3-31.7 copies/reaction and was evaluated against the field collected samples. The assay's performance was similar to a previously published probe based assay for detecting Ebola- and Marburgvirus. The developed pan-filovirus SYBR Green assay will allow for more affordable and sensitive detection of mammalian filoviruses in bat samples



DR KATHLEEN SUBRAMONEY

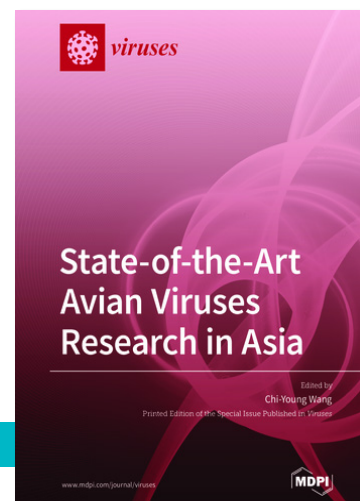
Molecular Epidemiology of SARS-CoV-2 during Five COVID-19 Waves and the Significance of Low-Frequency Lineages

Kathleen Subramoney, Nkhensani Mtileni, Jennifer Giandhari, Yeshnee Naidoo, Yajna Ramphal, Sureshnee Pillay, Upasana Ramphal, Akhil Maharaj, Derek Tshiabuila, Houriiyah Tegally, Eduan Wilkinson, Tulio de Oliveira, Burtram C. Fielding and Florette K. Treurnicht

Viruses

IMPACT FACTOR: 4,7

<https://doi.org/10.3390/v15061346>



ABSTRACT

SARS-CoV-2 lineages and variants of concern (VOC) have gained more efficient transmission and immune evasion properties with time. We describe the circulation of VOCs in South Africa and the potential role of low-frequency lineages on the emergence of future lineages. Whole genome sequencing was performed on SARS-CoV-2 samples from South Africa. Sequences were analysed with Nextstrain pangolin tools and Stanford University Coronavirus Antiviral & Resistance Database. In 2020, 24 lineages were detected, with B.1 (3%; 8/278), B.1.1 (16%; 45/278), B.1.1.348 (3%; 8/278), B.1.1.52 (5%; 13/278), C.1 (13%; 37/278) and C.2 (2%; 6/278) circulating during the first wave. Beta emerged late in 2020, dominating the second

wave of infection. B.1 and B.1.1 continued to circulate at low frequencies in 2021 and B.1.1 re-emerged in 2022. Beta was outcompeted by Delta in 2021, which was thereafter outcompeted by Omicron sub-lineages during the 4th and 5th waves in 2022. Several significant mutations identified in VOCs were also detected in low-frequency lineages, including S68F (E protein); I82T (M protein); P13L, R203K and G204R/K (N protein); R126S (ORF3a); P323L (RdRp); and N501Y, E484K, D614G, H655Y and N679K (S protein). Low-frequency variants, together with VOCs circulating, may lead to convergence and the emergence of future lineages that may increase transmissibility, infectivity and escape vaccine-induced or natural host immunity.



DR TENDESAYI KUFO-CHAKEZHA



PROF ADRIAN PURÉN

Syphilis screening coverage and positivity by HIV treatment status among South African pregnant women enrolled in the 2019 antenatal HIV sentinel survey.

Kufa T, Woldeesenbet S, Cheyip M, Ayalew K, Kularatne R, Manda S, Lombard C, Puren A.

Scientific reports.

IMPACT FACTOR: 4,6

<https://doi.org/10.3390/v15061346>

ABSTRACT

We describe coverage of maternal syphilis screening, syphilis positivity, coverage of treatment and their association with maternal HIV infection and antiretroviral treatment (ART) status among pregnant women attending South African antenatal clinics. The 2019 antenatal care sentinel survey was a cross-sectional survey conducted from 1 October to 15 November 2019 at 1589 sentinel sites in all nine provinces of the country and aimed to enrol 36,000 pregnant women ages 15-49 years regardless of HIV, ART or syphilis status. Data collection procedures included obtaining written informed consent, a brief interview, medical record review and blood specimen collection. Completed data collection forms and specimens were sent to designated regional laboratories for data capture and HIV serology testing. Data analysis determined four outcomes i) syphilis screening coverage ii) syphilis positivity iii) coverage of any treatment and iv) with Benzathine penicillin G (BPG). Multivariable logistic regression models with or without interaction between HIV infection and ART status with province were used to determine factors associated with syphilis positivity. Of the 41 598 women enrolled, 35 900

were included in the analysis for syphilis screening coverage. The weighted syphilis screening coverage was 96.4% [95% Confidence Interval (CI) 95.9-96.7%] nationally and was lowest among HIV positive women not on ART at 93.5% (95% CI 92.2-94.5%). Syphilis positivity was 2.6% (95% CI 2.4-2.9%) nationally. Among those who were syphilis positive, 91.9% (95% CI 89.8-93.7%) had documentation of syphilis treatment status, of whom 92.0% (95% CI 89.8-93.9%) were treated, with the majority treated with one or more doses of BPG [92.2% (95% CI 89.8-94.3%)]. HIV-positive women, not on ART [adjusted odd ratio (aOR) 2.24 (95% 1.71-2.93)] and those on ART [aOR 2.25 (95% CI 1.91-2.64)] were more likely to be syphilis positive compared to those who were HIV negative. The national syphilis screening coverage met the global screening target of 95%. Syphilis positivity was higher among HIV positive women compared to negative women. Introduction of rapid syphilis testing and ensuring a universal supply of appropriate treatment for syphilis will reduce the likelihood of mother-to-child transmission of syphilis.





DR NICOLE WOLTER

The impact of the SARS-CoV-2 pandemic on global influenza surveillance: Insights from 18 National Influenza Centers based on a survey conducted between November 2021 and March 2022

Lisa Staadegaard , Marco Del Riccio , Sytske Wiegersma , Clotilde El Guerche-Séblain , Erica Dueger , Meral Akçay , Jean-Sebastien Casalegno , Michel Dückers , Saverio Caini , John Paget ; NIC Collaborators; Vina Lea Arguelles, Inmaculada Cases, Julian Druce, Dominic E Dwyer, Joanna Ellis, José María Eiros, Ron Fouchier, Le Thi Quynh Mai, Michal Mandelboim, Adam Meijer, Pilailuk Okada, Varsha Potdar, Simona Puzelli, Marilda Siqueira, Cao Minh Thang, Martine Valette, David E Wentworth, **NIC collaborators: Nicole Wolter**



Influenza and other Respiratory Viruses

IMPACT FACTOR: 4,4

2023 May 11;17(5):e13140. PMID: 37180840 PMCID: PMC10173050

ABSTRACT

National Influenza Centers (NICs) have played a crucial role in the surveillance of SARS-CoV-2. The FluCov project, covering 22 countries, was initiated to monitor the impact of the SARS-CoV-2 pandemic on influenza activity.



DR ANTHONY SMITH

Enteric fever cluster identification in South Africa using genomic surveillance of *Salmonella enterica* serovar Typhi

Smith AM, Erasmus LK, Tau NP, Smouse SL, Ngomane HM, Disenyeng B, Whitelaw A, Lawrence CA, Sekwadi P, Thomas J

Microbial Genomics

IMPACT FACTOR: 3,9

<https://doi.org/10.1099/mgen.0.001044>



ABSTRACT

The National Institute for Communicable Diseases in South Africa participates in national laboratory-based surveillance for human isolates of *Salmonella* species. Laboratory analysis includes whole-genome sequencing (WGS) of isolates. We report on WGS-based surveillance of *Salmonella enterica* serovar Typhi (*Salmonella* Typhi) in South Africa from 2020 through 2021. We describe how WGS analysis identified clusters of enteric fever in the Western Cape Province of South Africa and describe the epidemiological investigations associated with these clusters. A total of 206 *Salmonella* Typhi isolates were received for analysis. Genomic DNA was isolated from bacteria and WGS was performed using Illumina NextSeq technology. WGS data were investigated using multiple bioinformatics tools, including those available at the Centre for

Genomic Epidemiology, Enterobase and Pathogenwatch. Core-genome multilocus sequence typing was used to investigate the phylogeny of isolates and identify clusters. Three major clusters of enteric fever were identified in the Western Cape Province; cluster one (n=11 isolates), cluster two (n=13 isolates), and cluster three (n=14 isolates). To date, no likely source has been identified for any of the clusters. All isolates associated with the clusters, showed the same genotype (4.3.1.1.EA1) and resistome (antimicrobial resistance genes: bla TEM-1B, catA1, sul1, sul2, dfrA7). The implementation of genomic surveillance of *Salmonella* Typhi in South Africa has enabled rapid detection of clusters indicative of possible outbreaks. Cluster identification allows for targeted epidemiological investigations and a timely, coordinated public health response.



DR KATHLEEN SUBRAMONEY

SARS-CoV-2 spike protein diversity at an intra-host level, among SARS-CoV-2 infected individuals in South Africa, 2020 to 2022

Kathleen Subramoney, Nkhensani Mtileni, Ashlyn Davis, Jennifer Giandhari, Houriiyah Tegally, Eduan Wilkinson, Yeshnee Naidoo, Yajna Ramphal, Sureshnee Pillay, Upasana Ramphal, Andiswa Simane, Bhaveshan Reddy, Bonolo Mashishi, Nonhlanhla Mbenenge, Tulio de Oliveira, Burtram C. Fielding, Florette K. Treurnicht

PLOS ONE

IMPACT FACTOR: 3,7

<https://doi.org/10.1371/journal.pone.0286373>

ABSTRACT

Intra-host diversity studies are used to characterise the mutational heterogeneity of SARS-CoV-2 infections in order to understand the impact of virus-host adaptations. This study investigated the frequency and diversity of the spike (S) protein mutations within SARS-CoV-2 infected South African individuals. The study included SARS-CoV-2 respiratory samples, from individuals of all ages, received at the National Health Laboratory Service at Charlotte Maxeke Johannesburg Academic hospital, Gauteng, South Africa, from June 2020 to May 2022. Single nucleotide polymorphism (SNP) assays and whole genome sequencing were performed on a random selection of SARS-CoV-2 positive samples. The allele frequency (AF) was determined using TaqMan Genotyper software for SNP PCR analysis and galaxy.eu for analysis of FASTQ reads from sequencing. The SNP assays identified 5.3% (50/948) of Delta cases with heterogeneity at delY144 (4%; 2/50), E484Q

(6%; 3/50), N501Y (2%; 1/50) and P681H (88%; 44/50), however only heterogeneity for E484Q and delY144 were confirmed by sequencing. From sequencing we identified 9% (210/2381) of cases with Beta, Delta, Omicron BA.1, BA.2.15, and BA.4 lineages that had heterogeneity in the S protein. Heterogeneity was primarily identified at positions 19 (1.4%) with T19IR (AF 0.2–0.7), 371 (92.3%) with S371FP (AF 0.1–1.0), and 484 (1.9%) with E484AK (0.2–0.7), E484AQ (AF 0.4–0.5) and E484KQ (AF 0.1–0.4). Mutations at heterozygous amino acid positions 19, 371 and 484 are known antibody escape mutations, however the impact of the combination of multiple substitutions identified at the same position is unknown. Therefore, we hypothesise that intra-host SARS-CoV-2 quasispecies with heterogeneity in the S protein facilitate competitive advantage of variants that can completely/partially evade host's natural and vaccine-induced immune responses.





DR HARRY MOULTRIE

The National COVID-19 Epi Model (NCEM): Estimating cases, admissions and deaths for the first wave of COVID-19 in South Africa

Silal SP, Pulliam JRC, Meyer-Rath G, Jamieson L, Nichols BE, Norman J, Hounsell R, Mayet S, Kagoro F, **Moultrie H**

PLOS Glob Public Health

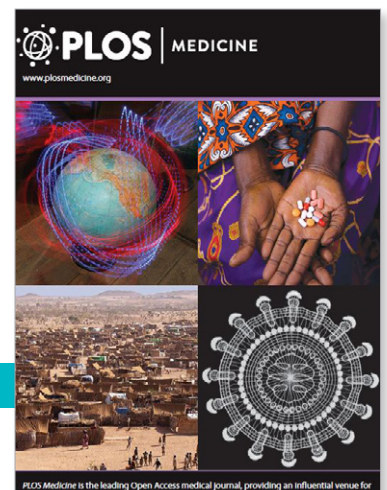
IMPACT FACTOR: 3.356

<https://doi.org/10.1371/journal.pgph.0001070>

ABSTRACT

In March 2020 the South African COVID-19 Modelling Consortium was formed to support government planning for COVID-19 cases and related healthcare. Models were developed jointly by local disease modelling groups to estimate cases, resource needs and deaths due to COVID-19. The National COVID-19 Epi Model (NCEM) while initially developed as a deterministic compartmental model of SARS-Cov-2 transmission in the nine provinces of South Africa, was adapted several times over the course of the first wave of infection in response to emerging local data and changing needs of government. By the end of the first wave, the NCEM had developed into a stochastic, spatially-explicit compartmental transmission model to estimate the total and reported incidence of COVID-19 across the 52 districts of South Africa. The model adopted a generalised Susceptible-Exposed-Infectious-Removed structure that accounted for the clinical profile of SARS-COV-2 (asymptomatic, mild, severe and critical cases) and avenues of treatment access (outpatient, and

hospitalisation in non-ICU and ICU wards). Between end-March and early September 2020, the model was updated 11 times with four key releases to generate new sets of projections and scenario analyses to be shared with planners in the national and provincial Departments of Health, the National Treasury and other partners. Updates to model structure included finer spatial granularity, limited access to treatment, and the inclusion of behavioural heterogeneity in relation to the adoption of Public Health and Social Measures. These updates were made in response to local data and knowledge and the changing needs of the planners. The NCEM attempted to incorporate a high level of local data to contextualise the model appropriately to address South Africa's population and health system characteristics that played a vital role in producing and updating estimates of resource needs, demonstrating the importance of harnessing and developing local modelling capacity.





DR SERISHA NAICKER

Epidemiology and susceptibility of *Nakaseomyces* (formerly *Candida*) *glabrata* bloodstream isolates from hospitalised adults in South Africa

Naicker SD, Shuping L, Zulu TG, **Mpembe RS**, Mhlanga M, **Tsotetsi EM**, Maphanga TG, **Govender NP**; MMed, FC Path SA, for GERMS-SA.

Medical Mycology

IMPACT FACTOR: 2,9

doi: 10.1093/mmy/myad057.

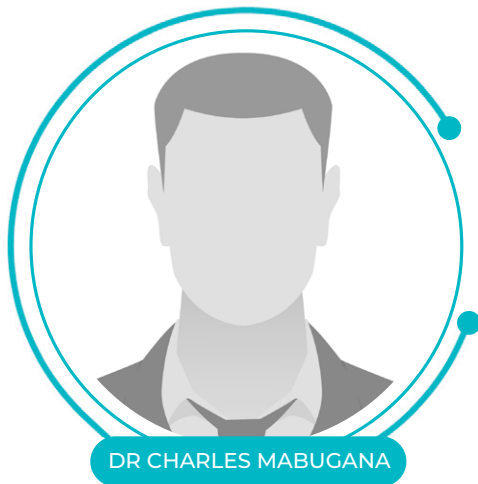


**Medical
Mycology**

ABSTRACT

During 2016-2017, *Nakaseomyces glabrata* (formerly *Candida glabrata*) caused 14% of cases of candidaemia in South Africa. We aimed to describe the clinical characteristics of adults with *N. glabrata* candidaemia at 20 sentinel hospitals (accounting for 20% (172/917) of cases) and the antifungal susceptibility of the corresponding isolates. A higher proportion of patients with *N. glabrata* candidaemia were older (median age: 55 years [interquartile range (IQR): 41-65 years] vs. 49 years [IQR: 35-63 years]; $p = 0.04$), female (87/164, 53% vs. 283/671, 42%; $p = 0.01$), admitted to a public-sector hospital (152/172, 88% vs. 470/745, 63%; $p < 0.001$), treated with fluconazole only (most with suboptimal doses) (51/95, 54% vs. 139/361, 39%;

$p < 0.001$), and had surgery (47/172, 27% vs. 123/745, 17%; $p = 0.001$) and a shorter hospital stay (median 7 days [IQR: 2-20 days] vs. 13 days [IQR: 4-27 days]; $p < 0.001$) compared to patients with other causes of candidaemia. Eight *N. glabrata* isolates (6%, 8/131) had minimum inhibitory concentrations in the intermediate or resistant range for ≥ 1 echinocandin and a R1377K amino acid substitution encoded by the hotspot 2 region of the FKS2 gene. Only 11 isolates (8%, 11/131) were resistant to fluconazole. Patients with confirmed *N. glabrata* candidaemia are recommended to be treated with an echinocandin (or polyene), thus further guideline training is required.



DR CHARLES MABUGANA

The evaluation of the Allplex™ BV molecular assay for the diagnosis of bacterial vaginosis in symptomatic South African females

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Diagnostic Microbiology and Infectious Disease,

IMPACT FACTOR: 2,9

<https://doi.org/10.1099/mgen.0.001044>



ABSTRACT

Bacterial vaginosis (BV) is a dysbiosis of vaginal microbiota characterized by a shift from *Lactobacillus* species predominance to a heterogeneous mixture of anaerobes. We compared the performance characteristics of the Allplex™ BV molecular assay with the reference test, Nugent score microscopy, for vaginal swab specimens from symptomatic South African women. A total of 213 patients were enrolled,

of whom 99 (46.5%) and 132 (62.0%) were diagnosed with BV by Nugent and Allplex™, respectively. The Allplex™ BV assay displayed a sensitivity of 94.9% (95% CI, 88.7%–97.8%) and a specificity of 66.7% (95% CI, 57.6%–74.6%), with an agreement of 79.8% (95% CI, 73.9%–84.7%) ($\kappa = 0.60$). Assay design may be enhanced for improved specificity by accounting for differences in healthy and BV-associated vaginal microbiomes among women of different ethnicities.



DR ANTHONY SMITH

Salmonella Enteritidis clades in South Africa: why we should be paying more attention. *Frontiers in Tropical Diseases*

Gallichan S, Ramalwa N, Thomas J, Feasey NA, **Smith AM**

Frontiers in Tropical Diseases

IMPACT FACTOR: n/a on WOS

4:1152422. doi: 10.3389/ftd.2023.1152422.



ABSTRACT

Sub-Saharan African (sSA) countries are under pressure to increase the production of affordable protein-rich foods often in a nascent regulatory environment with limited veterinary or environmental surveillance capabilities (1). Poultry has long been valued as an affordable source of animal protein in sSA. Previously poultry was predominantly produced by subsistence farmers, however intensive farming is rapidly emerging (2). A global epidemic of *Salmonella enterica* serotype Enteritidis (*S. Enteritidis*) began early in the 1980s, in association with consumption of contaminated poultry meat and eggs, which often results in *S. Enteritidis* infection in humans (3). That *S. Enteritidis* proliferates alongside the industrial production of poultry is well described, but its simultaneous expansion

in many parts of the world remains a mystery, although this has recently been linked to *S. Enteritidis* dissemination via centralized sourcing and international trade of breeding stocks (4). The lack of biosafety measures in poultry production has resulted in the NTS serovar, *S. Enteritidis* becoming the most reported foodborne pathogen in sSA (5). Generally, *S. Enteritidis* infections are associated with outbreaks of gastroenteritis in Europe and the United States (6). However, *S. Enteritidis* infections in sSA are additionally associated with life threatening bloodstream infections, known as invasive non-typhoidal *Salmonella* disease (hereafter named iNTS disease) (7). Indeed, in 2017, cases of iNTS disease in sSA were estimated to account for 79% of the global burden (8).

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