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Division of the National Health Laboratory Service

SCIENCE FOCUS

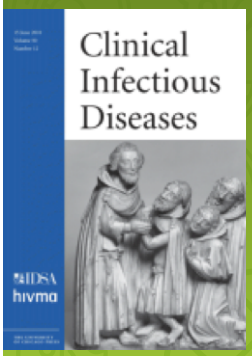
Science Focus acknowledges NICD members of staff who have published in peer-reviewed journals. The Science Focus is a compilation of scientific publications included in the quarterly reports submitted to the National Department of Health. It includes only publications where an NICD staff member is either the first or last author.

Prof Cheryl Cohen

The role of human immunodeficiency virus in influenza- and respiratory syncytial virus-associated hospitalisations in South African children, 2011-2016

McMorrow ML, Tempia S, Walaza S, Treurnicht FK, Moyes J, Cohen AL, Pretorius M, Hellferscee O, Wolter N, von Gottberg A, Nguweneza A4, McAnerney JM4, Naby F, Mekgoe O, Venter M, Madhi SA, ***Cohen C.***

Clinical Infectious Diseases
Impact Factor: 9.117



Background: Data describing influenza- or respiratory syncytial virus (RSV)-associated hospitalised illness in children aged <5 years in Africa are limited.

Methods: During 2011-2016, we conducted surveillance for severe respiratory illness (SRI) in children aged <5 years in 3 South African hospitals. Nasopharyngeal aspirates were tested for influenza and RSV using real-time reverse transcription polymerase chain reaction. We estimated rates of influenza- and RSV-associated hospitalised SRI by human immunodeficiency virus (HIV) status and compared children who tested positive for influenza vs. RSV using multivariable penalised logistic regression.

Results: Among 3650 hospitalised children, 203 (5.6%) tested positive for influenza viruses, 874 (23.9%) for RSV, and 19 (0.5%) for both. The median age of children hospitalised with influenza was 13.9 months vs. 4.4 months for RSV ($P < .01$). Annual influenza-associated hospitalisation rates per 100000 were highest among infants aged 6-11 months (545; 95% confidence interval [CI], 409-703), while RSV-associated hospitalisation rates were highest in infants aged 0-2 months (6593; 95% CI, 5947-7217). HIV exposure was associated with increased incidence of influenza- and RSV-associated hospitalisation in infants aged 0-5 months, with relative risk (RR) 2.2 (95% CI, 1.4-3.4) and 1.4 (95% CI, 1.3-1.6), respectively. HIV infection was associated with increased incidence of influenza- and RSV-associated hospitalisation in all age groups; RR 2.7 (95% CI, 2.0-3.5) and 3.8 (95% CI, 3.1-4.8), respectively.

Conclusions: Influenza- and RSV-associated hospitalisations are common among South African infants. HIV infection and HIV exposure in infants increase risk of influenza- and RSV-associated hospitalisation.

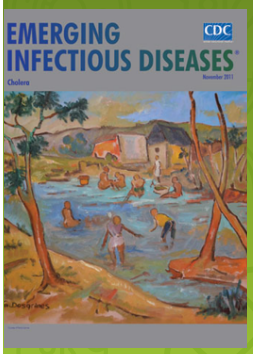
Dr Petrus Jansen van Vuren

Prof Janusz Paweska

Rift Valley fever reemergence after 7 years of quiescence, South Africa, May 2018

Jansen van Vuren P, *Kgaladi J, Msimang V,* ***Paweska JT.***

Emerging Infectious Diseases
Impact Factor: 7.422



Phylogenetic analysis of Rift Valley fever virus partial genomic sequences from a patient infected in South Africa in May 2018 suggests re-emergence of an endemic lineage different from that of the epidemic in South Africa during 2010–2011. Surveillance during interepidemic periods should be intensified to better predict future epidemics.

Dr Batsirai Mabvakure

Prof Penny Moore

Positive selection at key residues in the HIV envelope distinguishes broad and strain-specific plasma neutralising antibodies

Mabvakure BM, *Scheepers C, Garrett N, Abdool Karim S, Williamson C, Morris L,* ***Moore PL.***

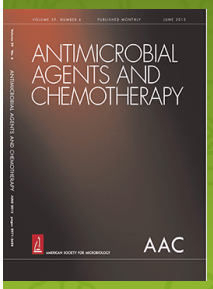
Journal of Virology
Impact Factor: 4.368

The development of HIV broadly neutralising antibodies (bNAbs) has previously been shown to be associated with viral evolution and high levels of genetic diversity in the HIV envelope (Env) glycoprotein. However, few studies have examined Env evolution in those who fail to develop neutralisation breadth in order to assess whether bNAbs result from distinct evolutionary pathways. We compared Env evolution in eight HIV-1-infected participants who developed bNAbs to six donors with similar viral loads who did not develop bNAbs over three years of infection. We focused on Env V1V2 and C3V4, as these are major targets for both strain-specific neutralising antibodies (nAbs) and bNAbs. Overall, evolutionary rates (ranging from 9.92×10-3 to 4.1×10-2 substitutions/site/year) and viral diversity (from 1.1% to 6.5%) across Env, and within targeted epitopes, did not distinguish bNAb donors from non-bNAb donors. However, bNAb participants had more positively selected residues within epitopes than those without bNAbs, and several of these were common among bNAb donors. A comparison of the kinetics of strain-specific nAbs and bNAbs indicated that selection pressure at these residues increased with the onset of breadth. These data suggest that highly targeted viral evolution rather than overall envelope diversity is associated with neutralisation breadth. The association of shared positively selected sites with the onset of breadth highlights the importance of diversity at specific positions in these epitopes for bNAb development, with implications for the development of sequential and cocktail immunisation strategies.

Importance: Millions of people are still being infected with HIV decades after the first recognition of the virus. Currently, no vaccine is able to elicit bNAbs that will prevent infection by global HIV strains. Several studies have implicated HIV Env diversity in the development of breadth. However, Env evolution in individuals who fail to develop breadth despite mounting potent strain-specific neutralising responses has not been well defined. Using longitudinal neutralisation, epitope mapping, and sequence data from 14 participants, we found that overall measures of viral diversity were similar in all donors. However, the number of positively selected sites within Env epitopes was higher in bNAb participants than in strain-specific donors. We further identified common sites that were positively selected as bNAbs developed. These data indicate that while viral diversity is required for breadth, this should be highly targeted to specific residues to shape the elicitation of bNAbs by vaccination.

Dr Shaheed Valley Omar

Clofazimine exposure in vitro selects efflux pump mutants and bedaquiline resistance



Ismail N, Peters RPH, Ismail NA, ***Omar SV.***

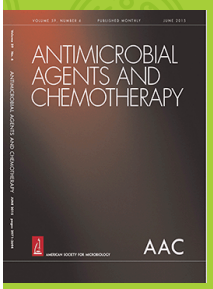
Antimicrobial Agents and Chemotherapy
Impact Factor: 4.257

Six in vitro clofazimine-resistant spontaneous mutants obtained from a wild-type or pyrazinamide-resistant ATCC reference strain were selected to evaluate bedaquiline cross-resistance. The reverse was conducted for bedaquiline mutants. All clofazimine mutants harboring an rv0678 mutation displayed phenotypic cross-resistance. We observed the same for rv0678 bedaquiline mutants; however, atpE bedaquiline mutants showed no phenotypic cross-resistance. This confirms that upfront clofazimine usage may impact subsequent bedaquiline use due to a shared efflux resistance pathway.

Dr Shaheed Valley Omar

Prof Nazir Ismail

Whole genome sequencing for drug resistance determination in *Mycobacterium tuberculosis*



Omar SV, *Joseph L, Said HM, Ismail F, Ismail N, Gwala TL,* ***Ismail NA.***

Antimicrobial Agents and Chemotherapy
Impact Factor: 4.256

Whole-genome sequencing allows rapid detection of drug-resistant *Mycobacterium tuberculosis* isolates. However, the availability of high-quality data linking quantitative phenotypic drug susceptibility testing (DST) and genomic data have thus far been limited. We determined drug resistance profiles of 176 genetically diverse clinical *M. tuberculosis* isolates from the Democratic Republic of the Congo, Ivory Coast, Peru, Thailand, and Switzerland by quantitative phenotypic DST for 11 antituberculous drugs using the BD Bactec MGIT 960 system and 7H10 agar dilution to generate a cross-validated phenotypic DST readout. We compared DST results with predicted drug resistance profiles inferred by whole-genome sequencing. Classification of strains by the two phenotypic DST methods into resistotype/wild-type populations was concordant in 73 to 99% of cases, depending on the drug. Our data suggest that the established critical concentration (5 mg/liter) for ethambutol resistance (MGIT 960 system) is too high and misclassifies strains as susceptible, unlike 7H10 agar dilution. Increased minimal inhibitory concentrations were explained by mutations identified by whole-genome sequencing. Using whole-genome sequences, we were able to predict quantitative drug resistance levels for the majority of drug resistance mutations. Predicting quantitative levels of drug resistance by whole-genome sequencing was partially limited due to incompletely understood drug resistance mechanisms. The overall sensitivity and specificity of whole-genome-based DST were 86.8% and 94.5%, respectively. Despite some limitations, whole-genome sequencing has the potential to infer resistance profiles without the need for time-consuming phenotypic methods.

Dr Petrus Jansen van Vuren

Prof Janusz Paweska

Phylodynamic analysis of Ebola virus disease transmission in Sierra Leone

Jansen van Vuren P, *Ladner J, Grobbelaar A, Wiley M, Lovett S, Allam M, Ismail A, Le Roux C, Weyer J, Moolla N, Storm N, Kgaladi J, Sanchez-Lockhart M, Conteh O, Palacios G,* ***Paweska JT.***

Viruses
Impact Factor: 3.761

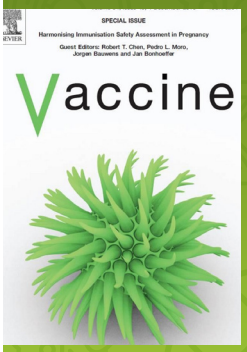
We generated genome sequences from 218 cases of Ebola virus disease (EVD) in Sierra Leone (SLE) during 2014–2015 to complement available datasets, particularly by including cases from a period of low sequence coverage during peak transmission of Ebola virus (EBOV) in the highly-affected Western Area division of SLE. The combined dataset was utilised to produce phylogenetic and phylodynamic inferences, to study sink–source dynamics and virus dispersal from highly-populated transmission hotspots. We identified four districts in SLE where EBOV was introduced and transmission occurred without onward exportation to other districts. We also identified six districts that substantially contributed to the dispersal of the virus and prolonged the EVD outbreak: five of these served as major hubs, with lots of movement in and out, and one acted primarily as a source, exporting the virus to other areas of the country. Positive correlations between case numbers, inter-district transition events, and district population sizes reaffirm that population size was a driver of EBOV transmission dynamics in SLE. The data presented here confirm the role of urban hubs in virus dispersal and of a delayed laboratory response in the expansion and perpetuation of the EVD outbreak in SLE.

Prof Cheryl Cohen

Prioritisation of risk groups for influenza vaccination in resource limited settings - a case study from South Africa

McMorrow ML, Tempia S, Walaza S, Treurnicht FK, Ramkrishna W, Azziz-Baumgartner E, Madhi SA, ***Cohen C.***

Vaccine
Impact Factor: 3.286



Background: Due to competing health priorities, low- and middle-income countries (LMIC) may need to prioritise between different influenza vaccine risk groups. Risk group prioritisation may differ in LMIC based upon programmatic feasibility, country-specific prevalence of risk conditions and influenza-associated morbidity and mortality.

Methods: In South Africa, we collected local disease burden data (both published and unpublished) and published vaccine efficacy data in risk groups and healthy adults. We used these data to aid policy makers with risk group prioritisation for influenza vaccination. We used the following formula to assess potential vaccine averted disease in each risk group: rate of influenza-associated hospitalisation (or death) per 100000 population * influenza vaccine efficacy (VE). We further estimated the cost per hospital day averted and the cost per year of life saved by influenza vaccination.

Results: Pregnant women, HIV-infected adults, and adults and children with tuberculosis disease had among the highest estimates of hospitalisations averted per 100 000 vaccinated and adults aged 65 years and older had the highest estimated deaths averted per 100000 vaccinated. However, when assessing both the cost per hospital day averted (range: USD148-1344) and the cost per year of life saved (range: USD112-1230); adults and children with TB disease, HIV-infected adults and pregnant women had the lowest cost per outcome averted.

Discussion: An assessment of the potential disease outcomes averted and associated costs may aid policymakers in risk group prioritisation for influenza vaccination.

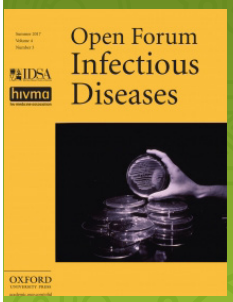
Dr Sibongile Walaza

Prof Cheryl Cohen

The impact of influenza and tuberculosis interaction on mortality among individuals aged ≥15 years hospitalised with severe respiratory illness in South Africa, 2010-2016

Walaza S, *Tempia S, Dawood H, Variava E, Wolter N, Dreyer A, Moyes J, Von Mollendorf C, McMorrow M, Von Gottberg A, Haffejee S5, Venter M, Treurnicht FK, Hellferscee O, Martinson NA, Ismail N,* ***Cohen C.***

Open Forum Infectious Diseases
Impact Factor: 3.240



Background: Data on the prevalence and impact of influenza-tuberculosis coinfection on clinical outcomes from high-HIV and -tuberculosis burden settings are limited. We explored the impact of influenza and tuberculosis coinfection on mortality among hospitalised adults with lower respiratory tract infection (LRTI).

Methods: We enrolled patients aged ≥15 years admitted with physician-diagnosed LRTI or suspected tuberculosis at 2 hospitals in South Africa from 2010 to 2016. Combined nasopharyngeal and oropharyngeal swabs were tested for influenza and 8 other respiratory viruses. Tuberculosis testing of sputum included smear microscopy, culture, and/or Xpert MTB/Rif.

Results: Among 6228 enrolled individuals, 4253 (68%) were tested for both influenza and tuberculosis. Of these, the detection rate was 6% (239/4253) for influenza, 26% (1092/4 253) for tuberculosis, and 77% (3113/4 053) for HIV. One percent (42/4 253) tested positive for both influenza and tuberculosis. On multivariable analysis, among tuberculosis-positive patients, factors independently associated with death were age group ≥65 years compared with 15-24 years (adjusted odds ratio [aOR], 3.6; 95% confidence interval [CI], 1.2-11.0) and influenza coinfection (aOR, 2.3; 95% CI, 1.02-5.2). Among influenza-positive patients, laboratory-confirmed tuberculosis was associated with an increased risk of death (aOR, 4.5; 95% CI, 1.5-13.3). Coinfection with other respiratory viruses was not associated with increased mortality in patients positive for tuberculosis (OR, 0.7; 95% CI, 0.4-1.1) or influenza (OR, 1.6; 95% CI, 0.4-5.6).

Conclusions: Tuberculosis coinfection is associated with increased mortality in individuals with influenza, and influenza coinfection is associated with increased mortality in individuals with tuberculosis. These data may inform prioritisation of influenza vaccines or antivirals for tuberculosis patients and inform tuberculosis testing guidelines for patients with influenza.

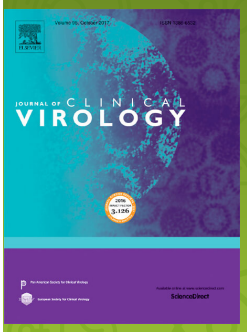
Dr Ahmad Mazanderani

Prof Gayle Sherman

Early infant diagnosis HIV-1 PCR cycle-threshold predicts infant viral load at birth

Mazanderani AH, *Kufa T, Technau KG, Strehlau R, Patel F, Shiau S, Burke M, Kuhn L, Abrams EJ,* ***Sherman GG.***

Journal of Clinical Virology
Impact Factor: 3.101



Background: HIV-1 viral load (VL) has been found to be an independent predictor for disease progression among untreated HIV-infected children. However, qualitative polymerase chain reaction (PCR) assays are routinely used for early infant diagnosis (EID).

Objectives: To predict HIV-1 VL at birth using qualitative EID real-time PCR cycle-threshold (Ct) values.

Study Design: This study was a secondary analysis of results from a cohort of intrauterine HIV-1 infected neonates. Neonates were enrolled at Rahima Moosa Mother & Child Hospital in Johannesburg, South Africa between June 2014 and November 2017. Laboratory EID HIV-1 PCR testing was performed at birth using COBAS AmpliPrep/COBAS TaqMan HIV-1 Qualitative Test v2.0 (EID CAP/CTM). Some infants had simultaneous EID point-of-care (POC) testing using Xpert HIV-1 Qualitative assay (EID Xpert). Neonates with a confirmed HIV-1 detected EID result and plasma HIV-1 RNA VL test were included in this analysis. Bland-Altman analysis was used to determine extent of agreement between Ct values of both EID assays. Multivariable linear regression models adjusting for time between EID and VL testing were used to describe the association between EID Ct values and VL and to predict VL at given EID Ct values.

Results: Among 107 HIV-1 infected neonates included in the study, 59 had POC EID testing. Median VL was 28400 copies per millilitre (cps/ml) (IQR: 1918-218 358) - two neonates had VL < 100 cps/ml prior to antiretroviral therapy initiation. There was good correlation between Ct values of both EID assays (Spearman correlation coefficient 0.9, 95% CI: 0.8-1.0). The limits of agreement between EID CAP/CTM and Xpert Ct values were 4-11 cycles. For every one cycle increase in Ct value there was 0.3 log10 RNA decrease (95% CI: -0.3 to -0.2) for both EID assays. An EID CAP/CTM Ct value ≤ 23 and an EID Xpert Ct value ≤ 31 predicted a VL of > 5.0 log10 cps/ml in 82.2% (95% CI: 73.9-88.3) and 84.7% (95% CI: 73.7-91.8) of cases, respectively.

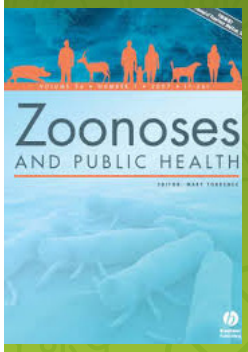
Conclusion: EID Ct values at birth predict VL and accurately identify infants with VL > 5.0 log10 cps/ml.

Prof Lucille Blumberg

Risk factors for bacterial zoonotic pathogens in acutely febrile patients in Mpumalanga Province, South Africa

Berrian AM, Martínez-López B, Quan V, Conrad PA, van Rooyen J, Simpson GJG, Frean J, Weyer J, Rossouw J, Knobel D, ***Blumberg L.***

Zoonoses Public Health
Impact Factor: 2.688



Endemic zoonoses, such as Q fever and spotted fever group (SFG) rickettsiosis, are prevalent in South Africa, yet often undiagnosed. In this study, we reviewed the demographics and animal exposure history of patients presenting with acute febrile illness to community health clinics in Mpumalanga Province to identify trends and risk factors associated with exposure to *Coxiella burnetii*, the causative agent of Q fever, and infection by SFG *Rickettsia* spp. Clinical and serological data and questionnaires elucidating exposure to animals and their products were obtained from 141 acutely febrile patients between 2012 and 2016. Exposure or infection status to *C. burnetii* and SFG *Rickettsia* spp. was determined by presence of IgG or IgM antibodies. Logistic regression models were built for risk factor analysis. Clinical presentation of patients infected by SFG rickettsiosis was described. There were 37/139 (27%) patients with a positive *C. burnetii* serology, indicative of Q fever exposure. Patients who had reported attending cattle inspection facilities ("dip tanks") were 9.39 times more likely to be exposed to Q fever (95% CI: 2.9–30.4). Exposure risk also increased with age (OR: 1.03, 95% CI: 1.002–1.06). Twenty-one per cent of febrile patients (24/118) had evidence of acute infection by SFG *Rickettsia* spp. Similarly, attending cattle inspection facilities was the most significant risk factor (OR: 8.48, 95% CI: 1.58–45.60). Seropositivity of females showed a significant OR of 8.0 when compared to males (95% CI: 1.49–43.0), and consumption of livestock was associated with a decreased risk (OR: 0.02, 95% CI: 0.001–0.54). A trend between domestic cat contact and SFG rickettsiosis was also noted, albeit borderline non-significant. In this endemic region of South Africa, an understanding of risk factors for zoonotic pathogens, including exposure to domestic animals, can help clinic staff with diagnosis and appropriate therapeutic management of acutely febrile patients as well as identify target areas for education and prevention strategies.

Dr Etienne Muller

Dr Ranmini Kularatne

Macrolide and fluoroquinolone resistance-associated mutations in *Mycoplasma genitalium* in Johannesburg, South Africa, 2007-2014

Muller EE, *Mahlangu MP, Lewis DA,* ***Kularatne RS.***

BMC Infectious Diseases
Impact Factor: 2.62

Background: Antimicrobial resistance in *Mycoplasma genitalium* is rising globally with resultant clinical treatment failure. We investigated the prevalence of mutations in the macrolide and fluoroquinolone resistance-determining regions of *M. genitalium* in Johannesburg, South Africa, and ascertained their association with HIV serostatus.

Methods: Stored *M. genitalium* positive specimens, collected from STI and HIV patients enrolled in the Gauteng STI National Microbiological Surveillance programme (2007-2014) and a large HIV outpatient clinic-based study (2007) in Johannesburg, were tested for antimicrobial resistance.

Results: We determined the prevalence of 23S rRNA gene mutations conferring macrolide resistance and mutations in the quinolone resistance-determining regions (QRDR) of the gyrA and parC genes in 266 *M. genitalium* positive DNA extracts. No macrolide resistance-associated mutations were detected in any of the specimens analysed. QRDR mutations with known *M. genitalium*-associated fluoroquinolone resistance were not detected in gyrA, however, one specimen (0.4%) contained a D87Y amino acid alteration in parC, which has been linked to fluoroquinolone treatment failure. The most common parC amino acid change detected, of unknown clinical significance, was P62S (18.8%). We found no significant association between QRDR mutations in M. genitalium and HIV-infection.

Conclusions: Ongoing antimicrobial resistance surveillance in *M. genitalium* is essential, as macrolide resistance may emerge given the recent incorporation of azithromycin into the 2015 South African national STI syndromic management guidelines.
of preparation.

Ms Johanna Venter

Dr Ranmini Kularatne

Comparison of an in-house real-time duplex PCR assay with commercial HOLOGIC® APTIMA assays for the detection of *Neisseria gonorrhoeae* and *Chlamydia trachomatis* in urine and extra-genital specimens

Venter JME, *Mahlangu PM, Müller EE, Lewis DA, Rebe K, Struthers H, McIntyre J,* ***Kularatne RS.***

BMC Infectious Diseases
Impact Factor: 2.620

Background: Extra-genital *Neisseria gonorrhoeae* and *Chlamydia trachomatis* infections are mostly asymptomatic, and important reservoir sites of infection as they often go undetected and may be more difficult to eradicate with recommended therapeutic regimens. Commercial nucleic acid amplification tests (NAATs) have not received regulatory approval for the detection of *N. gonorrhoeae* and *C. trachomatis* in extra-genital specimens. The HOLOGIC® APTIMA Combo2 assay for *N. gonorrhoeae* and *C. trachomatis* has performed well in evaluations using extra-genital specimens.

Methods: We assessed the performance of an in-house real-time duplex PCR assay for the detection of *N. gonorrhoeae* and *C. trachomatis* in urine and extra-genital specimens using the HOLOGIC® APTIMA assays as gold standard comparators. Urine, oropharyngeal and ano-rectal specimens were collected from each of 200 men-who-have-sex-with-men (MSM) between December 2011 and July 2012.

Results: For *N. gonorrhoeae* detection, the in-house PCR assay showed 98.5-100% correlation agreement with the APTIMA assays, depending on specimen type. Sensitivity for *N. gonorrhoeae* detection was 82.4% for ano-rectal specimens, 83.3% for oropharyngeal specimens, and 85.7% for urine; and specificity was 100% with all specimen types. The positive predictive value (PPV) for *N. gonorrhoeae* detection was 100% and the negative predictive value (NPV) varied with sample type, ranging from 98.5-99.5%. For *C. trachomatis* detection, correlation between the assays was 100% for all specimen types. The sensitivity, specificity, PPV and NPV of the in-house PCR assay was 100% for *C. trachomatis* detection, irrespective of specimen type.

Conclusion: The in-house duplex real-time PCR assay showed acceptable performance characteristics in comparison with the APTIMA® assays for the detection of extra-genital *N. gonorrhoeae* and *C. trachomatis*.

Prof John Frean

Household pets and the risk of zoonotic infections Update

Frean J.

Infectious Diseases Update

Impact Factor: 2.620

Zoonoses are animal infections that are transmissible to humans under natural conditions. The 'One Health' concept arose from the realisation that human health, animal health, and environmental health are interlinked. Most emerging or re-emerging infections come from animals, and therefore there are opportunities to protect individual and public health by being aware of the risks that exist when humans and animals share the same environment.

Dr Ranmini Kularatne

The management of male urethritis syndrome in South Africa

Kularatne RS.

Infectious Diseases Update

Impact Factor: 2.620

In South Africa, sexually transmitted infections (STIs) are treated in the context of syndromic management using standard treatment guidelines. A syndrome is a collection of consistent groups of symptoms and easily recognised signs that define a certain condition. The syndromic management approach for STIs provides treatment that will deal with the majority of, or the most serious, causative pathogens based on clinical manifestations. STI syndromic management is advocated by the World Health Organization as the most cost-effective means of treating STIs in resource-poor settings, which lack the resources or access to laboratory facilities for universal diagnostic testing.

Dr Sandrama Nadan

Prof Nicola Page

Epidemiology of human astroviruses among children younger than 5 years: prospective hospital-based sentinel surveillance in South Africa, 2009-2014

Nadan S, *Taylor MB, Groome MJ, Cohen C, Madhi SA,* ***Page NA.***

Journal of Medical Virology
Impact Factor: 1.988

Background: The epidemiology of human astroviruses (HAstVs) in hospitalised patients less than 5 years of age from selected sites in South Africa was investigated. Diarrheagenic stool specimens collected from April 2009 to May 2014 were screened retrospectively for selected viruses, bacteria and parasites.

Method: Patient data were analysed to identify epidemiologic factors most frequently detected with HAstV infections. The following case-comparisons were investigated; HAstV-positive and HAstV-negative children, human immunodeficiency virus (HIV)-infected and HIV-uninfected (HAstV-positive) children and HIV-exposed and unexposed (HAstV-positive HIV-uninfected) children.

Results: Astrovirus was identified in 7.0% (234/3340) of cases and most frequently in ages 7 to 12 months (9.2%; 90/975) compared with 5.8% to 6.6% in other 6-month age groups. No seasonal trends were observed. More HAstVs were detected in children from homes that used outdoor water sources (7.6%) compared to indoor sources [5.7%; adjusted odds ratio (aOR), 1.5; 95% CI, 1.1-2.1; P = 0.009]. Astroviruses were detected in 8.4% (67/799) of HIV-uninfected patients that were exposed to HIV compared with 5.9% (74/1257) of HIV-unexposed patients (P = 0.032).

Conclusion: Astroviruses were most prevalent in children aged 7 to 12 months and were detected throughout the study period. The study was limited as only hospitalised patients were investigated and no comparisons were made to diarrhoea-free control groups. Future HAstV surveillance should include community-based studies and children presenting at outpatient facilities.

Mrs Mahlape Mahlangu

Dr Ranmini Kularatne

The prevalence of *Mycoplasma genitalium* and association with HIV infection in symptomatic patients, Johannesburg, South Africa, 2007-2014

Mahlangu MP, *Venter JME, Maseko DV, Muller EE,* ***Kularatne RS.***

Sexually Transmitted Diseases
Impact Factor: 1.981

Background: *Mycoplasma genitalium* is associated with genital discharge syndrome, but limited prevalence data is available in South Africa. The prevalence rates of *M. genitalium* infection and HIV co-infection were determined in urogenital specimens collected from male and female patients presenting with genital discharge syndrome to a primary health care centre in Johannesburg, South Africa from 2007 through 2014.

Methods: Genital specimens from 4731 patients were tested by a validated in-house multiplex real-time PCR assay for the detection of *Neisseria gonorrhoeae*, *Chlamydia trachomatis*, *Trichomonas vaginalis* and *M. genitalium*. Sera were tested for HIV infection using the Determine™ HIV 1/2 and Unigold™ assays.

Results: The relative prevalence of *M. genitalium* in males and females was 8.9% and 10.6%, respectively. The prevalence of HIV infection in those infected with *M. genitalium*, without other sexually transmitted infections (STIs), was significantly higher than in those without *M. genitalium* infection (48.9% v 40.5%, p=0.014). This significant difference in HIV seroprevalence was particularly observed among females in the study cohort.

Conclusion: The relative prevalence of *M. genitalium* and its association with prevalent HIV among females with vaginal discharge syndrome (VDS) calls for further research on the potential role of *M. genitalium* in the transmission and acquisition of HIV.

Ms Blazenka Letinic

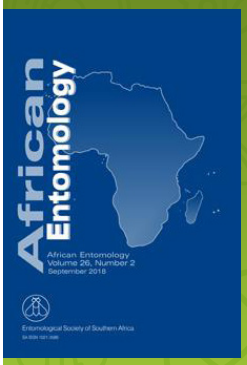
Prof Lizette Koekemoer

Inoculation protocol for the African malaria vector, *Anopheles arabiensis*, by means of nano-injection

Letinic BD, *Kemp A, Christian RN,* ***Koekemoer LL.***

African Entomology
Impact Factor: 0.508

Inoculation by means of injection has become a prominent bio-manipulation technique. This physical delivery system offers an advantage over other techniques by introducing precise quantities of inoculate into any life stage of an organism. However, this technique is intricate, laborious and requires extensive optimisation. Factors such as the location of injection, age of the organism, injection volume, and nutritional status of the organism prior to injection are variables that will likely differ between species. Bio-manipulation studies have been performed on the major African malaria vector mosquito species, *Anopheles gambiae s.s.*, yet they are still lacking for the closely related vector *An. arabiensis*. This study established a method of nano-injection procedure for *An. arabiensis* mosquitoes and found that the highest rate of survival was achieved when 1-day-old mosquitoes, fed on a 10 % sucrose solution prior to injection, were intra-thoracically injected using an inoculation volume of 69 nl.



Prof Basil Brooke

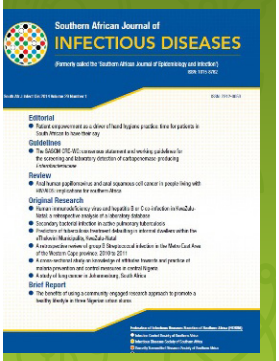
Editorial Commentary: Malaria control is not simply a matter of killing mosquitoes

Brooke BD.

Southern African Journal of Infectious Diseases
Impact Factor: 0.390

South Africa has a particularly long history of controlling malaria in its affected provinces – KwaZulu-Natal, Mpumalanga and Limpopo. Suppressing malaria vector mosquitoes with insecticides, accurate and timely diagnosis of infected persons, and subsequent case management with appropriate treatment regimens have reduced the incidence of malaria by at least 95% over the past seven decades. This level of success has placed South Africa in a particularly strong position to eliminate malaria within its borders in the near future (the current target is 2023).

There is of course a 'however' to this statement. Malaria elimination does not mean business as usual. Stabilising and maintaining the baseline level of control whilst scaling up current interventions, and adding new elements, is costly, logistically challenging and a tough project to sell in the face of competing public health priorities. The necessary stakeholder commitments have nevertheless been made, a revised elimination strategy for the period 2019 to 2023 has been developed and a detailed business case for eliminating malaria in South Africa is in the final stages of preparation.



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