



**NATIONAL INSTITUTE FOR
COMMUNICABLE DISEASES**

Division of the National Health Laboratory Service

SCIENCE FOCUS

A quarterly nexus of
scientific insights

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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

Expanding recognition: Honouring all NICD researchers

In previous issues, Science Focus highlighted staff members who were the first or last authors in peer-reviewed publications. Moving forward, we are expanding our approach. Starting with this issue, we will include a dedicated section acknowledging all publications where a National Institute for Communicable Diseases (NICD) staff member contributed, even if they were not the first or last author.

As an organisation, we recognise the significant effort and collaboration that goes into research. Many of our staff members play vital roles in groundbreaking studies, contributing expertise and dedication to advance scientific knowledge. It is only fitting that we acknowledge their contributions each quarter. That said, our primary focus will continue to be on profiling first and last authors.

This issue covers peer-reviewed publications from the last quarter (October to December), featuring 29 diverse studies across NICD centres. As always, these publications offer valuable insights into various health and science disciplines.

Among the key articles featured is a study from the NICD's Sequencing Core Facility, a cutting-edge department enhancing our genomic surveillance and public health research. Titled "Whole genome sequencing assisted outbreak investigation of Salmonella Enteritidis at a hospital in South Africa, September 2022", the study demonstrates how whole genome sequencing (WGS) was used to analyse bacterial isolates, supporting an epidemiological investigation. Using Illumina NextSeq technology, researchers applied advanced bioinformatics tools to generate critical insights.

Another notable publication, "Reducing colorectal cancer mortality in South Africa: experiences and progress from the South African National Cancer Prevention Services", examines the rising incidence and disproportionately high mortality rates of colorectal cancer in the country. Researchers from the National Cancer Registry argue that identifying and monitoring high-risk family members could significantly reduce cancer-related deaths.

Additionally, the Centre for Respiratory Diseases and Meningitis contributed an important study, "Home-based testing as an approach to estimate influenza vaccine effectiveness in South Africa, 2021-2022—A pilot study." This research explores the feasibility of home-based testing for influenza and its potential role in improving surveillance programmes for respiratory pathogens. The findings suggest that home-based swabbing is both practical and well-received, offering a promising method for gathering vaccine effectiveness data.

We invite you to explore this issue for these and many other insightful contributions to the field of health and science.

On behalf of the team,

Vuyo Sabani
Senior Communications Manager



DR NOSIPHO SHANGASE

Quality of caregiver-adolescent relationship on HIV, Herpes Simplex Virus type-2, and on pregnancy among young women in South Africa enrolled in HIV prevention trials network 068

Nosipho Shangase, Jess Edwards, Brian Pence, Allison Aiello, Xavier Gómez-Olivé, Kathleen Kahn, Marie Stoner, Audrey Pettifor

Journal of Adolescent Health

IMPACT FACTOR: 5.5

<https://doi.org/10.1016/j.jadohealth.2024.08.015>

Purpose: Adolescent girls and young women (AGYW) are at an increased risk of acquiring HIV and HSV-2, and unintended pregnancies are high in AGYW. Despite the protective impact of caregiver-adolescent relationships on risk behaviors, less attention has been paid to the association of these relationships and sexually transmitted infections (STIs) and pregnancy.

Methods: We used longitudinal data from HIV Prevention Trial Network 068, which was conducted among 2,533 AGYW (13 – 20 years) over 5 years in Agincourt, South Africa. Kaplan-Meier and Cox models were used to estimate the effect of quality of caregiver-adolescent relationships (caring and closeness) on STIs and pregnancy. Also, we assessed effect measure modification by age (14–19 vs. 20–25 years) for STI risk using stratum-specific estimates and likelihood ratio tests, with a p value <.1 indicative of effect measure modification.

Results: There were no significant differences in the hazard of HIV by our exposures (caring: hazard ratio (HR): 1.03, 95% CI: 0.75, 1.42; closeness: HR: 0.80, 95% CI: 0.57, 1.11). Among 14–19-year-olds, those who reported caregiver caring were less likely to acquire HSV-2 (HR: 0.69, 95% CI: 0.51, 0.94, likelihood ratio tests= 3.89, p-value = .0487), in contrast, there were no significant differences among 20 – 25-year-olds. AGYW who reported high-quality relationships had a lower hazard of pregnancy incidence (caring: HR: 0.79, 95% CI: 0.68, 0.93; closeness: HR: 0.76; 95% CI: 0.64, 0.91).

Discussion: Positive caregiver-adolescent relationships are associated with reduced risk of HSV-2 among younger AGYW and pregnancy incidence.





MS CHENOË SANKAR



DR KERRIGAN MCCARTHY

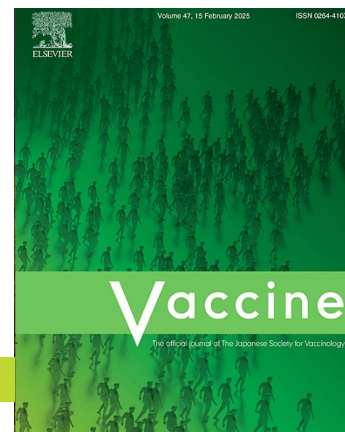
Vaccine safety surveillance in South Africa through COVID-19: A journey to systems strengthening

Chenoa Sankar, Johanna C. Meyer, Marione Schönfeldt, Hannah Gunter, Halima Dawood, Victoria Sekiti, Naseera Pickard, Lawrence Mubaiwa, Dini Mawela, Siphon Dlamini, Jonny Peter, David Spencer, Clive Gray, Vinod Patel, Lesley Bamford, Tohlang Sehloho,
Kerrigan McCarthy

Elsevier

IMPACT FACTOR: 4.5

<https://doi.org/10.1016/j.vaccine.2024.126535>



Background: Surveillance systems for monitoring and reporting adverse events following immunisation (AEFI) and adverse events of special interest (AESI) are vital in understanding safety profiles of post-marketed vaccines. Evaluation of surveillance systems is necessary for systems strengthening. We conducted the first evaluation of the South African AEFI surveillance system in its current form, established in 2018.

Methods: Using CDC guidelines for evaluation of surveillance systems, we conducted a cross-sectional evaluation of system attributes, including quantitative analyses of AEFI/AESI data from 17 May 2021 to 31 December 2022 and qualitative analyses through semi-structured interviews with AEFI surveillance personnel. Findings were used to generate recommendations for system strengthening.

Results: The system collects and manages AEFI data, employs investigative tools and has an established AEFI review committee conducting causality assessment, thus meeting WHO minimal capacity for vaccine safety. System adaptation through inclusion of digital applications facilitated public reporting,

whilst increasing complexity of database management. Respondents demonstrated engagement with the system through accounts of their roles in AEFI surveillance. Between 17 May 2021 and 31 December 2022, 37,537,009 COVID-19 vaccine doses (BNT162b2 and Ad26.COV2.S) were administered, and 3846 AEFI reported in relation to these vaccines (reporting rate: 10.2/100,000 doses). AEFI reporting rates varied considerably across provinces, ranging from 1.6 to 59.5 AEFI/100,000 doses. In this time period 283 AEFI were reported in relation to non-COVID-19 vaccines. By 31 December 2022, 73.5 % of severe cases that were investigated were causality assessed.

Conclusion: We observed a functional, useful, flexible system with high reported stakeholder and public acceptability levels. System challenges included low reporting rates from particular provinces, weak coordination between paper and digital reporting and human resource constraints. Recommendations include integration of paper-based and digital surveillance reporting systems to enhance signal detection and eliminate data duplication, provision of dedicated human and financial resources at provincial level and inclusion of active AEFI surveillance through cohort event monitoring.



DR JOCELYN MOYES



PROF. CHERYL COHEN

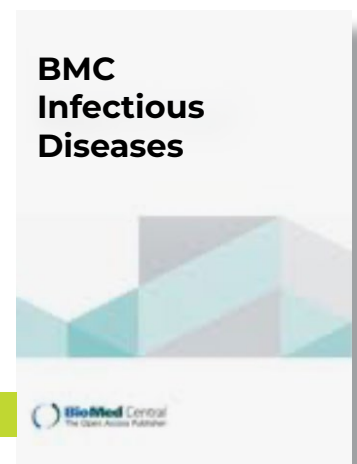
Risk factors for severe respiratory syncytial virus-associated respiratory tract infection in a high HIV prevalence setting, South Africa, 2012 - 2018

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

BMC Infectious Diseases

IMPACT FACTOR: 4.3

<https://doi.org/10.1186/s12879-024-10024-9>



Background: Identifying risk factors for respiratory syncytial virus (RSV)-associated severe acute respiratory illness (SARI) will assist with targeting vaccine interventions.

Methods: Using surveillance data from South Africa (2012-2018), we compared the characteristics of individuals with RSV-associated influenza-like illness (ILI) (reference group) to those with RSV-associated SARI to describe factors associated with SARI using a multivariable analysis.

Results: RSV was detected in 6% (483/7792) of ILI cases and 15% (844/5672) of SARI cases. Factors associated with SARI in children included age < 2 months, compared to age 2-4 years (adjusted

odds ratio (aOR) 54.4; 95% confidence interval (CI) 23.5-125.8), malnutrition (aOR 1.9; 95% CI 1.2-3.2), prematurity (aOR 2.4; 95% CI 1.3-4.6) and living with HIV (LWH) (aOR 22.5; 95% CI 2.9-174.3). In individuals ≥ 5 years, factors associated with SARI included age ≥ 65 years compared to age 5-24 years (aOR 10.7; 95% CI 1.1-107.5), symptom duration ≥ 5 days (aOR 2.7; 95% CI 1.1-6.3), underlying illness (aOR 2.7; 95% CI 1.5-26.1) and LWH (aOR 16.8, 95% CI: 4.8-58.2).

Conclusion: Individuals at the extremes of age and those with identified risk factors might benefit most from RSV prevention interventions.



MS NIKAYLA BATOHI



MS CHRISTINA F. THOBAKGALE

HIV-1 Elite controllers are characterized by elevated levels of CD69-expressing natural killer cells

Nikayla Batohi, Sharon Shalekoff, Neil A. Martinson, Ebrahim Osman, Caroline T. Tiemessen, Christina F. Thobakgale

Journal of Acquired Immune Deficiency Syndrome (JAIDS)

IMPACT FACTOR: 2.9

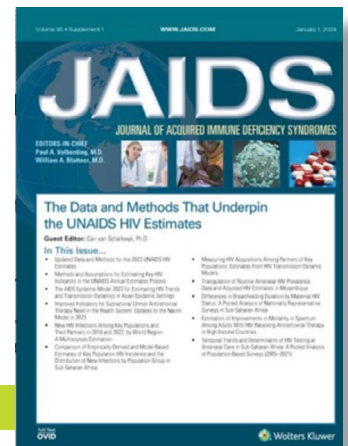
<https://doi.org/10.1097/qai.0000000000003518>

Background: HIV type 1 ((human immunodeficiency virus) HIV-1) elite controllers (ECs) are a rare subset of people living with HIV-1 (PLWH) who control viral replication in the absence of antiretroviral treatment (ART) and may provide a model for a functional cure. We investigated the role of natural killer (NK) cells in HIV-1 ECs from South Africa.

Methods: Phenotypic (CD69, CD38, CD57, PD-1), functional (CD107a, IFN- γ (interferon gamma)), and nutrient transporter profiles (glucose transporter 1, CD98) of NK cells from ECs (n = 20), viremic progressors (VPs; n = 19), PLWH on ART (n = 20), and people without HIV-1 (PWOH; n = 21) were analyzed using flow cytometry. The Kruskal–Wallis test and followed by the Mann–Whitney U test were used to determine differences among the study groups. The Spearman rank correlation coefficient was used to determine significant associations.

Results: Compared with the other study groups, the percentage of CD69-expressing NK cells was higher in ECs, whereas the percentage of CD38-expressing NK cells was higher in VPs. Percentages of CD69+CD38– NK cells were elevated in ECs compared with VPs (P = 0.003), but were not different to PLWH on ART and PWOH. Differentiation, exhaustion, and metabolic profiles were not different in ECs compared with PLWH on ART and PWOH; however, NK cell function was lower than in PWOH.

Conclusions: These findings demonstrate that NK cells from ECs have an activated, mature profile with low levels of immune exhaustion and a reduced metabolic phenotype suggesting functional competence. This insight could inform the development of novel immunotherapeutic strategies for treating HIV-1.





MS ALAINE A. MARSDEN



DR CATHRINE SCHEEPERS

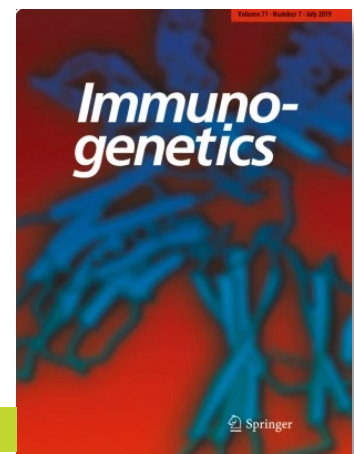
Novel polymorphic and copy number diversity in the antibody IGH locus of South African individuals

Alaine A. Marsden, Martin Corcoran, Gunilla Karlsson Hedestam, Nigel Garrett, Salim S. Abdool Karim, **Penny L. Moore**, Dale Kitchin, Lynn Morris & Cathrine Scheepers

Immunogenetics

IMPACT FACTOR: 2.9

<https://doi.org/10.1007/s00251-024-01363-7>



ABSTRACT

The heavy chain of an antibody is crucial for mediating antigen binding. IGHV genes, which partially encode the heavy chain of antibodies, exhibit vast genetic diversity largely through polymorphism and copy number variation (CNV). These genetic variations impact population-level expression levels. In this study, we analyzed expressed antibody transcriptomes and matched germline IGHV genes from donors from KwaZulu-Natal, South Africa. Amplicon NGS targeting germline IGHV sequences was performed on genomic DNA from 70 participants, eight of whom had matched datasets of expressed antibody transcriptomes.

Germline IGHV sequencing identified 161 unique IGHV alleles, of which 32 were novel. A further 21 novel IGHV alleles were detected in the expressed transcriptomes of these donors. We also examined the datasets for CNV, uncovering gene duplications of 10 IGHV genes from germline sequencing and 33 genes in the expressed transcriptomes. Many of the IGHV gene duplications have not been described in other populations. This study expands our understanding of genetic differences in distinct populations and suggests the potential impact of genetic diversity on immune responses.



MS TSHIAMA M. MWAMBA



PROF. LIZETTE L. KOEKEMOER

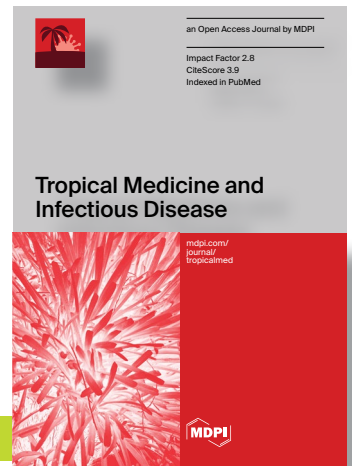
Host preferences and impact of climate on blood feeding in *Anopheles funestus* group from South Africa

Tshiama Maria Mwamba, Yael Dahan-Moss, Givemore Munhenga, Innocent Maposa, Lizette Leonie Koekemoer

Tropical Medicine and Infectious Disease

IMPACT FACTOR: 2.8

<https://doi.org/10.3390/tropicalmed9100251>



ABSTRACT

Anopheles vaneedeni and *Anopheles parensis* (members of the *An. funestus* group) are generally not considered malaria vectors. However, both species were recently identified as potential vectors in South Africa. A critical factor needed to determine their role in malaria transmission is their preference for human blood. The human blood index of *An. vaneedeni* and *An. parensis* and their potential role in the ongoing residual malaria transmission in South Africa is unknown. This study aimed to identify host blood meals from the wild-caught *An. funestus* group in a longitudinal study, and to establish the relationship between temperature, relative humidity, and precipitation on host feeding preferences. *Anopheles lesoni*, *An. parensis*, *An. vaneedeni*, and *Anopheles rivulorum* were collected, and

females mainly fed on cattle. Climatic parameters did not influence the host feeding preferences of these four members of the *An. funestus* group, but impacted the proportion of females that took a blood meal. Significant changes in feeding proportions were driven by relative humidity, temperature, and precipitation. The role of these species in the ongoing residual malaria transmission in South Africa needs further investigation, as no human blood meals were identified. It is recommended that vector surveillance teams incorporate climatic monitoring and host blood meal identification into their routine activities. This information could provide the malaria vector control programmes with scientific evidence to evaluate the importance of the *An. funestus* group in residual malaria transmission.



DR RUVIMBO CHINGONZOH

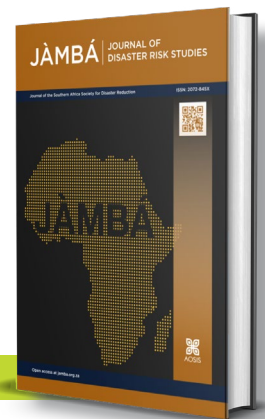
Public health surveillance perspectives from provincial COVID-19 experiences, South Africa 2021

Ruvimbo Chingonzoh, Yvonne Gixela, Bontle Motloutung, Nosiphiwo Mgobo, Zonwabele Merile, Thomas Dlamini

Jàmbá: Journal of Disaster Risk Studies

IMPACT FACTOR: 1.3

<https://doi.org/10.4102/jamba.v16i1.1625>



ABSTRACT

Previous pandemics, recent outbreaks, and imminent public health events are a clarion call for functional public health surveillance systems that timeously detect public health events, guide interventions, and inform public health policy. We reviewed the Eastern Cape Provincial coronavirus disease 2019 (COVID-19) surveillance approach to determine best practices and opportunities to strengthen public health surveillance. We conducted a document review of COVID-19 surveillance reports, tools and guidelines prepared between March 2020 and November 2021. Iterative content and thematic analysis were applied to identify strengths and shortcomings of provincial COVID-19 surveillance. Strengths and shortcomings of the provincial COVID-19 surveillance process, and human, technical, and technological resources for surveillance were described. The existence of local surveillance networks, local availability of national-level surveillance guidelines, the ability to describe and,

track COVID-19 epidemiology, and provincial access to a national web-based centralised COVID-19 surveillance data system were strengths identified. Shortcomings included poor data quality, data disharmony between sub-national reporting levels, under-resourced surveillance capacity at district level, and suboptimal use of the routine surveillance system for COVID-19 surveillance. The review determined the need for a web-based, integrated surveillance system that was agile in meeting evolving surveillance needs and accessible at all health reporting levels for response and decision-making.

Contribution: The review identified opportunities to advance the existing routine public health surveillance system and improve public health surveillance and response. This qualitative review articulates local knowledge that should be translated into strategies and actions to bolster public health preparedness.



MR WENLONG C. CHEN

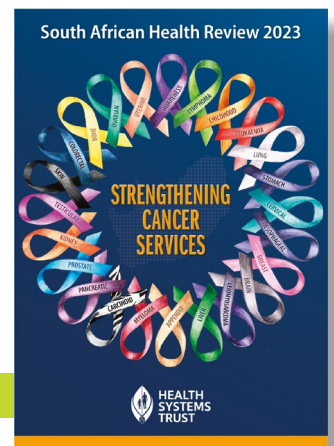
Reducing colorectal cancer mortality in South Africa: experiences and progress from the South African National Cancer Prevention Services

Wenlong C. Chen, Abrie van Wyk, Ursula Algar, Mazvita Muchengeti, Ines Buccimazza, Francois Malherbe, Nomonde Mbatani, Raj Ramesar, Paul A. Goldberg

South African Health Review

IMPACT FACTOR: N/A

<https://doi.org/10.61473/001c.119023>



Aim: The incidence rates of colorectal cancer are rapidly increasing in South Africa. Previous studies have shown that the prevalence of inherited colorectal cancer in South Africa is 3-5 times higher than in high-income countries. Targeted screening and surveillance programmes for individuals with known colorectal cancer-causing mutations have resulted in increased life expectancy. The South African National Cancer Prevention Services (SANCaPS), was established to implement national systems for identifying individuals with inherited cancers, improving their clinical management, and reducing the overall disease burden.

Methods: Using colorectal cancer as an example, SANCaPS aimed to extend surveillance and management practices from the Western Cape to a national level. The goals included improving the quality of pathology reporting, establishing counselling systems for at-risk individuals, developing cost-effective mutation detection protocols, identifying and counselling at-risk family members, providing mutation testing, organising endoscopic

surveillance programmes for high-risk individuals, setting ethical frameworks for research, and extrapolating learnings from the inherited colorectal cancers surveillance programme to other cancers with known hereditary predispositions.

Results: SANCaPS initiated the standardisation of national pathology reporting for colorectal cancers. Currently, a minimum core pathology dataset collection is being piloted in the National Health Laboratory Service's TrakCare system. Subsequently, SANCaPS aims for broader adoption through stakeholder engagements. This will help to identify patients with mismatch repair-deficient colorectal cancers, facilitate research, and improve reporting.

Conclusions: To improve patient outcomes, this consultative process and framework will be replicated to introduce standardised management workflows for other common cancers, including breast, prostate, uterine, and others.



MR BRIAN BRÜMMER

Whole genome sequencing assisted outbreak investigation of *Salmonella Enteritidis*, at a hospital in South Africa, September 2022

Brian Brümmer, Anthony Marius Smith, Motshabi Modise, Juno Thomas, Hetani Mdose, Ramasedi Mokoena and Dikeledi Balen

Access Microbiology

IMPACT FACTOR: N/A

<https://doi.org/10.1099/acmi.0.000835.v3>



ABSTRACT

Our Health authorities were notified of a suspected outbreak of foodborne disease in a hospital in South Africa, where staff and patients reported acute onset of abdominal cramps, diarrhoea, fever and rigours after eating a chicken pasta meal. The aim of this report is to discuss the use of whole genome sequencing (WGS) analysis of bacterial isolates to support an epidemiological investigation. An epidemiological investigation led by the Infection Control Manager of the hospital and supported by an outbreak response team was conducted. Standard microbiological procedures were used to process stool samples and culture/identify diarrhoeal pathogens. Bacterial cultures were investigated using WGS performed using Illumina NextSeq technology, and WGS data were analysed using multiple bioinformatics tools, including those available at the Center for

Genomic Epidemiology and EnteroBase. Core genome multilocus sequence typing (cgMLST) was used to investigate the phylogeny of isolates. Forty-nine cases were identified, with stool samples collected from 21 cases, and nontyphoidal *Salmonella* isolated from 19 out of 21 (90%) of the samples. All isolates were identified as *Salmonella enterica* serovar Enteritidis and differed from each other by ≤ 2 allele differences on cgMLST, indicating that isolates are highly genetically related. Delays in testing of food retention samples rendered the negative test results of limited value. A case-control study was conducted; eating chicken pasta was strongly associated with developing gastroenteritis (odds ratio (OR) = 15.4, Chi-Square test with Yates correction p value = 0.02). The epidemiological evidence suggests that the chicken pasta was the likely vehicle of transmission in this outbreak, although the source of *S. enterica* serovar Enteritidis remains unknown.



DR SHŪNÉ V. OLIVER

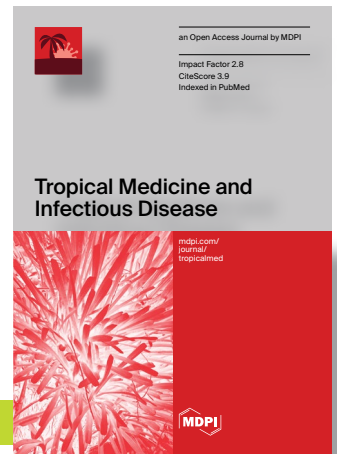
The effect of larval exposure to heavy metals on the Gut Microbiota composition of adult *Anopheles arabiensis* (Diptera: Culicidae)

Ashmika Singh, Shristi Misser, Mushal Allam, Wai-Yin Chan, **Arshad Ismail, Givemore Munhenga, Shūné V. Oliver**

Tropical Medicine and Infectious Disease

IMPACT FACTOR: N/A

<https://doi.org/10.3390/tropicalmed9100249>



ABSTRACT

Anopheles arabiensis is a highly adaptable member of the *An. gambiae* complex. Its flexible resting behaviour and diverse feeding habits make conventional vector control methods less effective in controlling this species. Another emerging challenge is its adaptation to breeding in polluted water, which impacts various life history traits relevant to epidemiology. The gut microbiota of mosquitoes play a crucial role in their life history, and the larval environment significantly influences the composition of this bacterial community. Consequently, adaptation to polluted breeding sites may alter the gut microbiota of adult mosquitoes. This study aimed to examine how larval exposure to metal pollution affects the gut microbial dynamics of *An. arabiensis* adults. Larvae of *An. arabiensis* were exposed to either cadmium chloride or copper nitrate, with larvae reared in untreated water serving as a control. Two laboratory strains (SENN: insecticide

unselected, SENN-DDT: insecticide selected) and F1 larvae sourced from KwaZulu-Natal, South Africa, were exposed. The gut microbiota of the adults were sequenced using the Illumina Next Generation Sequencing platform and compared. Larval metal exposure affected alpha diversity, with a more marked difference in beta diversity. There was evidence of core microbiota shared between the untreated and metal-treated groups. Bacterial genera associated with metal tolerance were more prevalent in the metal-treated groups. Although larval metal exposure led to an increase in pesticide-degrading bacterial genera in the laboratory strains, this effect was not observed in the F₁ population. In the F₁ population, *Plasmodium*-protective bacterial genera were more abundant in the untreated group compared to the metal-treated group. This study therefore highlights the importance of considering the larval environment when searching for local bacterial symbionts for paratransgenesis interventions.



DR JOCELYN MOYES



PROF. CHERYL COHEN

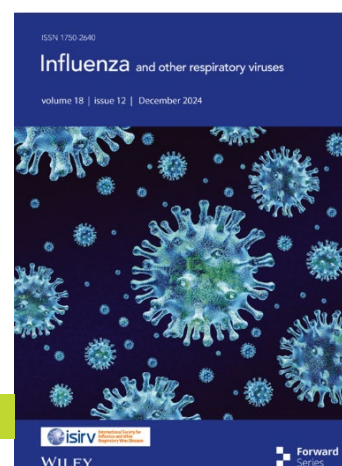
Home-based Testing as an approach to estimate influenza vaccine effectiveness in South Africa, 2021-2022-A pilot study

Jocelyn Moyes, Mvuyo Makhazi, Sibongile Walaza, Phiwokuhle Ntombela, Fahima Moosa, Anne von Gottberg, Nicole Wolter, Mignon du Plessis, Gillian Hunt, Cherie Cawood, Erica Dueger, Cheryl Cohen

Influenza and Other Respiratory Viruses

IMPACT FACTOR: N/A

<https://doi.org/10.1111/irv.70034>



Background: Surveillance programmes for influenza and other respiratory pathogens are important to generate vaccine effectiveness (VE) estimates and to inform vaccine composition. We aimed to explore the feasibility and acceptability of home-based testing.

Methods: In three out of nine provinces in South Africa, we established a self-referral system for individuals aged ≥ 18 years with respiratory symptoms of ≤ 10 days duration. Following consent, swab collection material was delivered to participants who also completed a questionnaire including self-reported vaccination status. Swabs were tested by PCR for influenza, respiratory syncytial virus (RSV) and SARS-CoV-2. A test-negative methodology was used to estimate influenza VE.

Results: Of 1456 samples collected between 19 November 2021 and 3 September 2022, 73 (5%) tested positive for influenza, 38 (3%) tested positive for RSV and 394 (27%) for SARS-CoV-2. We

subtyped 55% (40/73) of the influenza positive specimens; 16/40 (40%) were influenza A(H1N1)pdm09; 10/40 (25%) A(H3N2)) and all 14/40 (35%) influenza B were B/Victoria. Only 20% (279/1451) of participants reported influenza-like illness case definition symptoms of fever and cough. Influenza vaccine coverage was 11% (157/1454). The overall influenza VE was 26% (95% confidence interval: -73%, 69%). Of the completed acceptability questionnaires, 123/127 (97%) participants would make use of the service again; 90% (1306) were recruited via the COVID-19 testing centre (call in, social media, webpage), and 7% (99/1306) through *CoughWatchSA*.

Conclusion: Home-based swabbing was feasible and acceptable. We were able to calculate an influenza VE, although a larger sample size and verification of vaccine status may improve the VE estimates in the future.

Other publications highlighting NICD staff contributions



DR KEEREN LUTCHMINARAIN

Southern African HIV Clinicians Society guideline on the management of non-tuberculous mycobacteria in people with HIV

Halima Dawood, Lauren Richards, **Keeren Lutchminarain**, Arifa Parker, Camilla Wattrus, Nosisa Sipambo, Jeremy Nel, Thandekile Manzini, Kogieleum Naidoo

Southern African Journal of HIV Medicine

<https://doi.org/10.4102/sajhivmed.v25i1.1657>



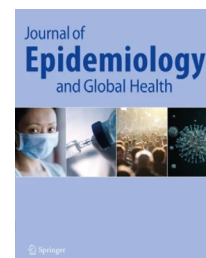
PROF. ANTHONY M. SMITH

Molecular Epidemiology and AMR Perspective of Diarrhoeagenic *Escherichia coli* in Africa: A Systematic Review and Meta-analysis

John Bosco Kalule, Linda A. Bester, Daniel L. Banda, Firehiwot Abera Derra, Chisomo Msefula, **Anthony M. Smith**, Abraham Ajayi, Happiness Kumburu, Geoffrey Kwenda, Kaunda Yamba, John Mwaba, Yasmina J. Fakim, Nyasha Sithole, Aquillah M. Kanzi, Patrick M. K. Njage, Francis Chikuse, Sofonias K. Tessema, Stella I. Smith, Ebenezer Foster-Nyarko

Journal of Epidemiology and Global Health

<http://dx.doi.org/10.1007/s44197-024-00301-w>



DR ISMAIL ARSHAD



PROF. ANTHONY M. SMITH

Genomics sequence data of a drug-resistant *Pseudomonas aeruginosa* producing Tripoli Metallo- β -lactamase 1 isolated from Sudan

Mohammed SE, Hamid O, Abdelrahim M, **Ismail Arshad**, **Smith Anthony M.**, Allam M.

Data in Brief

<https://doi.org/10.1016/j.dib.2024.111040>



Other publications highlighting NICD staff contributions



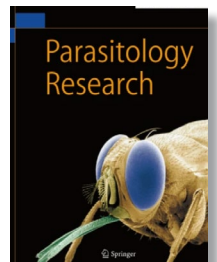
PROF. LIZETTE L. KOEKEMOER

Only incandescent light significantly decreases feeding of *Anopheles funestus* s.s. (Diptera: Culicidae) mosquitos under laboratory conditions.

Layla van Zyl, Ashley M. Burke, **Lizette L. Koekemoer**, Bernard W.T. Coetzee.

Parasitology Research

<http://doi.org/10.1007/s00436-024-08370-3>



PROF. GOVENDER P. NELESH

Exploring polyamine metabolism of the yeast-like fungus, *Emergomyces africanus*

Koroleva E, Toplis B, Taylor M, van Deventer C, Steffen HC, van den Heever C, **Govender Nelesh P.**, de Hoog S, Botha A.

FEMS Yeast Research

<https://doi.org/10.1093/femsyr/foae038>



PROF. OLGA PEROVIC

The challenges of difficult-to-treat *Acinetobacter* infections

Richards GA, **Perovic O**, Brink AJ.

Clinical Microbiol Reviews

<https://doi.org/10.1128/cmr.00093-24>



Other publications highlighting NICD staff contributions



PROF. GAYLE SHERMAN

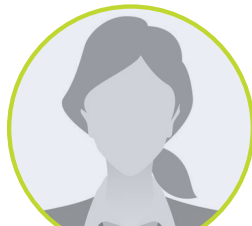
Are social protection and food security accelerators for adolescents to achieve the Global AIDS targets?

Lucie Cluver, Siyanai Zhou, Olanrewaju Edun, Allison Oman Lawi, Nontokozi Langwenya, David Chipanta, **Gayle Sherman**, Lorraine Sherr, Mona Ibrahim, Rachel Yates, Louise Gordon, and Elona Toska

Journal of the International AIDS Society
<https://doi.org/10.1002/jia2.26369>



DR SIMONE I. RICHARDSON

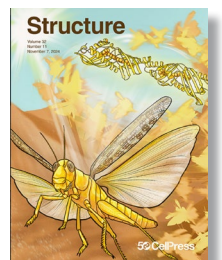


DR NELIA P. MANAMELA

Discovery and characterization of a pan-betacoronavirus S2-binding antibody

Nicole V. Johnson, Steven C. Wall, Kevin J. Kramer, Clinton M. Holt, Sivakumar Periasamy, **Simone I. Richardson**, **Nelia P. Manamela**, Naveenchandra Suryadevara, Emanuele Andreano, Ida Paciello, Giulio Pierleoni, Giulia Piccini, Ying Huang, Pan Ge, James D. Allen, Naoko Uno, Andrea R. Shiakolas, Kelsey A. Pilewski, Rachel S. Nargi, Rachel E. Sutton, Alexandria A. Abu-Shmais, Robert Parks, Barton F. Haynes, Robert H. Carnahan, James E. Crowe, Jr., Emanuele Montomoli, Rino Rappuoli, Alexander Bukreyev, Ted M. Ross, Giuseppe A. Sautto, Jason S. McLellan, Ivelin S. Georgiev

Structure
<https://doi.org/10.1016/j.str.2024.08.022>



DR NISHI PRABDIAL-SING



PROF. ANNE VON GOTTBERG

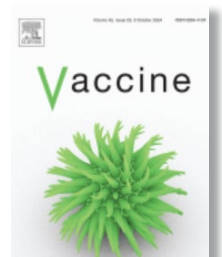


DR KERRIGAN MCCARTHY

Estimation of the poliovirus type 2 immunity gap in South Africa

Lauren Brown, Jeremy Bingham, Juliet Pulliam, Zinhle Mthombothi, Tumelo Sereo, Mercy Kamupira, Sonia Botha, Koko Molema, Elizabeth Maseti, Marione Schönfeldt, Nicoletta Mabhena, **Nishi Prabdial-Sing**, **Anne von Gottberg**, **Kerrigan McCarthy**, Cari van Schalkwyk

Vaccine
<https://www.sciencedirect.com/science/article/pii/S0264410X24007035>



Other publications highlighting NICD staff contributions



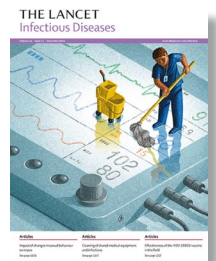
PROF. CHERYL COHEN

The respiratory syncytial virus vaccine and monoclonal antibody landscape: the road to global access

Jonne Terstappen, Sarah F Hak, Anant Bhan, Debby Bogaert, Louis J Bont, Ursula J Buchholz, Andrew D Clark, **Cheryl Cohen**, Ron Dagan, Daniel R Feikin, Barney S Graham, Anuradha Gupta, Pradeep Haldar, Rose Jalang'o, Ruth A Karron, Leyla Kragten, You Li, Yvette N Löwensteyn, Patrick K Munywoki, Rosemary Njogu, Ab Osterhaus, Andrew J Pollard, Luiza Reali Nazario, Charles Sande, Ashish R Satav, Padmini Srikantiah, Renato T Stein, Naveen Thacker, Rachael Thomas, Marta Tufet Bayona, Natalie I Mazur

The Lancet Infectious Diseases

[https://doi.org/10.1016/S1473-3099\(24\)00455-9](https://doi.org/10.1016/S1473-3099(24)00455-9)



DR SHAHEED V. OMAR



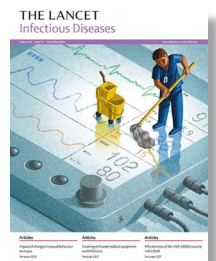
MS LAVANIA JOSEPH

Evaluating culture-free targeted next-generation sequencing for diagnosing drug-resistant tuberculosis: a multicentre clinical study of two end-to-end commercial workflows

Rebecca E Colman, Marva Seifert, Andres De la Rossa, Sophia B Georghiou, Christine Hoogland, Swapna Uplekar, Sacha Laurent, Camilla Rodrigues, Priti Kambli, Nestani Tukvadze, Nino Maghradze, **Shaheed V Omar**, **Lavania Joseph**, Anita Suresh, Timothy C Rodwell

The Lancet Infectious Diseases

[https://doi.org/10.1016/S1473-3099\(24\)00586-3](https://doi.org/10.1016/S1473-3099(24)00586-3)



MR WENLONG C. CHEN



DR MUCHENGETI MAZVITA

Heterogeneous genetic architectures of prostate cancer susceptibility in sub-Saharan Africa.

Janivara R, **Chen Wenlong C.**, Hazra U, Baichoo S, Agalliu I, Kachambwa P, Simonti CN, Brown LM, Tambe SP, Kim MS, Harlemon M, Jalloh M, Muzondiwa D, Naidoo D, Ajayi OO, Snyder NY, Niang L, Diop H, Ndoeye M, Mensah JE, Abrahams AOD, Biritwum R, Adjei AA, Adebisi AO, Shittu O, Ogunbiyi O, Adebayo S, Nwegbu MM, Ajibola HO, Oluwole OP, Jamda MA, Pentz A, Haiman CA, Spies PV, van der Merwe A, Cook MB, Chanock SJ, Berndt SI, Watya S, Lubwama A, **Muchengeti Mazvita**, Doherty S, Smyth N, Lounsbury D, Fortier B, Rohan TE, Jacobson JS, Neugut AI, Hsing AW, Gusev A, Aisuodionoe-Shadrach OI, Joffe M, Adusei B, Gueye SM, Fernandez PW, McBride J, Andrews C, Petersen LN, Lachance J, Rebbeck TR

Nature Genetics

<https://doi.org/10.1038/s41588-024-01931-3>



Other publications highlighting NICD staff contributions



DR NICOLE WOLTER

Challenges and approaches to establishing multi-pathogen serosurveillance: Findings from the 2023 serosurveillance summit

Andrea C Carcelen , Alex C Kong , Saki Takahashi, Sonia Hegde, Thomas Jaenisch, May Chu, Rosemary Rochford, Natalya Kostandova, Emily S Gurley, Amy Wesolowski, Andrew S Azman , Fiona R M van der Klis , Gerco den Hartog , Christopher Drakeley, Christopher D Heaney, Amy K Winter, Henrik Salje, Isabel Rodriguez-Barraquer , Daniel T Leung , Sammy M Njenga, Eunice Wangeci Kagucia, Kondwani C Jambo, **Nicole Wolter**, Richelle C Charles , Martha-Idalí Saboyá-Díaz, Diana L Martin, William J Moss

Public Med

<https://pubmed.ncbi.nlm.nih.gov/39226906/>



MR WENLONG C. CHEN

Serum free light chains in a racially diverse population including African Americans and populations from South Africa

Bertamini L, Alberge JB, Lee DJ, El-Khoury H, Kim S, Fleming G, Murphy CSM, Colchie J, Davis MI, Perry J, Lightbody ED, Allam S, Goqwana LN, Philip V, Smyth NA NA, Sakrikar D, Perkins MC, Harding S, Troske D, Getz G, Karlson EW, Munshi NC, Anderson KC, Trippa L, Marinac CR, **Chen Wenlong C**, Joffe M, Ghobrial IM.

Blood

<https://doi.org/10.1182/blood.2024026078>



MR WENLONG C. CHEN



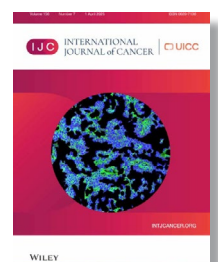
DR MUCHENGETI MAZVITA

Smokeless tobacco (snuff) and site-specific cancer risks in adult Black South African women: Findings from the Johannesburg Cancer Study

Motlhale M, Sitas F, de Villiers CB, Simba H, Feliu A, **Chen Wenlong C**, Schüz J, **Muchengeti Mazvita**, McCormack V.

International Journal of Cancer

<https://doi.org/10.1002/ijc.35293>



Other publications highlighting NICD staff contributions



MR WENLONG C. CHEN

The association of HIV status with triple-negative breast cancer in patients with breast cancer in South Africa: a cross-sectional analysis of case-only data from a prospective cohort study

Dubner J, Neugut AI, Joffe M, O'Neil DS, Ayeni OA, **Chen Wenlong C.**, Buccimazza I, Čačala SR, Stopforth LW, Farrow HA, Nietz S, Murugan N, Phakathi B, Jacobson JS, Crew KD, McCormack V, Ruff P, Cubasch H, Pumpalova YS.

The Lancet Global Health

[https://doi.org/10.1016/S2214-109X\(24\)00376-0](https://doi.org/10.1016/S2214-109X(24)00376-0)



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PROF. PENNY L. MOORE

Safety, effectiveness and immunogenicity of heterologous mRNA-1273 boost after prime with ad26.cov2.s among healthcare workers in South Africa: the single-arm, open-label, phase 3 SHERPA study

Garrett N, Reddy T, Yende-Zuma N, Takalani A, Woeber K, Bodenstein A, Jonas P, Engelbrecht I, Jassat W, Moultrie H, Bradshaw D, Seocharan I, Odhiambo J, Khuto K, **Richardson Simone I**, Omondi MA, Nesamari R, Keeton RS, Riou C, **Moyo-Gwete Thandeka**, Innes C, Zwane Z, Barnabas S, Lombaard J, Gill K, Nchabeleng M, Snyman E, Petrick F, Spooner E, Naidoo L, Kalonji D, Naicker V, Singh N, Maboja R, Mda P, Malan D, Nana A, Malahlena M, Kotze P, Allagappen JJ, Diacon AH, Kruger GM, Patel D, **Moore Penny L**, Burgers WA, Anteyi K, Leav B, Bekker L, Gray GE, Goga A, the SHERPA study team

PLOS Global Public Health

<https://doi.org/10.1371/journal.pgph.0003260>



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MS TINASHA TOMBE-NYAHUMA



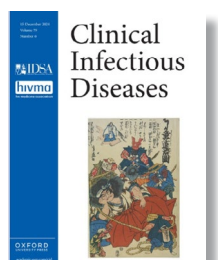
DR MUCHENGETI MAZVITA

HIV-1 Viremia and Cancer Risk in 2.8 Million People: the South African HIV Cancer Match Study

Ruffieux Y, **Mwansa-Kambafwile Judith**, **Metekoua Carole**, **Tombe-Nyahuma Tinasha**, Bohlius J, **Muchengeti Mazvita**, Egger M, Rohner E.

Clinical Infectious Diseases

<https://doi.org/10.1093/cid/ciae652>





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