

Issue 18 - September 2021



NATIONAL INSTITUTE FOR
COMMUNICABLE DISEASES

Division of the National Health Laboratory Service

SCIENCE FOCUS

Bridging the gap between scientists and communities



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.



Editor's Note

Notable research achievements of the National Institute for Communicable Diseases (NICD) are highlighted in the latest Science Focus. This issue features outstanding statistical findings, the number of peer-reviewed articles produced, the top three published authors and high impact factor score articles.

The Science Focus kicks off with a feature by Dr Givemore Munhenga and Pinky Manana, which focuses on bringing science to communities. The article delves into how community engagement was mobilised in the KwaZulu-Natal province in preparation for a pilot Sterile Insect Technique release programme. Dubbed the "Maskandi experience", the use of a cultural song was used to share information at community level. Prof Penny Moore and Dr Thandeka Moyo-Gwete's collaboration on *Cross-reactive neutralizing antibody responses elicited by SARS-CoV-2 501Y.V2 (B.1.351)* guarantees to be an interesting read. The article unpacks how the neutralization escape by SARS-CoV-2 variants has impacted the efficacy of first generation COVID-19 vaccines.

In a population cohort study, *Asymptomatic transmission and high community burden of seasonal influenza in an urban and a rural community in South Africa, 2017-18 (PHIRST)*, Prof Cheryl Cohen and Prof Stefano Tempia found that individuals with asymptomatic influenza transmitted infection to 29 (6%) of 509 household contacts.

In an interesting read, *HIV infection as risk factor for death among hospitalized persons with candidemia, South Africa, 2012-2017*, Prof Nelesh Govender and Prof Cheryl Cohen determine the effect of HIV infection on deaths among persons over 18 months of age with culture-confirmed candidemia at 29 sentinel hospitals in South Africa during 2012-2017. It was found that of 1,040 case-patients with documented HIV status and in-hospital survival data, 426 (41%) were HIV-seropositive.

It is evident that NICD researchers continue to pave the way in publishing important public health papers and high-impact publications in, to name a few, the New England Journal of Medicine, The Lancet Global Health, The Center for Disease Control and Prevention's Emerging Infectious Diseases, Journal of Fungi and the Bio Med Central.

NICD staff members are encouraged to continue to send their comments to the Communications Unit.

Enjoy reading!

On behalf of the team,

Sinenhlanhla Jimoh
Senior Communications Manager

Bridging the gap between scientists and communities: Community engagement in preparation for a pilot Sterile Insect Technique release programme for malaria vector control in KwaZulu-Natal Province, South Africa

Dr Givemore Munhenga and Pinky Manana

Science is grounded on the need to solve society's problems. Against this background, any scientific or technological solutions should be a participatory effort between communities and scientists. Unfortunately, the traditional scientist approach has primarily been prescriptive, in most instances, side-lining the communities in which the research is intended. This has created a gap between research and practice leading to suboptimal benefits from scientific research and new technologies. This was at the back of our minds when we initiated the development of the Sterile Insect Technique (SIT) as a possible supplementary malaria vector control method to accelerate the malaria elimination agenda. Investigations on the applicability of SIT under a South African setting are now approaching the piloting stage.

The Sterile Insect Technique is a vector control technology that uses ionising radiation to sterilise mass-produced insects. The sterile insects are released in infested areas where they mate with the native population producing non-viable offspring. Consistent application of this technology can suppress and, in some instances, eliminate vector populations. Naturally, releasing laboratory-reared genetically modified mosquitoes into communities will generate debate, raising social, ethical, and regulatory concerns. Experiences from similar technology attempts showed that failure to involve resulted in mistrust and the total collapse of an SIT initiative (<https://doi.org/10.1111/dewb.12147>). At the same time, connecting with communities on the ground resulted in improved acceptability of releasing mosquitoes in their communities. This clearly shows that failure to consider the beliefs and perceptions of the community may lead to negative attitudes and the inability to achieve the intended goals. Therefore, the NICD SIT project needed to engage and work collaboratively with the community to enhance the uptake of the technology.

The engagement activities for the project commenced in early 2015 where knowledge, attitudes and practices survey to understand the beliefs and perceptions of the community regarding the possibility of releasing mosquitoes in their communities as a malaria control strategy (<https://bmcpublichealth.biomedcentral.com/articles/10.1186/s12889-017-4583-2>). This exercise allowed us to identify appropriate ways to introduce SIT research in Mamfene communities. Because of its richness in the Zulu heritage and importance to the Zulu tribe, we explored the indigenous music genre "Maskandi" to engage the community. The song was composed and produced together with a popular local "Maskandi" band. Using one of their own to write a song in the famous traditional Zulu genre made the community better understand the complexity of the SIT technology. The song was well received and informative, increasing knowledge on malaria transmission and the SIT (<https://malariajournal.biomedcentral.com/articles/10.1186/s12936-021-03736-9>).



Figure 1: Ms Manana participating in a phone-in a radio interview to answer question on the Sterile Insect Technique

Furthermore, we are exploring using an SIT radio short story, "Umdlayo womoya", to engage the community. This SIT tale was developed in collaboration with a native drama team. The story was played on a local community radio station for two weeks. Evaluation of its impact in increasing knowledge on malaria transmission and SIT technology is underway. In addition to these innovative approaches, we supplemented the community engagement exercise using existing channels used by the local malaria control programme, including distributing pamphlets, radio interviews using the local radio station, lectures at schools, community meetings and halls, roadshows and door to door campaigns.

In conclusion, our experience working with the Mamfene community generated a wealth of information and tools that can be used to bridge the gap between the public and scientists. Most importantly, it has taught us that for any public intervention to be accepted, the community needs a general scientific understanding of the intervention and that the penalty for scientific illiteracy by the community can be costly.



Figure 2: Mr Zikhali, a community liaison officer for the SIT project, explaining the concepts of SIT technology to out-patients at a primary health care facility in Mamfene

EXCEPTIONAL RESEARCH STATISTICS

TOP 3

MOST PUBLISHED AUTHORS IN Q1 OF 2021/2022

1



PROF ANNE VON
GOTTBERG

2



PROF CHERYL
COHEN

3



PROF PENNY
MOORE

3



PROF CAROLINE
TIEMESSEN

3



DR JINAL
BHIMAN

3



MS JACKIE
KLEYNHANS

FEATURED RESEARCH ABSTRACTS FOR THE FIRST QUARTER OF 2021/2022



Dr Thandeka Moyo-Gwete

Cross-reactive neutralizing antibody responses elicited by SARS-CoV-2 501Y.V2 (B.1.351)

Moyo-Gwete T, Madzivhandila M, Makhado Z, Ayres F, Mhlanga D, Oosthuysen B, Lambson BE, Kgagudi P, Tegally H, Iranzadeh A, Doolabh D, Tyers L, Chinhoi LR, Mennen M, Skelem S, Marais G, Bhiman JN, Ueckermann V, Rossouw T, Boswell M, de Oliveira T, Williamson C, Burgers WA, Ntusi N, Morris L, Moore PL

The New England Journal of Medicine
Impact Factor: 91.245

Neutralization escape by SARS-CoV-2 variants, as has been observed in the 501Y.V2 (B.1.351) variant, has impacted the efficacy of first generation COVID-19 vaccines. Here, the antibody response to the 501Y.V2 variant was examined in a cohort of patients hospitalized with COVID-19 in early 2021 - when over 90% of infections in South Africa were attributed to 501Y.V2. Robust binding and neutralizing antibody titers to the 501Y.V2 variant were detected and these binding antibodies showed high levels of cross-reactivity for the original variant, from the first wave. In contrast to an earlier study where sera from individuals infected with the original variant showed dramatically reduced potency against 501Y.V2, sera from 501Y.V2-infected patients maintained good cross-reactivity against viruses from the first wave. Furthermore, sera from 501Y.V2-infected patients also neutralized the 501Y.V3 (P.1) variant first described in Brazil, and now circulating globally. Collectively these data suggest that the antibody response in patients infected with 501Y.V2 has a broad specificity and that vaccines designed with the 501Y.V2 sequence may elicit more cross-reactive responses.





Prof Cheryl Cohen



Prof Stefano Tempia

Asymptomatic transmission and high community burden of seasonal influenza in an urban and a rural community in South Africa, 2017-18 (PHIRST): a population cohort study

Cohen C, Kleynhans J, Moyes J, McMorrow ML, Treurnicht FK, Hellferscee O, Mathunjwa A, von Gottberg A, Wolter N, Martinson NA, Kahn K, Lebina L, Mothlaoleng K, Wafawanaka F, Gómez-Olivé FX, Mkhencele T, Mathee A, Piketh S, Language B, **Tempia S**

The Lancet Global Health
Impact Factor: 26.763

Background: Data on influenza community burden and transmission are important to plan interventions especially in resource-limited settings. However, data are limited, particularly from low-income and middle-income countries. We aimed to evaluate the community burden and transmission of influenza in a rural and an urban setting in South Africa.

Methods: In this prospective cohort study approximately 50 households were selected sequentially from both a rural setting (Agincourt, Mpumalanga Province, South Africa; with a health and sociodemographic surveillance system) and an urban setting (Klerksdorp, Northwest Province, South Africa; using global positioning system data), enrolled, and followed up for 10 months in 2017 and 2018. Different households were enrolled in each year. Households of more than two individuals in which 80% or more of the occupants agreed to participate were included in the study. Nasopharyngeal swabs were collected twice per week from participating household members irrespective of symptoms and tested for influenza using real-time RT-PCR. The primary outcome was the incidence of influenza infection, defined as the number of real-time RT-PCR-positive episodes divided by the person-time under observation. Household cumulative infection risk (HCIR) was defined as the number of subsequent infections within a household following influenza introduction.

Findings: 81 430 nasopharyngeal samples were collected from 1116 participants in 225 households (follow-up rate 88%). 917 (1%) tested positive for influenza; 178 (79%) of 225 households had one or more influenza-positive individual. The incidence of influenza infection was 43.6 (95% CI 39.8–47.7) per 100 person-seasons. 69 (17%) of 408 individuals who had one influenza infection had a repeat influenza infection during the same season. The incidence (67.4 per 100 person-seasons) and proportion with repeat infections (22 [23%] of 97 children) were highest in children younger than 5 years and decreased with increasing age ($p < 0.0001$). Overall, 268 (56%) of 478 infections were symptomatic and 66 (14%) of 478 infections were medically attended. The overall HCIR was 10% (109 of 1088 exposed household members infected [95% CI 9–13%]). Transmission (HCIR) from index cases was highest in participants aged 1–4 years (16%; 40 of 252 exposed household members) and individuals with two or more symptoms (17%; 68 of 396 exposed household members). Individuals with asymptomatic influenza transmitted infection to 29 (6%) of 509 household contacts. HIV infection, affecting 167 (16%) of 1075 individuals, was not associated with increased incidence or HCIR.

Interpretation: Approximately half of influenza infections were symptomatic, with asymptomatic individuals transmitting influenza to 6% of household contacts. This suggests that strategies, such as quarantine and isolation, might be ineffective to control influenza. Vaccination of children, with the aim of reducing influenza transmission might be effective in African settings given the young population and high influenza burden.





Prof Nelesh Govender



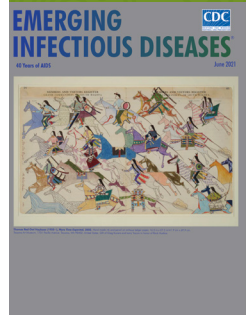
Prof Cheryl Cohen

HIV Infection as Risk Factor for Death among Hospitalized Persons with Candidemia, South Africa, 2012–2017

Nelesh P. Govender, Jim Todd, Jeremy Nel, Mervyn Mer, Alan Karstaedt, **Cheryl Cohen**, for **GERMS-SA**

Emerging Infectious Diseases
Impact Factor: 6.883

We determined the effect of HIV infection on deaths among persons >18 months of age with culture-confirmed candidemia at 29 sentinel hospitals in South Africa during 2012–2017. Of 1,040 case-patients with documented HIV status and in-hospital survival data, 426 (41%) were HIV-seropositive. The in-hospital case-fatality rate was 54% (228/426) for HIV-seropositive participants and 37% (230/614) for HIV-seronegative participants (crude odds ratio [OR] 1.92, 95% CI 1.50–2.47; $p < 0.001$). After adjusting for relevant confounders ($n = 907$), mortality rates were 1.89 (95% CI 1.38–2.60) times higher among HIV-seropositive participants than HIV-seronegative participants ($p < 0.001$). Compared with HIV-seronegative persons, the stratum-specific adjusted mortality OR was higher among HIV-seropositive persons not managed in intensive care units (OR 2.27, 95% CI 1.47–3.52; $p < 0.001$) than among persons who were (OR 1.56, 95% CI 1.00–2.43; $p = 0.05$). Outcomes among HIV-seropositive persons with candidemia might be improved with intensive care.





Ms Serisha Naicker



Prof Nelesh Govender

Genotype, Antifungal Susceptibility, and Virulence of Clinical South African *Cryptococcus neoformans* Strains from National Surveillance, 2005–2009

Serisha D. Naicker, Rindidzani E. Magobo, Tsidiso G. Maphanga, Carolina Firacative, Erika van Schalkwyk, Juan Monroy-Nieto, Jolene Bowers, David M. Engelthaler, Liliwe Shuping, Wieland Meyer and **Nelesh P. Govender**

Journal of Fungi

Impact Factor: 5.816

In South Africa, *Cryptococcus neoformans* is the most common cause of adult meningitis. We performed multi locus sequence typing and fluconazole susceptibility testing of clinical *C. neoformans* isolates collected from 251 South African patients with cryptococcosis through national surveillance from 2005 to 2009. We examined the association between clinical characteristics of patients and genotype, and the effect of genotype on in-hospital mortality. We performed whole genome phylogenetic analysis of fifteen *C. neoformans* isolates with the molecular type VNB and tested their virulence in a *Galleria mellonella* model. Most isolates had the molecular type VNI (206/251, 82%), followed by VNBII (25/251, 10%), VNB (15/251, 6%), and VNBIV (5/251, 2%); 67 sequence types were identified. There were no differences in fluconazole minimum inhibitory concentration (MIC) values among molecular types and the majority of strains had low MIC values (MIC₅₀ of 1 µg/mL and MIC₉₀ of 4 µg/mL). Males were almost twice as likely of being infected with a non-VNI genotype (adjusted odds ratio [OR]: 1.65, 95% confidence interval [CI]: 0.25–10.99; $p = 0.61$). Compared to patients infected with a VNI genotype, those with a non-VNI genotype had a 50% reduced adjusted odds of dying in hospital (95% CI: 0.03–7.57; $p = 0.62$). However, for both these analyses, our estimates had wide confidence intervals spanning 1 with large p -values. Fifteen VNB strains were not as virulent in a *G. mellonella* larval model as the H99 reference strain. A majority of these VNB strains belonged to the VNBII clade and were very closely related by phylogenetic analysis.





Ms Thembekile Zwane



Prof Olga Perovic

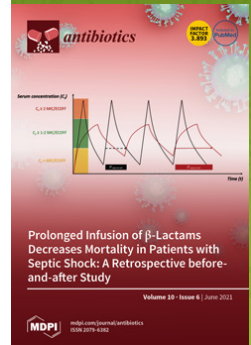
Etiology and Antimicrobial Susceptibility of Pathogens Associated with Urinary Tract Infections among Women Attending Antenatal Care in Four South African Tertiary-Level Facilities, 2015–2019

Thembekile Zwane, **Liliwe Shuping** and **Olga Perovic**

Antibiotics

Impact Factor: 4.693

In South Africa, uncomplicated community-acquired UTIs (CA-UTIs) are treated empirically; however, the extent of antibiotic resistance among these pathogens is not well known. We conducted a descriptive cross-sectional study of women attending ANCs at four tertiary public-sector hospitals in Gauteng. Female patients aged 15–49 years, with urine cultures performed between January 2015 and December 2019, were included. A case of culture-confirmed UTI was defined as any woman with ≤ 2 uropathogens with a bacterial count of $\geq 10^5$ colony-forming units per ml for at least one pathogen. We identified 3558 cases of culture-confirmed UTIs in women with a median age of 30 years (interquartile range; 25–35). *E. coli* accounted for most infections (56% (1994/3558)), followed by *E. faecalis*, with a prevalence of 17% (609/3558). The prevalence of *K. pneumoniae* was 5% (193/3558), 5% (186/3558) for *S. agalactiae*, and 5% (179/3558) for *P. mirabilis*. Ninety-five percent (1827/1927) of the *E. coli* and 99% of the *E. faecalis* (301/305) isolates were susceptible to nitrofurantoin. Common uropathogens showed high susceptibility to first-line antibiotics, gentamicin and nitrofurantoin, as recommended for use in primary healthcare settings. Overall, our study provided an indication of the level of antimicrobial resistance in the four facilities.





Prof Anne von Gottberg

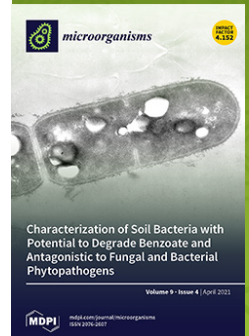
Serotype distribution of remaining pneumococcal meningitis in the mature PCV10/13 period: Findings from the PSERENADE Project

*Quesada MG, Yang Y, Bennett JC, Hayford K, Zeger SL, Feikin DR, Peterson ME, Cohen AL, Almeida SCG, Ampofo K, Ang M, Bar-Zeev N, Bruce MG, Camilli R, Chacón GC, Ciruela P, Cohen C, Corcoran M, Dagan R, De Wals P, Desmet S, Diawara I, Gierke R, Guevara M, Hammitt LL, Hilty M, Ho PL, Jayasinghe S, Kleynhans J, Kristinsson KG, Ladhani SN, McGeer A, Mwenda JM, Pekka Nuorti J, Oishi K, Ricketson LJ, Sanz JC, Savrasova L, Setchanova LP, Smith A, Valentiner-Branth P, Valenzuela MT, van der Linden M, van Sorge NM, Varon E, Winje BA, Yildirim I, Zintgraff J, Knoll MD, Zahin Amin-Chowdhury, Born R, Brandileone MCC, Bruden D, Byington CL, Cameron C, Castilla J, Chan G, Chow KH, Dalby T, Danis K, de Gouveia L, de Miguel S, Deceuninck G, Del Manso M, Díaz J, Dimina E, Erlendsdottir H, Givon-Lavi N, Kellner JD, Knol MJ, Lefebvre B, Mereckiene J, Muñoz-Almagro C, Napoli D, Nzoyikorera N, Pelton SI, Pennington K, Pilishvili T, Ploy MC, Puentes R, Suga S, Sutcliffe CG, Swarthout TD, Thoon KC, Toropainen M, Vestheim DF, **von Gottberg A***

Microorganisms

Impact Factor: 4.128

Pneumococcal conjugate vaccine (PCV) introduction has reduced pneumococcal meningitis incidence. The Pneumococcal Serotype Replacement and Distribution Estimation (PSERENADE) project described the serotype distribution of remaining pneumococcal meningitis in countries using PCV10/13 for least 5–7 years with primary series uptake above 70%. The distribution was estimated using a multinomial Dirichlet regression model, stratified by PCV product and age. In PCV10-using sites (N = 8; cases = 1141), PCV10 types caused 5% of cases <5 years of age and 15% among ≥5 years; the top serotypes were 19A, 6C, and 3, together causing 42% of cases <5 years and 37% ≥5 years. In PCV13-using sites (N = 32; cases = 4503), PCV13 types caused 14% in <5 and 26% in ≥5 years; 4% and 13%, respectively, were serotype 3. Among the top serotypes are five (15BC, 8, 12F, 10A, and 22F) included in higher-valency PCVs under evaluation. Other top serotypes (24F, 23B, and 23A) are not in any known investigational product. In countries with mature vaccination programs, the proportion of pneumococcal meningitis caused by vaccine-in-use serotypes is lower (≤26% across all ages) than pre-PCV (≥70% in children). Higher-valency PCVs under evaluation target over half of remaining pneumococcal meningitis cases, but questions remain regarding generalizability to the African meningitis belt where additional data are needed.





Ms Nozuko P. Blasich



Prof Nelesh Govender

Association of semi-quantitative cryptococcal antigen results in plasma with subclinical cryptococcal meningitis and mortality among patients with advanced HIV disease

Blasich N, Wake R, Rukasha I, Prince Y, Govender NP

Medical Mycology

Impact Factor: 4.621

Blood cryptococcal antigen (CrAg) titers >160 are associated with concurrent subclinical cryptococcal meningitis (CM). When lumbar puncture (LP) is not immediately available in a CrAg screening program, semi-quantitative CrAg assays may provide risk stratification for CM. Two semi-quantitative assays (SQ [Immuno-Mycologics, Norman, OK, USA] and CryptoPS [Biosynex, Strasbourg, France]) were evaluated against a qualitative lateral flow assay (LFA) using 194 plasma samples from a cohort of HIV-seropositive individuals with CD4 counts <100 cells/ μ l. We compared SQ and CryptoPS results to titers for LFA-positive samples. Among patients with LP, we examined the association between semi-quantitative CrAg results and CM. We used a Cox proportional hazards model to determine the association between SQ score and mortality. Of 194 participants, 60 (31%) had positive LFA results, of whom 41 (68%) had a titer of ≤ 160 and 19 (32%) a titer >160 . Fifty individuals with antigenemia had an LP; a clinically useful SQ score that identified all ten cases of subclinical CM was ≥ 3 (100% sensitivity, 55% specificity). Patients with an SQ score of 3 or 4 also had a 2.2-fold increased adjusted hazards of 6-month mortality (95% CI: 0.79–6.34; $p = 0.13$) versus those with score of <3 . Nine of ten patients with subclinical CM had a strong-positive CryptoPS result versus 10/40 without subclinical CM ($p < 0.001$). Semi-quantitative assays offered a sensitive though not specific means of gauging the risk of concurrent CM in this patient population.



**Medical
Mycology**



Ms Tafadzwa Dhokotera

Spatiotemporal modelling and mapping of cervical cancer incidence among HIV positive women in South Africa : a nationwide study

Tafadzwa Dhokotera, Riou Julien, Bartels Lina, Rohner Eliane, Chammartin Frederique, Johnson Leigh, Singh Elvira, Olago Victor, Sengayi Muchengeti Mazvita, Egger Matthias, Bohlius Julia, and Konstantinoudis Garyfallos

International Journal of Health Geographics

Impact Factor: 3.918

Background: Disparities in invasive cervical cancer (ICC) incidence exist globally, particularly in HIV positive women who are at elevated risk compared to HIV negative women. We aimed to determine the spatial, temporal, and spatiotemporal incidence of ICC and the potential risk factors among HIV positive women in South Africa.

Methods: We included ICC cases in women diagnosed with HIV from the South African HIV cancer match study during 2004–2014. We used the Thembisa model, a mathematical model of the South African HIV epidemic to estimate women diagnosed with HIV per municipality, age group and calendar year. We fitted Bayesian hierarchical models, using a reparameterization of the Besag-York-Mollié to capture spatial autocorrelation, to estimate the spatiotemporal distribution of ICC incidence among women diagnosed with HIV. We also examined the association of deprivation, access to health (using the number of health facilities per municipality) and urbanicity with ICC incidence. We corrected our estimates to account for ICC case underascertainment, missing data and data errors.

Results: We included 17,821 ICC cases and demonstrated a decreasing trend in ICC incidence, from 306 to 312 in 2004 and from 160 to 191 in 2014 per 100,000 person-years across all municipalities and corrections. The spatial relative rate (RR) ranged from 0.27 to 4.43 in the model without any covariates. In the model adjusting for covariates, the most affluent municipalities had a RR of 3.18 (95% Credible Interval 1.82, 5.57) compared to the least affluent ones, and municipalities with better access to health care had a RR of 1.52 (1.03, 2.27) compared to municipalities with worse access to health.

Conclusions: The results show an increased incidence of cervical cancer in affluent municipalities and in those with more health facilities. This is likely driven by better access to health care in more affluent areas. More efforts should be made to ensure equitable access to health services, including mitigating physical barriers, such as transportation to health centres and strengthening of screening programmes.





Dr Maria Paximadis



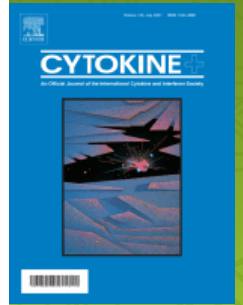
Prof Caroline Tiemessen

Interleukin-8 genetic diversity, haplotype structure and production differ in two ethnically distinct South African populations

Maria Paximadis, Anabela C.P. Picton, Dhriti Sengupta, Michele Ramsay, Adrian Puren, **Caroline T. Tiemessen**

Cytokine
Impact Factor: 3.861

A single nucleotide polymorphism (SNP), 251 bases upstream from the IL-8 transcription start ($-251A>T$, rs4073), has been extensively investigated in cancers and inflammatory and infectious diseases in predominantly European and Asian populations. We sequenced the IL-8 gene of 109 black and 32 white South African (SA) individuals and conducted detailed characterization of gene variation and haplotype structure. IL-8 production in phytohaemagglutinin (PHA)-stimulated peripheral blood mononuclear cells (PBMCs) of a subset (black: $N = 22$; white: $N = 32$) of these individuals was measured using ELISA. Select variants were genotyped for additional black individuals ($N = 141$), and data from the 1000 Genomes Project were used for haplotype analysis and comparative purposes. In white individuals, the $-251A>T$ SNP formed part of a prevalent six-variant haplotype [haplotype frequency (HF): 61%], Hap-1C, involving the following variants: $-251A>T$; $+394T>G$ (rs2227307); $+780C>T$ (rs2227306); $+1240->A$ (rs2227541); $+1635C>T$ (rs2227543) and $+2770A>T$ (rs2227543). Hap-1C ($-251T+394T+780C+1240+A+1635C+2770A$) was composed of two three-variant sub-haplotypes [Hap-1Ca: $-251T+394T+1240+A$; Hap-1Cb: $+780C+1635C+2770A$] sharing similarities with haplotypes identified in the black population. Hap-1C was found to be present in European, East and South Asian populations. Four haplotypes were identified in the black population with the two prevalent haplotypes each comprised of two variants: Hap-1B [$-251A>T$ and $+1240->A$; $-251T+1240+A$; HF: 14%] and Hap-2B [$-743T>C$ (rs2227532) and $+2452A>C$ (rs2227545); $-743C+2452C$; HF: 13%]. Populations did not differ in unstimulated PBMC IL-8 production. Upon PHA stimulation, PBMCs from white individuals produced more IL-8 ($P = 0.04$), suggesting the $-251T$ allele is responsible for higher production, however further analysis revealed that Hap-1C (and constituent sub-haplotypes), did not associate with IL-8 production. Populations did however differ in monocyte number with the white population having significantly more monocytes compared to the black population ($P = 0.025$), and furthermore monocyte number strongly correlated with IL-8 production in both population groups (black: $p = 0.0002$, $r = 0.71$; white: $P = 0.0005$, $r = 0.59$). Hap-1B, Hap-2B, and a SNP located one base pair upstream of the IL-8 ATG start codon, $+100C>T$ SNP (rs2227538), all associated with higher IL-8 production in the black population - individuals harbouring at least one of these haplotypes/variant associated with higher IL-8 production ($P = 0.003$) compared to individuals without. The black population was enriched for individuals harbouring Hap-1B and/or Hap-2B compared to the 1000 Genomes project sub-Saharan African population ($P = 0.006$), suggesting that SA black individuals may be high IL-8 producers. Given the paucity of IL-8-related studies that have been conducted in populations from sub-Saharan Africa, this study has significantly increased our understanding of this important chemokine in the South African population.





Dr Halima Said

Distribution and clonality of drug-resistant tuberculosis in South Africa

Halima Said, John Ratabane, Linda Erasmus, Yasmin Gardee, Shaheed Omar, Andries Dreyer, Farzana Ismail, Zaheda Bhyat, Tiisetso Lebaka, Minty van der Meulen, Thabisile Gwala, Adeboye Adelekan, Karidia Diallo and Nazir Ismail

BMC Microbiology
Impact Factor: 3.605

Background: Studies have shown that drug-resistant tuberculosis (DR-TB) in South Africa (SA) is clonal and is caused mostly by transmission. Identifying transmission chains is important in controlling DR-TB. This study reports on the sentinel molecular surveillance data of rifampicin-resistant (RR) TB in SA, aiming to describe the RR-TB strain population and the estimated transmission of RR-TB cases.

Method: RR-TB isolates collected between 2014 and 2018 from eight provinces were genotyped using combination of spoligotyping and 24-loci mycobacterial interspersed repetitive-units-variable-number tandem repeats (MIRU-VNTR) typing.

Results: Of the 3007 isolates genotyped, 301 clusters were identified. Cluster size ranged between 2 and 270 cases. Most of the clusters (247/301; 82.0%) were small in size (<5 cases), 12.0% (37/301) were medium sized (5–10 cases), 3.3% (10/301) were large (11–25 cases) and 2.3% (7/301) were very large with 26–270 cases. The Beijing genotype was responsible for majority of RR-TB cases in Western and Eastern Cape, while the East-African-Indian-Somalian (EAI1_SOM) genotype accounted for a third of RR-TB cases in Mpumalanga. The overall proportion of RR-TB cases estimated to be due to transmission was 42%, with the highest transmission-rate in Western Cape (64%) and the lowest in Northern Cape (9%).

Conclusion: Large clusters contribute to the burden of RR-TB in specific geographic areas such as Western Cape, Eastern Cape and Mpumalanga, highlighting the need for community-wide interventions. Most of the clusters identified in the study were small, suggesting close contact transmission events, emphasizing the importance of contact investigations and infection control as the primary interventions in SA.





Sharon Shalekoff



Prof Caroline Tiemessen

Normalization of B Cell Subsets but Not T Follicular Helper Phenotypes in Infants With Very Early Antiretroviral Treatment

Sharon Shalekoff, Shayne Loubser, Bianca Da Costa Dias, Renate Strehlau, Stephanie Shiao, Shuang Wang, Yun He, Elaine J. Abrams, Louise Kuhn and **Caroline T. Tiemessen**

Frontiers in Pediatrics
Impact Factor: 3.418

Introduction: Infant HIV-1-infection is associated with high morbidity and mortality if antiretroviral treatment (ART) is not initiated promptly. We characterized development of circulating T follicular helper cells (cTfh) and their relationship to naïve/memory B cell subsets in a cohort of neonates initiating ART within the first week of life.

Methods: Infants were diagnosed within 48 hours of birth and started ART as soon as possible. The frequency and phenotype of cTfh and B cells were analyzed at enrollment (birth –19 days) and at 4, 12, and 72 weeks of age in blood of 27 HIV-1-intrauterine-infected and 25 HIV-1 exposed uninfected (HEU) infants as part of a study in Johannesburg, South Africa. cTfh cells were divided into Tfh1, Tfh2, and Tfh17 subsets. B cell phenotypes were defined as naïve, resting memory, activated memory and tissue-like memory cells.

Results: HIV-1-infected infants had higher frequencies of cTfh cells than HEU infants up to 12 weeks of age and these cTfh cells were polarized toward the Tfh1 subset. Higher frequencies of Tfh1 and lower frequencies of Tfh2 and Tfh17 correlated with lower CD4+ T cell percentages. Lower frequencies of resting memory, with corresponding higher frequencies of activated memory B cells, were observed with HIV-1 infection. Importantly, dysregulations in B cell, but not cTfh cell, subsets were normalized by 72 weeks.

Conclusion: Very early ART initiation in HIV-1-infected infants normalizes B cell subsets but does not fully normalize perturbations in cTfh cell subsets which remain Tfh1 polarized at 72 weeks. It remains to be determined if very early ART improves vaccine antibody responses despite the cTfh and B cell perturbations observed over the time course of this study.





Ms Jackie Kleynhans

A cross-sectional study measuring contact patterns using diaries in an urban and a rural community in South Africa, 2018

Kleynhans J, Tempia S, McMorrow ML, von Gottberg A, Martinson NA, Kahn K, Moyes J, Mkhencele T, Lebina L, Gómez-Olivé FX, Wafawanaka F, Mathunjwa A, Cohen C, Buys A, Mathee A, Language B, Maake L, Treurnicht F, Mothlaoleng K, Carrim M, Wolter N, Hellferscee O, Wagner RG, Piketh S

BMC Public Health

Impact Factor: 3.295

Background: Describing contact patterns is crucial to understanding infectious disease transmission dynamics and guiding targeted transmission mitigation interventions. Data on contact patterns in Africa, especially South Africa, are limited. We measured and compared contact patterns in a rural and urban community, South Africa. We assessed participant and contact characteristics associated with differences in contact rates.

Methods: We conducted a cross-sectional study nested in a prospective household cohort study. We interviewed participants to collect information on persons in contact with for one day. We described self-reported contact rates as median number people contacted per day, assessed differences in contact rates based on participant characteristics using quantile regression, and used a Poisson model to assess differences in contact rates based on contact characteristics within age groups. We also calculated cumulative person hours in contact within age groups at different locations.

Results: We conducted 535 interviews (269 rural, 266 urban), with 17,252 contacts reported. The overall contact rate was 14 (interquartile range (IQR) 9–33) contacts per day. Those ≤ 18 years had higher contact rates at the rural site (coefficient 17, 95% confidence interval (95%CI) 10–23) compared to the urban site, for those aged 14–18 years (13, 95%CI 3–23) compared to < 7 years. No differences were observed for adults. There was a strong age-based mixing, with age groups interacting more with similar age groups, but also interaction of participants of all ages with adults. Children aged 14–18 years had the highest cumulative person hours in contact (116.3 rural and 76.4 urban).

Conclusions: Age played an important role in the number and duration of contact events, with children at the rural site having almost double the contact rate compared to the urban site. These contact rates can be utilized in mathematical models to assess transmission dynamics of infectious diseases in similar communities.





Dr Selamawit Woldesenbet

Recent HIV infection among pregnant women in the 2017 antenatal sentinel cross-sectional survey, South Africa: Assay-based incidence measurement

Woldesenbet, S, Kufa-Chakezha T, Lombard C, Manda S, Cheyip M, Ayalew K, et al.

PLOS ONE

Impact Factor: 3.24

Introduction: New HIV infection during pre-conception and pregnancy is a significant contributor of mother-to-child transmission of HIV in South Africa. This study estimated HIV incidence (defined as new infection within the last one year from the time of the survey which included both new infections occurred during pregnancy or just before pregnancy) among pregnant women and described the characteristics of recently infected pregnant women at national level.

Methods: Between 1 October and 15 November 2017, we conducted a national cross-sectional survey among pregnant women aged 15–49 years old attending antenatal care at 1,595 public facilities. Blood specimens were collected from pregnant women and tested for HIV in a centralised laboratory. Plasma viral load and limiting antigen avidity enzyme immunosorbent assay (LAg) tests were further performed on HIV positive specimens to differentiate between recent and long-term infections. Recent infection was defined as infection that occurred within one year from the date of collection of blood specimen for the survey. Data on age, age of partner, and marital status were collected through interviews. Women whose specimens were classified as recent by LAg assay and with viral loads >1,000 copies/mL were considered as recently infected. The calculated proportion of HIV positive women with recent infection was adjusted for assay-specific parameters to estimate annual incidence. Survey multinomial logistic regression was used to examine factors associated with being recently infected using HIV negative women as a reference group. Age-disparate relationship was defined as having a partner 5 or more years older.

Results: Of 10,049 HIV positive participants with LAg and viral load data, 1.4% (136) were identified as recently infected. The annual HIV incidence was 1.5% (95% confidence interval (CI): 1.2–1.7). In multivariable analyses, being single (adjusted odds ratio, aOR: 3.4, 95% CI: 1.8–6.2) or cohabiting (aOR: 3.8, 95% CI: 1.8–7.7), compared to being married as well as being in an age-disparate relationship among young women (aOR: 3.1, 95% CI: 2.0–4.7; reference group: young women (15–24years) whose partners were not 5 years or more older) were associated with higher odds of recent infection.

Conclusions: Compared to previous studies among pregnant women, the incidence estimated in this study was substantially lower. However, the UNAIDS target to reduce incidence by 75% by 2020 (which is equivalent to reducing incidence to <1%) has not been met. The implementation of HIV prevention and treatment interventions should be intensified, targeting young women engaged in age-disparate relationship and unmarried women to fast track progress towards the UNAIDS target.



Ms Pinky Manana



Dr Givemore Munhenga

“Maskandi experience”: exploring the use of a cultural song for community engagement in preparation for a pilot Sterile Insect Technique release programme for malaria vector control in KwaZulu-Natal Province, South Africa 2019

Pinky N. Manana, Sara Jewett, Jabulani Zikhali, Dumisani Dlamini, Nondumiso Mabaso, Zothile Mlambo, Roxanne Ngobese and **Givemore Munhenga**

Malaria Journal

Impact Factor: 2.979

Background: An assessment of the Sterile Insect Technique (SIT) as a complementary malaria vector control tool, is at an advanced stage in South Africa. The technique involves the release of laboratory-reared sterilized male mosquitoes of the major malaria vector *Anopheles arabiensis*, raising social, ethical and regulatory concerns. Therefore, its implementation largely depends on community participation and acceptance. Against this background, it is critical that robust and effective community strategies are developed. This study describes the development of a cultural song to engage the community and increase awareness on SIT and malaria control in KwaZulu-Natal, South Africa.

Methods: An exploratory concurrent mixed-methods study was conducted to get opinions about the effectiveness of a cultural song developed to engage communities and increase acceptability of the SIT technology. Two self-administered surveys (expert and community) were conducted. Additionally, more in depth opinions of the song and its effectiveness in conveying the intended information were investigated through three community dialogue sessions with community members in the study area.

Results: A total of 40 experts and 54 community members participated in the survey. Four themes were identified in relation to the appropriateness and effectiveness of the song, with a fifth theme focused on recommendations for adaptations. Overall, the song was well received with the audience finding it entertaining and informative. Responses to unstructured questions posed after the song showed an increase in the knowledge on malaria transmission and SIT technology. In particular, the explanation that male mosquitoes do not bite allayed anxiety and fears about the SIT technology.

Conclusion: The song was deemed both culturally appropriate and informative in engaging community members about the SIT technology. It proved useful in promoting health messages and conveying SIT technology as a complementary malaria vector control tool. With minor adaptations, the song has potential as an area-wide community engagement tool in areas targeted for sterile male releases.



BMC



Bianca E Silva



Dr Yael Dahan-Moss

Microbiota identified from preserved *Anopheles*

Bianca E. Silva, Zvifadzo Matsena Zingoni, Lizette L. Koekemoer, and **Yael L. Dahan-Moss**

Malaria Journal
Impact Factor: 2.979

Background: Mosquito species from the *Anopheles gambiae* complex and the *Anopheles funestus* group are dominant African malaria vectors. Mosquito microbiota play vital roles in physiology and vector competence. Recent research has focused on investigating the mosquito microbiota, especially in wild populations. Wild mosquitoes are preserved and transported to a laboratory for analyses. Thus far, microbial characterization post-preservation has been investigated in only *Aedes vexans* and *Culex pipiens*. Investigating the efficacy of cost-effective preservatives has also been limited to AllProtect reagent, ethanol and nucleic acid preservation buffer. This study characterized the microbiota of African *Anopheles* vectors: *Anopheles arabiensis* (member of the *An. gambiae* complex) and *An. funestus* (member of the *An. funestus* group), preserved on silica desiccant and RNAlater® solution.

Methods: Microbial composition and diversity were characterized using culture-dependent (midgut dissections, culturomics, MALDI-TOF MS) and culture-independent techniques (abdominal dissections, DNA extraction, next-generation sequencing) from laboratory (colonized) and field-collected mosquitoes. Colonized mosquitoes were either fresh (non-preserved) or preserved for 4 and 12 weeks on silica or in RNAlater®. Microbiota were also characterized from field-collected *An. arabiensis* preserved on silica for 8, 12 and 16 weeks.

Results: *Elizabethkingia anophelis* and *Serratia oryzae* were common between both vector species, while *Enterobacter cloacae* and *Staphylococcus epidermidis* were specific to females and males, respectively. Microbial diversity was not influenced by sex, condition (fresh or preserved), preservative, or preservation time-period; however, the type of bacterial identification technique affected all microbial diversity indices.

Conclusions: This study broadly characterized the microbiota of *An. arabiensis* and *An. funestus*. Silica- and RNAlater®-preservation were appropriate when paired with culture-dependent and culture-independent techniques, respectively. These results broaden the selection of cost-effective methods available for handling vector samples for downstream microbial analyses.





Dr Shayne Loubser



Prof Caroline Tiemessen

Lack of association of KIR2DL1-R²⁴⁵ and KIR2DL1-C²⁴⁵ with HIV-1 control in black South Africans with HLA-C2

Shayne Loubser, Bianca Da Costa Dias, Sharon Shalekoff, Nikki L. Gentle, **Caroline T. Tiemessen**

Human Immunology
Impact Factor: 2.850

Activating/inhibitory killer-cell immunoglobulin-like receptors (KIRs) partly regulate natural killer (NK) cells. KIR2DL1 allotypes with cysteine at position-245 (KIR2DL1-C²⁴⁵) express at lower levels and demonstrate weaker inhibitory signaling compared to allotypes with arginine at position-245 (KIR2DL1-R²⁴⁵). The functional consequence of either allotype in infectious diseases is unknown. Since NK cells mediate antiviral immunity, we investigated KIR2DL1-R²⁴⁵ and KIR2DL1-C²⁴⁵ in association with HIV-1 virological control in untreated immunocompetent black South Africans. Allotype carriage, determined by KIR2DL1 sequencing, was similar between uninfected South Africans (n = 104) and other black African populations, but differed significantly from Europeans, while no significant differences were noted between uninfected and HIV-1-infected individuals (n = 52). KIR2DL1 expression, measured by flow cytometry, in uninfected individuals showed higher KIR2DL1-R²⁴⁵ expression compared to KIR2DL1-C²⁴⁵ in white donors (n = 27), while black donors (n = 21) generally expressed lower levels of both allotypes. KIR2DL1 expression was reduced in HLA-C2 carriers, most evident in black HLA-C2/C2 donors. KIR2DL1-R²⁴⁵ and KIR2DL1-C²⁴⁵ did not associate with viral load when HLA-C2 ligands were present, however in HLA-C1 homozygotes, individuals with only KIR2DL1-R²⁴⁵, showed lower viral loads compared to carriers of both allotypes. The lack of association of KIR2DL1-R²⁴⁵ or KIR2DL1-C²⁴⁵ with HIV-1 control in HLA-C2 carriers may relate to lower KIR2DL1 expression levels in a population with high HLA-C2 prevalence.





Prof Maureen Coetzee

New distribution record of *Anopheles rivulorum*-like from Sadiola, Mali, with notes on malaria vector insecticide resistance

Sue-Ellen Wragge, Nelius Venter, Dramane Toure, Richard H. Hunt, and **Maureen Coetzee**

Transactions of the Royal Society of Tropical Medicine and Hygiene

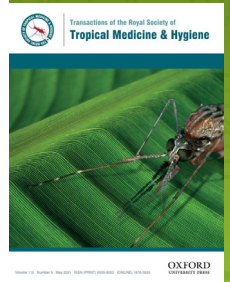
Impact Factor: 2.184

Background: The SEMOS gold mine in Sadiola, southwestern Mali, has been implementing a malaria vector control programme for 15 y using indoor residual house spraying and sporadic larval control. Periodic screening of the vector populations have been carried out over the years to provide information to the control programme, mainly on vector species present and their insecticide resistance status. The data from five entomological surveys, carried out in 2006, 2011, 2014, 2016 and 2018, are presented.

Methods: Adult mosquitoes were collected resting on walls inside houses and on verandas. Insecticide susceptibility assays were carried out and mosquitoes subsequently identified by species using molecular assays.

Results: The major malaria vector mosquitoes, *Anopheles gambiae* and *Anopheles arabiensis* were abundant at each sampling period with *Anopheles coluzzii* and *Anopheles funestus* being rare or absent. *Anopheles rivulorum* was identified in 2006 and *Anopheles lesoni* in 2016. The presence of *Anopheles rivulorum*-like, identified for the first time in 2018, was not screened for in previous surveys. Insecticide susceptibility bioassays showed resistance in both *A. gambiae* and *A. arabiensis* to pyrethroids, carbamates and dichlorodiphenyltrichloroethane over the 12 y.

Conclusions: This is the first record of *A. rivulorum*-like west of Côte d'Ivoire. Resistance levels to the three classes of insecticides were variable but appeared to decrease after pyrethroids were discontinued for house spraying.



OXFORD
UNIVERSITY PRESS



Dr Simone Richardson



Prof Penny Moore

Targeting Fc effector function in vaccine design

Richardson SI, Moore PL

Expert Opinion on Therapeutic Targets

Impact Factor: 0.96

Introduction: Antibodies mediate pathogen neutralization in addition to several cytotoxic Fc functions through engaging cellular receptors and recruiting effector cells. Fc effector functions have been well described in disease control and protection against infectious diseases including HIV, Ebola, malaria, influenza and tuberculosis, making them attractive targets for vaccine design.

Areas Covered: We briefly summarize the role of Fc effector functions in disease control and protection in viral, bacterial and parasitic infectious diseases. We review Fc effector function in passive immunization and vaccination, and primarily focus on strategies to elicit and modulate these functions as part of a robust vaccine strategy.

Expert Opinion: Despite their known correlation with vaccine efficacy for several diseases, only recently have seminal studies addressed how these Fc effector functions can be elicited and modulated in vaccination. However, gaps remain in assay standardization and the precise mechanisms of diverse functional assays. Furthermore, there are inherent difficulties in the translation of findings from animal models to humans, given the difference in sequence, expression and function of Fc receptors and Fc portions of antibodies. However, overall it is clear that vaccine development to elicit Fc effector function is an important goal for optimal prevention against infectious disease.





Ms Faith Moyo



Prof Gayle Sherman

Maternal HIV viral load testing during pregnancy and postpartum care in Gauteng Province, South Africa

F Moyo, A H Mazanderani, T Kufa, G G Sherman

South African Medical Journal
Impact Factor: 0.566

Background: Pregnant and breastfeeding women living with HIV (WLHIV) are a target population for elimination of mother-to-child transmission of HIV (eMTCT). However, there are limited data on maternal virological responses during pregnancy and the postpartum period in South Africa (SA).

Objectives: To review compliance of viral load (VL) testing with national guidelines and suppression rates during pregnancy and up to 9 months postpartum among WLHIV delivering in four tertiary hospitals in Gauteng Province, SA.

Methods: All women who had a point-of-care HIV VL test using Xpert HIV-1 VL (Cepheid, USA) at delivery in four tertiary obstetric units in Gauteng between June 2018 and February 2020 were included. HIV VL tests of eligible women performed up to 9 months before and after delivery were extracted from the National Health Laboratory Service's Corporate Data Warehouse. Proportions of women delivering who had antenatal and postpartum VL tests performed and their suppression rates were determined and expressed as percentages.

Results: Of 4 989 eligible WLHIV (median age 31.1 years), 917 (18.4%) had a VL performed during the antenatal period; of these, 335 (36.5%) had a VL ≥ 50 copies/mL and 165 (18.0%) a VL $\geq 1\ 000$ copies/mL. At delivery, 1 911 women (38.3%) had a VL ≥ 50 copies/mL and 1 028 (20.6%) a VL $\geq 1\ 000$ copies/mL. Among 627 women (12.6%) with a VL test postpartum, 234 (37.3%) had a VL ≥ 50 copies/mL and 93 (14.8%) a VL $\geq 1\ 000$ copies/mL. Overall, having a VL test performed during the antenatal period was associated with viral suppression at delivery and receiving a VL test postpartum ($p < 0.001$). Women with a VL ≥ 50 copies/mL at delivery were more likely to be younger and to remain virally unsuppressed postpartum ($p < 0.001$) compared with women with a VL < 50 copies/mL.

Conclusions: Fewer than 5% of WLHIV with a VL at the time of delivery received VL monitoring during the antenatal and postpartum periods in accordance with national guidelines. More than 80% of WLHIV delivering had no evidence of VL monitoring during the antenatal period, and they were more likely than women who received monitoring during the antenatal period to be virally unsuppressed at delivery and to receive no VL monitoring postpartum. Women with a high VL at delivery were likely to remain virally unsuppressed postpartum. These results emphasise the need for closer monitoring of and rapid reaction to high maternal VLs during pregnancy, at delivery and postpartum for attainment of eMTCT.





Dr Waasila Jassat

A call to action: Temporal trends of COVID-19 deaths in South African Muslims

Waasila Jassat, Zameer Brey, Muhammad Wadee, Shoyab Wadee, Shabir A Madhi

South African Medical Journal

Impact Factor: 0.566



Compared to whites, South Africans identified of Indian ancestry have a 35% increased risk of dying of COVID-19 when hospitalised, whilst black-Africans and “coloured” race have a 23-24% higher risk of death following COVID-19 hospitalization. Compared with all other race groups, South Africans of Indian ancestry have an 11% increased risk of death following COVID-19 hospitalization.

During the third epidemic wave of COVID-19 in SA, the highest number of new cases of COVID-19 were reported in Gauteng. Statistics gathered by Muslim community organisations across the country report daily numbers of known COVID-19 deaths to a co-ordinating group known as Muslim Stats. By 10 June 2021, 2,747 COVID-19 deaths were recorded in the Muslim community which constitutes 4.8% recorded COVID-19 deaths nationally. The Muslim community represent approximately 1.9% of South Africa’s 59.6 million population.

In Gauteng, comparing Muslim deaths, weekly hospital deaths reported to DATCOV and excess natural deaths reported by the MRC, a sharp and steeply rising increase in deaths was evident among Muslims in early May 2021. The weekly number of deaths in the Gauteng Muslim communities surpassed the peak weekly deaths reported in the community during the first and second waves.

These findings provide circumstantial evidence that gatherings at the end of Ramadaan and Eid-ul-Fitr (April to May 2021) likely led to super-spreader events among Muslims in Gauteng, that has resulted in a large number of avoidable deaths. The SARS-CoV-2 Delta variant, may have contributed to the early outbreak in this community, as the variant is approximately 60% more transmissible and likely more virulent than ancestry SARS-CoV-2.

It is important that adequate mitigation strategies be adopted nationally, including in the Muslim and other religious communities, to avoid further preventable COVID-19 deaths. Public health and social measures to limit transmission such as mask wearing, physical distancing and hand sanitising are important. Notably, super-spreader events are directly or indirectly responsible for greater than 80% of SARS-CoV-2 infection. Such super-spreader events can occur due to gatherings of even a few people in poorly ventilated indoor spaces, particularly in the absence of wearing face masks (including when socialising). Most importantly, those who are at most risk, people over 60 years, are advised to seize the opportunity to be vaccinated.



Dr Shune Oliver

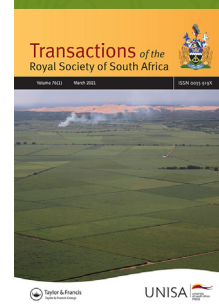
The effect of larval cigarette exposure on the life history of the major malaria vector *Anopheles arabiensis*

Shune V. Oliver

Transactions of the Royal Society of South Africa

Impact Factor: 0.049

Anopheles arabiensis typically breeds in clean, temporary bodies of water. This species, however, is adapting to breeding in polluted water. This has the effect of pollutants being non-insecticidal forms of selection pressure driving insecticide resistance. Cigarette butts are common plastic pollutants which are complex toxicants that would include nicotine pollutants. This is of concern as the neonicotinoid clothianidin is suggested as a potential vector control insecticide. As such, there is a risk that larval exposure to cigarette pollution could alter the efficacy of this insecticide. This study aimed to examine the effect of larval cigarette exposure on the life history of laboratory-reared *An. arabiensis*, as well as elucidate the role of nicotine in these effects. Two laboratory strains of *An. arabiensis* were used, the insecticide susceptible SENN and the resistant SENN-DDT strain. The effects of cigarette and nicotine exposure on key life history traits were assessed. SENN-DDT laid more eggs in cigarette-polluted water than SENN but developed significantly slower in polluted water. Larval cigarette selection increased adult longevity in SENN-DDT, but reduced longevity in SENN. Larval selection did not alter neonicotinoid tolerance in males of either strain, or female SENN. Nicotine selection increased tolerance to both neonicotinoids, but cigarette selection only increased clothianidin tolerance in SENN-DDT females. Insecticide resistant *An. arabiensis* therefore had an advantage in cigarette polluted environments. Selection for cigarette tolerance only increased neonicotinoid tolerance where insecticide resistance was already present. Therefore, larval cigarette exposure may only have a limited effect on neonicotinoid efficacy for malaria control.





Dr Blaženka Letinić



Prof Lizette Koekemoer

Additional evidence on the efficacy of different Akirin vaccines assessed on *Anopheles arabiensis*

Blaženka D. Letinic, Marinela Contreras, Yael Dahan-Moss, Ingrid Linnekugel, Jose de la Fuente and **Lizette L. Koekemoer**

Parasites and Vectors

Impact Factor: n/a

Background: *Anopheles arabiensis* is an opportunistic malaria vector that rests and feeds outdoors, circumventing current indoor vector control methods. Furthermore, this vector will readily feed on both animals and humans. Targeting this vector while feeding on animals can provide an additional intervention for the current vector control activities. Previous results have displayed the efficacy of using Subolesin/Akirin ortholog vaccines for the control of multiple ectoparasite infestations. This made Akirin a potential antigen for vaccine development against *An. arabiensis*.

Methods: The efficacy of three antigens, namely recombinant Akirin from *An. arabiensis*, recombinant Akirin from *Aedes albopictus*, and recombinant Q38 (Akirin/Subolesin chimera) were evaluated as novel interventions for *An. arabiensis* vector control. Immunisation trials were conducted based on the concept that mosquitoes feeding on vaccinated balb/c mice would ingest antibodies specific to the target antigen. The antibodies would interact with the target antigen in the arthropod vector, subsequently disrupting its function.

Results: All three antigens successfully reduced *An. arabiensis* survival and reproductive capacities, with a vaccine efficacy of 68–73%.

Conclusions: These results were the first to show that hosts vaccinated with recombinant Akirin vaccines could develop a protective response against this outdoor malaria transmission vector, thus providing a step towards the development of a novel intervention for *An. arabiensis* vector control.



Editorial and production team:

Sinenhlanhla Jimoh
Thapelo Marutla
Carina Kriel
Prof John Freaan
Nileen Gale

**Thank you for your contributions!
Kindly continue to send your
contributions to:**

NileenG@nicd.ac.za



**NATIONAL INSTITUTE FOR
COMMUNICABLE DISEASES**

Division of the National Health Laboratory Service