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

Science Focus

"TAKE A DEEP DIVE INTO THE LATEST RESEARCH AND CUTTING-EDGE SOLUTIONS DRIVING PUBLIC HEALTH FORWARD."

ISSUE 25 | Q4 2022/2023

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

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Our unwavering mission remains to foster a culture of excellence, provide a platform for the brightest minds, and promote scientific advancements that positively impact society.

MS SINENHLANHLA JIMOH
SENIOR COMMUNICATIONS MANANGER

Celebrating Achievements and Scientific Advancements that benefit our communities

We are thrilled to share the NICD Community's extraordinary achievements and ground-breaking research in this issue of the Science Focus. In FY 2022/23, a total of 252 peer-reviewed publications were published, exceeding the target by an amazing 112 articles. This achievement exemplifies our researchers' passion and commitment to creating exceptional work that is subjected to stringent review processes.

In this issue of the Science Focus, we take pride in recognising the accomplishments of our esteemed researchers who have obtained their National Research Foundation (NRF) rating. The NRF rating is a valuable tool for benchmarking the quality of NICD researchers against the best in the world. NRF ratings are allocated based on a researcher's recent research outputs and impact as perceived by international peer reviewers.

Among those rated we acknowledge Dr Kurt Wibmer, Dr Jessica Coertse, Dr Orienka Hellferscee and Dr Shuné Oliver as the talented young researchers identified with a Y rating, symbolising the bright future of scientific advancements at the NICD. We eagerly anticipate witnessing the growth and contributions of these young researchers as they continue to push the boundaries of knowledge.

This edition features research output in quarter four of FY 2022/2023. We highlight, among other works, the study by Prof Cheryl Cohen and a colleague on "COVID-19 infection, reinfection, and the transition to endemicity", which was published in The Lancet. Prof. Cohen and colleague have attained a high impact factor score of 202,731. Their study delves into critical aspects of the ongoing COVID-19 pandemic. Prof Cohen's exceptional work has positioned her as a top publisher for the quarter, emphasising the importance and impact of her findings.

Additionally, we feature the study titled "Unmasking pneumococcal carriage in a high human immunodeficiency virus (HIV) prevalence population in two community cohorts in South Africa, 2016-2018: the PHIRST Study." Co-authored by Ms Maimuna Carrim and Dr Nicole Wolter, this study, published in Clinical Infectious Diseases, addresses the limited longitudinal pneumococcus colonization data in high HIV prevalence settings following pneumococcal conjugate vaccine introduction. Their research sheds light on crucial aspects of pneumococcal carriage in vulnerable populations, contributing to the understanding of public health immunization strategies.

As we celebrate these remarkable achievements, we extend our heartfelt congratulations to our colleagues and all the researchers who have contributed to this edition of Science Focus. Their dedication, innovation, and commitment to advancing scientific knowledge serve as an inspiration.

Our unwavering mission remains to foster a culture of excellence, provide a platform for the brightest minds, and promote scientific advancements that positively impact society. With each passing quarter, we are privileged to witness the remarkable strides made within our scientific community, and we eagerly anticipate the discoveries and breakthroughs that lie ahead.

We hope you find this edition insightful as you explore the latest achievements within the NICD community.

On behalf of the team,

Sinenhlanhla Jimoh
Senior Communications Manager

Disclaimer: Impact factor scores contained in this publication were compiled in February/March 2023.

PEER REVIEWED PUBLICATION STATISTICS

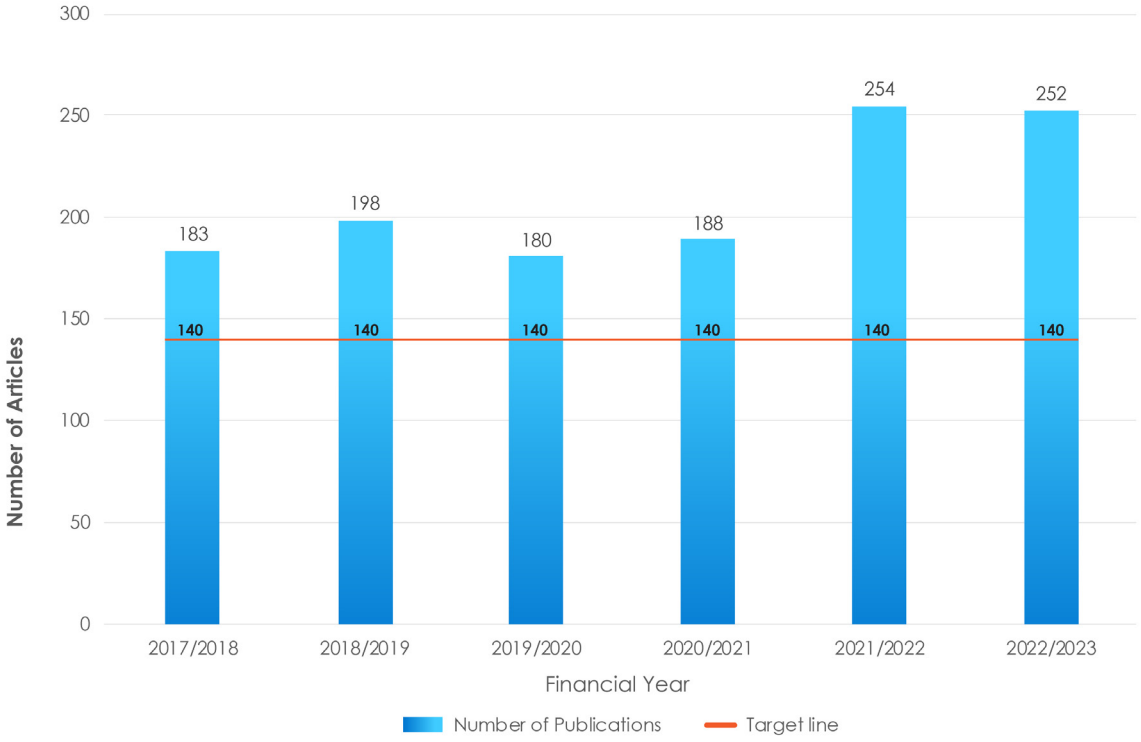


Figure 1: The peer-reviewed publications from the 2017/18 fiscal year through to the 2022/23 fiscal year are compared in the figure above. Based on this comparison, the yearly objective of 140 publications was exceeded during a six-year period.

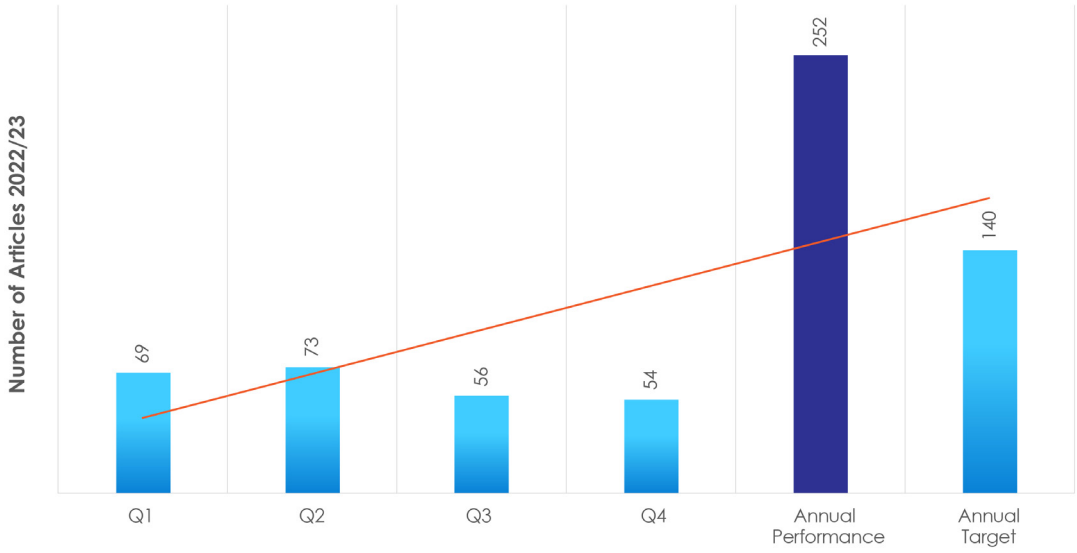


Figure 2: The peer-reviewed publications from the 2022/23 fiscal year from Q1 through to Q4 are compared in the figure above. The yearly target of 140 publications was exceeded for the 2022/23 fiscal year.

Top Published Authors for Q4 2022/2023

1 PROF CHERYL COHEN

2 PROF ANNE VON GOTTBERG

3 DR NICOLE WOLTER

DR JACKIE KLEYNHANS

4 DR SIBONGILE WALAZA

5

PROF PENNY MOORE

DR JINAL BHIMAN

DR JOCELYN MOYES

MS MAIMUNA CARRIM

Disclaimer: Impact factor scores contained in this publication were compiled in November/December 2022.

NRF Rated Researchers

B – Internationally acclaimed researchers


PROF ADRIAN PUREN


DR ANTHONY SMITH


PROF ANNE VON GOTTBERG


PROF BASIL BROOKE


PROF CHERYL COHEN


PROF CAROLINE TIEMESSEN


PROF NELESH GOVENDER

C – Established researchers


DR ETIENNE MÜLLER


DR GIVEMORE MUNHENGA


DR HALIMA SAID


DR JAISHREE RAMAN


DR JACQUELINE WEYER


DR MIGNON DU PLESSIS


DR MICHELLE GROOME


PROF NICOLA PAGE


DR NISHI PRABDIAL-SING


DR NICOLE WOLTER

Y – Promising young researchers


DR JESSICA COERTSE

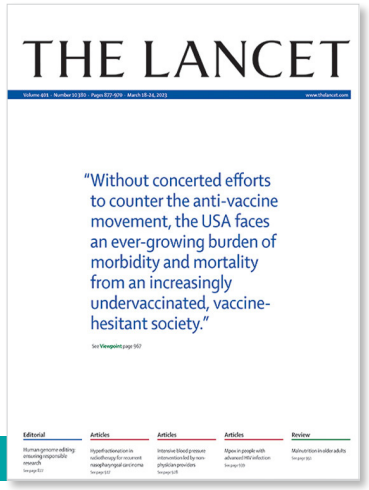

DR ORIENKA HELLFERSCEE


DR CK WIBMER


DR SHUNÉ OLIVER

Disclaimer: Impact factor scores contained in this publication were compiled in February/March 2023.

PROF CHERYL COHEN



COVID-19 infection, reinfection, and the transition to endemicity

Cheryl Cohen, Juliet Pulliam

Lancet

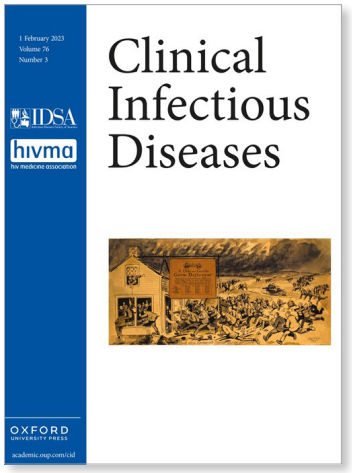
IMPACT FACTOR: 202,731

Understanding the protection conferred by previous infection against repeat infection, illness, and severe disease is key to projecting the future epidemiology of COVID-19 and to guiding vaccine policy decisions. In The Lancet, The COVID-19 Forecasting Team1 report data from a systematic review and meta-analysis of 65 studies from 19 different countries estimating the reduction in COVID-19 risk among individuals with previous SARS-CoV-2 infection, compared with those without a previous infection. Although there have been several previous systematic reviews that address this question, the current study adds substantial new information through the inclusion of an analysis of the change in protection conferred by previous infection with time since infection and an analysis stratified by SARS-CoV-2 variant. This analysis is particularly important following the emergence of the omicron variant in late 2021, with rapid spread globally. Currently, in most parts of the world, COVID-19 is dominated by different omicron sublineages, with ongoing emergence of new sublineages demonstrating the importance of potential immune escape.2

The COVID-19 Forecasting Team1 found a high level of protection against reinfection and symptomatic disease for ancestral, alpha, beta, and delta variants (mean pooled estimate >82%) but substantially lower protection (approximately 45%) for the omicron BA.1 variant. Protection against severe disease was high for all variants evaluated (>85% at 40 weeks). Protection against reinfection with alpha, beta, and delta variants waned over time but remained higher than 75% at 40 weeks. By contrast, protection against reinfection by omicron BA.1 waned more rapidly, decreasing to 36% at 40 weeks. The data available for the omicron sublineages BA.2, BA.4, and BA.5, although limited, suggested that protection against these sublineages was lower if the past infection was with a pre-omicron variant compared with omicron; however, reinfection of those with a past omicron infection was higher for BA.4 and BA.5, highlighting the ongoing importance of immune evasion as a selective pressure driving the emergence of new subvariants.

DR JACKIE KLEYNHANS

PROF CHERYL COHEN



Household Transmission of Severe Acute Respiratory Syndrome Coronavirus 2 From Adult Index Cases With and Without Human Immunodeficiency Virus in South Africa, 2020-2021: A Case-Ascertained, Prospective, Observational Household Transmission Study

Jackie Kleynhans, Sibongile Walaza , Neil A Martinson , Mzimasi Neti , Anne von Gottberg , Jinal N Bhiman , Dylan Toi, Daniel G Amoako , Amelia Buys , Kedibone Ndlangisa , Nicole Wolter , Leisha Genade , Lucia Maloma , Juanita Chewparsad , Limakatso Lebina , Linda de Gouveia , Retshidisitswe Kotane , Stefano Tempia , **Cheryl Cohen**

Clinical Infectious Diseases

IMPACT FACTOR: 20,999

BACKGROUND

In South Africa, 19% of adults are living with human immunodeficiency virus (HIV; LWH). Few data on the influence of HIV on severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) household transmission are available.

METHODS

We performed a case-ascertained, prospective household transmission study of symptomatic adult index SARS-CoV-2 cases LWH and not living with HIV (NLWH) and their contacts from October 2020 to September 2021. Households were followed up 3 times a week for 6 weeks to collect nasal swabs for SARS-CoV-2 testing. We estimated household cumulative infection risk (HCIR) and duration of SARS-CoV-2 positivity (at a cycle threshold value <30 as proxy for high viral load).

RESULTS

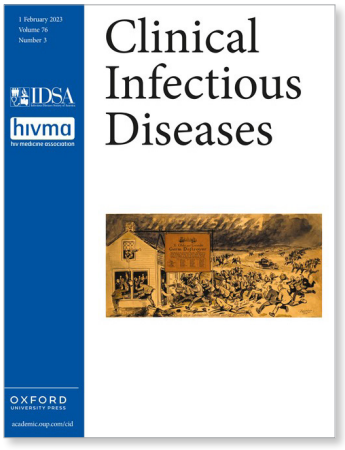
HCIR was 59% (220 of 373), not differing by index HIV status (60% LWH vs 58% NLWH). HCIR increased with index case age (35-59 years: adjusted OR [aOR], 3.4; 95% CI, 1.5-7.8 and ≥60 years: aOR, 3.1; 95% CI, 1.0-10.1) compared with 18-34 years and with contacts' age, 13-17 years (aOR, 7.1; 95% CI, 1.5-33.9) and 18-34 years (aOR, 4.4; 95% CI, 1.0-18.4) compared with <5 years. Mean positivity was longer in cases LWH (adjusted hazard ratio, 0.4; 95% CI, .1-.9).

CONCLUSIONS:

Index HIV status was not associated with higher HCIR, but cases LWH had longer positivity duration. Adults aged >35 years were more likely to transmit and individuals aged 13-34 to be infected SARS-CoV-2 in the household. As HIV infection may increase transmission, health services must maintain HIV testing and antiretroviral therapy initiation.

MS MAIMUNA CARRIM

DR NICOLE WOLTER



Unmasking pneumococcal carriage in a high human immunodeficiency virus (HIV) prevalence population in two community cohorts in South Africa, 2016-2018: the PHIRST Study

Maimuna Carrim, Stefano Tempia , Deus Thindwa , Neil A Martinson, Kathleen Kahn , Stefan Flasche, Orienka Hellferscee , Florette K Treurnicht, Meredith L McMorrow, Jocelyn Moyes , Thulisa Mkhencele , Azwifarwi Mathunjwa , Jackie Kleynhans , Limakatso Lebina , Katlego Mothlaoleng , Floidy Wafawanaka , Francesc Xavier Gómez-Olivé , Cheryl Cohen , Anne von Gottberg , **Nicole Wolter ; PHIRST group**

Clinical Infectious Diseases

IMPACT FACTOR: 20,999

BACKGROUND

Longitudinal pneumococcus colonization data in high human immunodeficiency virus (HIV) prevalence settings following pneumococcal conjugate vaccine introduction are limited.

METHODS

In 327 randomly selected households, 1684 individuals were enrolled and followed-up for 6 to 10 months during 2016 through 2018 from 2 communities. Nasopharyngeal swabs were collected twice weekly and tested for pneumococcus using quantitative lytA real-time polymerase chain reaction. A Markov model was fitted to the data to define the start and end of an episode of colonization. We assessed factors associated with colonization using logistic regression.

RESULTS

During the study period, 98% (1655/1684) of participants were colonized with pneumococcus at least once. Younger age (<5 years: adjusted odds ratio [aOR], 14.1; 95% confidence [CI], 1.8-111.3, and 5-24 years: aOR, 4.8, 95% CI, 1.9-11.9, compared with 25-44 years) and HIV infection (aOR, 10.1; 95% CI, 1.3-77.1) were associated with increased odds of colonization. Children aged <5 years had fewer colonization episodes (median, 9) than individuals ≥5 years (median, 18; P < .001) but had a longer episode duration (<5 years: 35.5 days; interquartile range, 17-88) vs. ≥5 years: 5.5 days (4-12). High pneumococcal loads were associated with age (<1 year: aOR 25.4; 95% CI, 7.4-87.6; 1-4 years: aOR 13.5, 95% CI 8.3-22.9; 5-14 years: aOR 3.1, 95% CI, 2.1-4.4 vs. 45-65 year old patients) and HIV infection (aOR 1.7; 95% CI 1.2-2.4).

CONCLUSIONS

We observed high levels of pneumococcus colonization across all age groups. Children and people with HIV were more likely to be colonized and had higher pneumococcal loads. Carriage duration decreased with age highlighting that children remain important in pneumococcal transmission.

DR SIMONE RICHARDSON

PROF PENNY MOORE

Antibody-dependent cellular cytotoxicity against SARS-CoV-2 Omicron sub-lineages is reduced in convalescent sera regardless of infecting variant

Richardson SI, Kgagudi P, Manamela NP, Kaldine H, Venter EM, Pillay T, Lambson BE, van der Mescht MA, Hermanus T, Burgers W, Ntusi N, Ueckermann V, Rossouw TM, Boswell MT, **Moore PL**

Cell Reports Medicine

IMPACT FACTOR: 16,988

ABSTRACT

The severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) Omicron BA.4 and BA.5 variants caused major waves of infections. Here, we assess the sensitivity of BA.4 to binding, neutralization, and antibody-dependent cellular cytotoxicity (ADCC) potential, measured by FcγRIIIa signaling, in convalescent donors infected with four previous variants of SARS-CoV-2, as well as in post-vaccination breakthrough infections (BTIs) caused by Delta or BA.1. We confirm that BA.4 shows high-level neutralization resistance regardless of the infecting variant. However, BTIs retain activity against BA.4, albeit at reduced titers. BA.4 sensitivity to ADCC is reduced compared with other variants but with smaller fold losses compared with neutralization and similar patterns of cross-reactivity. Overall, the high neutralization resistance of BA.4, even to antibodies from BA.1 infection, provides an immunological mechanism for the rapid spread of BA.4 immediately after a BA.1-dominated wave. Furthermore, although ADCC potential against BA.4 is reduced, residual activity may contribute to observed protection from severe disease.

DR WAASILA JASSAT

PROF CHERYL COHEN

A cohort study of post-COVID-19 condition across the Beta, Delta, and Omicron waves in South Africa: 6-month follow-up of hospitalized and nonhospitalized participants

Jassat W, Mudara C, Vika C, Welch R, Arendse T, Dryden M, Blumberg L, Mayet N, Tempia S, Parker A, Nel J, Perumal R, Groome MJ, Conradie F, Ndjeka N, Sigfrid L, Merson L, **Cohen C**

Int J Infect Dis

IMPACT FACTOR: 12,073

ABSTRACT

Objectives: The study aimed to describe the prevalence of and risk factors for post-COVID-19 condition (PCC).

METHODS

This was a prospective, longitudinal observational cohort study. Hospitalized and nonhospitalized adults were randomly selected to undergo telephone assessment at 1, 3, and 6 months. Participants were assessed using a standardized questionnaire for the evaluation of symptoms and health-related quality of life. We used negative binomial regression models to determine factors associated with the presence of ≥1 symptoms at 6 months.

RESULTS

A total of 46.7% of hospitalized and 18.5% of nonhospitalized participants experienced ≥1 symptoms at 6 months (P ≤0.001). Among hospitalized people living with HIV, 40.4% had persistent symptoms compared with 47.1% among participants without HIV (P = 0.108). The risk factors for PCC included older age, female sex, non-Black race, presence of a comorbidity, greater number of acute COVID-19 symptoms, hospitalization/COVID-19 severity, and wave period (lower risk of persistent symptoms for the Omicron compared with the Beta wave). There were no associations between self-reported vaccination status with persistent symptoms.

CONCLUSION

The study revealed a high prevalence of persistent symptoms among South African participants at 6 months but decreased risk for PCC among participants infected during the Omicron BA.1 wave. These findings have serious implications for countries with resource-constrained health care system.

DR MELITAH MOTLHALE

Kaposi sarcoma-associated herpesvirus, HIV-1 and Kaposi sarcoma risk in black South Africans diagnosed with cancer during antiretroviral treatment rollout.

Motlhale M, Muchengeti M, Bradshaw D, Chen WC, Singini MG, de Villiers CB, Lewis CM, Bender N, Mathew CG, Newton R, Waterboer T, Singh E, Sitas F.

Int J Cancer

IMPACT FACTOR: 7,316

ABSTRACT

Kaposi sarcoma-associated herpesvirus (KSHV) causes Kaposi sarcoma (KS). The risk of KS is amplified in HIV-immunosuppressed individuals and antiretroviral therapy (ART) reduces KS incidence. Reliable data on the relationship between these factors are lacking in Africa. We used questionnaires and serum from 7886 black South Africans (18-74 years) with incident cancer, recruited between 1995 and 2016. ART rollout started in 2004. We measured associations between KS, HIV-1 and KSHV before and after ART rollout. We measured seropositivity to HIV-1, KSHV latency-associated nuclear antigen (LANA) and glycoprotein (K8.1) and calculated case-control-adjusted odds ratios (ORadj) and 95% confidence intervals (CI) in relation to KS and KSHV infection, before (1995-2004), early (2005-2009) and late (2010-2016) ART rollout periods. KSHV seropositivity

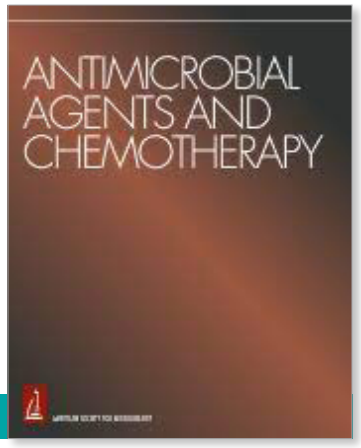
among 1237 KS cases was 98%. Among 6649 controls, KSHV seropositivity was higher in males (ORadj = 1.4 [95%CI 1.23-1.52]), in persons with HIV, (ORadj = 4.2 [95%CI 3.74-4.73]) and

lower in high school leavers (ORadj = 0.7 [95%CI 0.59-0.83]). KSHV seropositivity declined over the three ART rollout periods (37%, 28% and 28%, Ptrend < .001) coinciding with increases in high school leavers over the same periods (46%, 58% and 67%, Ptrend < .001). HIV-1 seroprevalence increased from 10% in the pre-ART period to 22% in the late ART period (Ptrend < .001). Compared to HIV-1 and KSHV seronegatives, KSHV seropositives yielded an OR for KS of 26 (95%CI 11-62) in HIV-1 seronegative participants and an OR of 2501 (95%CI 1083-5776) in HIV-1 seropositive participants. HIV-1 increases the risk of KS in those infected with KSHV by 100-fold. Declines in KSHV seroprevalence coincide with ART rollout and with improvements in educational standards and general hygiene.

DR SHAHEED VALLY OMAR

Emergence of Canonical and NoncanonicalGenomic Variants following In Vitro Exposure of Clinical Mycobacterium tuberculosis Strains to Bedaquiline or Clofazimine

Ismail N, Dippenaar A, Warren RM, Peters RPH, **Omar SV**



Antimicrobial Agents & Chemotherapy

IMPACT FACTOR: 5,938

ABSTRACT

In Mycobacterium tuberculosis, bedaquiline and clofazimine resistance occurs primarily through Rv0678 variants, a gene encoding a repressor protein that regulates mmpS5/mmpL5 efflux pump gene expression. Despite the shared effect of both drugs on efflux, little else is known about other pathways affected. We hypothesized that in vitro generation of bedaquiline- or clofazimine-resistant mutants could provide insight into additional mechanisms of action. We performed whole-genome sequencing and determined phenotypic MICs for both drugs on progenitor and mutant progenies. Mutants were induced through serial passage on increasing concentrations of bedaquiline or clofazimine. Rv0678 variants were identified in both clofazimine- and bedaquiline-resistant mutants, with concurrent atpE SNPs occurring in the latter. Of concern was the acquisition of variants in the F420 biosynthesis pathway in clofazimine-resistant mutants obtained from either a fully susceptible (fbiD: del555GCT) or rifampicin mono-resistant (fbiA: 283delTG and T862C) progenitor. The acquisition of these variants possibly implicates a shared pathway between clofazimine and nitroimidazoles. Pathways associated with drug tolerance and persistence, F420 biosynthesis, glycerol uptake and metabolism, efflux, and NADH homeostasis appear to be affected following exposure to these drugs. Shared genes affected by both drugs include Rv0678, glpK, nuoG, and uvrD1. Genes with variants in the bedaquiline resistant mutants included atpE, fadE28, truA, mmpL5, glnH, and pks8, while clofazimine-resistant mutants displayed ppsD, fbiA, fbiD, mutT3, fadE18, Rv0988, and Rv2082 variants. These results show the importance of epistatic mechanisms as a means of responding to drug pressure and highlight the complexity of resistance acquisition in M. tuberculosis.

KEYWORDS

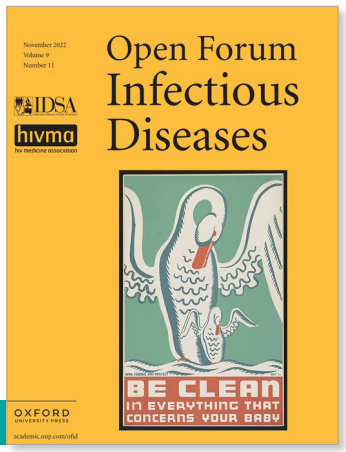
Mycobacterium tuberculosis; bedaquiline; canonical; clofazimine; geneti

PROF OLGA PEROVIC

DR MICHELLE LOWE

In Vitro activity of Ceftolozane-Tazobactam against Escherichia Coli, Klebsiella Pneumoniae and Pseudomonas Aeruginosa obtained from blood Cultures from Sentinel Public Hospitals in South Africa.

Perovic O, Singh-Moodley A, **Lowe M**



Antibiotics

IMPACT FACTOR: 5,222

ABSTRACT

Multidrug-resistant (MDR) Gram-negative bacteria are responsible for the majority of healthcare-associated infections and pose a serious threat as they complicate and prolong clinical care. A novel cephalosporin-β-lactamase-inhibitor combination, ceftolozane-tazobactam (C/T) was introduced in 2014, which improved the treatment of MDR pathogens. This study aimed to evaluate the activity of C/T against Escherichia coli (n = 100), Klebsiella pneumoniae (n = 100), and Pseudomonas aeruginosa (n = 100) blood culture isolates in South Africa (SA). Isolates were sequentially selected (2010 to 2020) from the Group for Enteric, Respiratory, and Meningeal Diseases Surveillance (GERMS) programme in SA. Organism identification was performed using the matrix-assisted laser desorption/ionisation-time of flight mass spectrometry (MALDI-TOF MS) instrument (Microflex, Bruker Daltonics, Bremen, Germany), and antibiotic susceptibility was performed using the Sensititre instrument (Trek Diagnostic Systems, East Grinstead, UK). C/T resistance was reported in 16 E. coli, 28 K. pneumoniae and 13 P. aeruginosa isolates. Fifty percent of the C/T resistant isolates were subjected to whole-genome sequencing (WGS). According to the whole genome multilocus sequence typing (MLST) analysis, the E. coli isolates (n = 8) belonged to sequence type (ST)10, ST131, ST405, and ST410, the K. pneumoniae isolates (n = 14) belonged to ST1, ST37, ST73, ST101, ST231, ST307, ST336 and ST6065 (novel ST), and the P. aeruginosa isolates (n = 7) belonged to ST111, ST233, ST273, and ST815. The WGS data also showed that all the E. coli isolates harboured aminoglycoside (aph (3")-Ib, aph (6)-Id), macrolide (mdfA, mphA), and sulphonamide (sul2) antibiotic resistance genes, all the K. pneumoniae isolates harboured β-lactam (blaCTX-M-15), and sulphonamide (sul2) antibiotic resistance genes, and all the P. aeruginosa isolates harboured aminoglycoside (aph (3')-IIb), β-lactam (PAO), fosfomycin (fosA), phenicol (catB7), quinolone (crpP), and disinfectant (qacE) antibiotic resistance genes. It is evident that E. coli, K. pneumoniae and P. aeruginosa can adapt pre-existing resistance mechanisms to resist newer β-lactam molecules and inhibitors, since these isolates were not exposed to ceftolozane-tazobactam previously.

DR JINAL BHIMAN

PROF PENNY MOORE

Novavax NVX-CoV2373 triggers neutralization of Omicron sub-lineages

Bhiman J, Richardson SI, Lambson BE, Kgagudi P, Mzindle N, Kaldine H, Crowther C, Gray G, Bekker L, Nonovax trial clinical lead author group, Shinde V, Bennett C, Glenn GM, Madhi SA, **Moore PL**

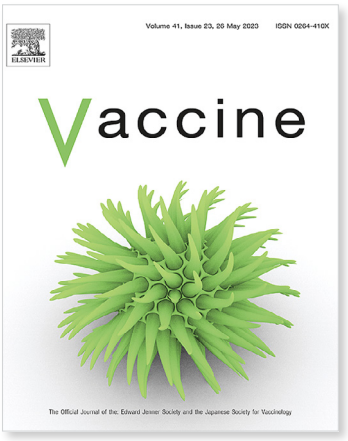
Scientific Reports

IMPACT FACTOR: 4,997

ABSTRACT

The SARS-CoV-2 Omicron (B.1.1.529) Variant of Concern (VOC) and its sub-lineages (including BA.2, BA.4, BA.5, BA.2.12.1) contain spike mutations that confer high level resistance to neutralizing antibodies induced by vaccination with ancestral spike or infection with previously circulating variants. The NVX-CoV2373 vaccine, a protein nanoparticle vaccine containing the ancestral spike sequence, has value in countries with constrained cold-chain requirements. Here we report neutralizing titers following two or three doses of NVX-CoV2373. We show that after two doses, Omicron sub-lineages BA.1 and BA.4/BA.5 were resistant to neutralization by 72% (21/29) and 59% (17/29) of samples respectively. However, after a third dose of NVX-CoV2373, we observed high titers against Omicron BA.1 (GMT: 1,197) and BA.4/BA.5 (GMT: 582), with responses similar in magnitude to those triggered by three doses of an mRNA vaccine. These data are of particular relevance as BA.4/BA.5 is dominating in multiple locations, and highlight the potential utility of the NVX-CoV2373 vaccine as a booster in resource-limited environments.

PROF PENNY MOORE



A research and development (R&D) roadmap for broadly protective coronavirus vaccines: A pandemic preparedness stategy

Moore KA, Leighton T, Ostrowsky JT, Anderson CJ, Danila RB, Ulrich AK, Lackritz EM, Mehr AJ, Baric RS, Baylor NW, Gellin BG, Gordon JL, Krammer F, Perlman S, Rees HV, Saville M, Weller CL, Osterholm MT, The Coronavirus Vaccines R&D Roadmap Taskforce **(Moore PL).**

Vaccine

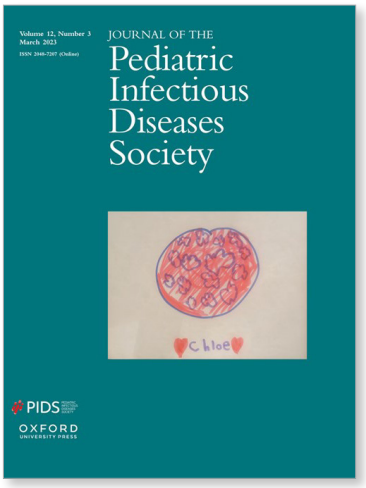
IMPACT FACTOR: 4,169

ABSTRACT

Broadly protective coronavirus vaccines are an important tool for protecting against future SARS-CoV-2 variants and could play a critical role in mitigating the impact of future outbreaks or pandemics caused by novel coronaviruses. The Coronavirus Vaccines Research and Development (R&D) Roadmap (CVR) is aimed at promoting the development of such vaccines. The CVR, funded by the Bill & Melinda Gates Foundation and The Rockefeller Foundation, was generated through a collaborative and iterative process, which was led by the Center for Infectious Disease Research and Policy (CIDRAP) at the University of Minnesota and involved 50 international subject matter experts and recognized leaders in the field. This report summarizes the major issues and areas of research outlined in the CVR and identifies high-priority milestones. The CVR covers a 6-year timeframe and is organized into five topic areas: virology, immunology, vaccinology, animal and human infection models, and policy and finance. Included in each topic area are key barriers, gaps, strategic goals, milestones, and additional R&D priorities. The roadmap includes 20 goals and 86 R&D milestones, 26 of which are ranked as high priority. By identifying key issues, and milestones for addressing them, the CVR provides a framework to guide funding and research campaigns that promote the development of broadly protective coronavirus vaccines.

DR NICOLA CHIWANDIRE

PROF CHERYL COHEN



Changing epidemiology of COVID-19 in children and adolescents over four successive epidemic waves in South Africa, 2020-2022

Chiwandire N, Jassat W, Groome M, Kufa T, Walaza S, Wolter N, von Gottberg A, Zar HJ, Reubenson G, Tempia S, Ebonwu J, Govender N, Ntshoe G, Shonhiwa AM, Blumberg L, **Cohen C**

J Pediatric Infect Dis Soc

IMPACT FACTOR: 3,806

BACKGROUND

South Africa experienced four waves of SARS-CoV-2 infection, dominated by Wuhan-Hu, Beta, Delta, and Omicron (BA.1/BA.2). We describe the trends in SARS-CoV-2 testing, cases, admissions, and deaths among children and adolescents in South Africa over successive waves.

METHODS

We analyzed national SARS-CoV-2 testing, case, and admissions data from March 2020 to February 2022 and estimated cumulative rates by age group for each endpoint. The severity in the third versus the fourth wave was assessed using multivariable logistic regression.

RESULTS

Individuals ≤18 years comprised 35% (21,008,060/60,142,978) of the population but only 12% (424,394/3,593,644) of cases and 6% (26,176/451,753) of admissions. Among individuals ≤18 years, infants had the highest admission (505/100,000) rates. Testing, case, and admission rates generally increased successively in the second (Beta) and third (Delta) waves among all age groups. In the fourth (Omicron BA.1/BA.2) wave, the case rate dropped among individuals ≥1 year but increased among those <1 year. Weekly admission rates for children <1 year (169/100,000) exceeded rates in adults (124/100,000) in the fourth wave. The odds of severe COVID-19 in all admitted cases were lower in the fourth wave versus the third wave in each age group, but they were twice as high in admitted cases with at least one comorbidity than those without.

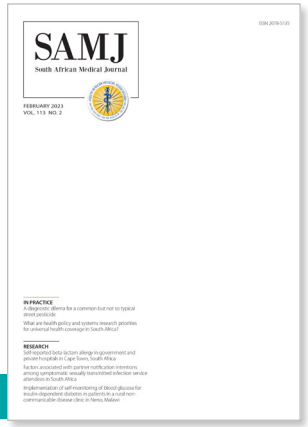
CONCLUSIONS

The admission rate for children <5 years was higher in the fourth wave than in previous waves, but the overall outcomes were less severe. However, children with at least one comorbidity had increased odds of severe disease, warranting consideration of prioritizing this group for vaccination.

DR BIANCA DA COSTA DIAS

Factors associated with partner notification intentions among symptomatic sexually transmitted infection service attendees in South Africa

Bianca Da Costa Dias, T Kufa,R S Kularatne



South African Medical Journal

IMPACT FACTOR: 0,566

BACKGROUND

In South Africa (SA), a client-initiated partner notification (PN) approach is implemented for the management of sexual partners of patients presenting with sexually transmitted infections (STIs) or STI syndromes.

OBJECTIVES

To explore the demographic, sexual behavioural and clinical characteristics associated with PN intentions among symptomatic STI service attendees at sentinel primary healthcare facilities in three SA provinces.

METHODS

We analysed cross-sectional data obtained from 1 293 adults enrolled into STI aetiological surveillance during 2019 - 2020 in Gauteng, KwaZulu-Natal and Western Cape provinces. Self-reported sexual practices, PN intentions and clinical data were collected using nurse-administrated questionnaires. We assessed gender-stratified factors associated with the index case's willingness to notify their sexual partners of their STI syndrome diagnosis. Univariable and multivariable Poisson regression models with robust error variance were used to determine factors associated with gender-stratified PN intentions.

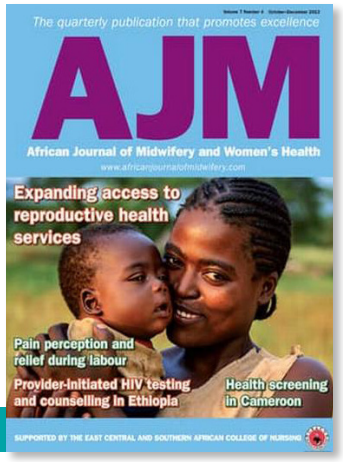
RESULTS

The enrolled participants comprised 887 male (68.6%) and 406 female (31.4%) STI clients. Self-reported PN intentions were higher among women than men (83.5% v. 64.4%; p<0.001). Multivariable analyses revealed that casual sex partnerships during the preceding 3-month period and enrolment at the KwaZulu-Natal site were independent barriers to PN intent among male participants. For females, enrolment at the Gauteng site was independently associated with lower PN intentions, while presenting with genital ulcer syndrome was a motivator towards PN intent. The primary reasons cited for non-disclosure across both genders were casual sexual encounters, followed by geographically distant partnerships and fear of disclosure.

CONCLUSION

We show that demographic and behavioural characteristics, as well as relationship dynamics, may influence the PN intentions of STI service attendees in SA. Alternative PN strategies should be considered, based on the reported barriers, to increase overall STI notification, strengthen partner management and ultimately reduce STI incidence.

PROF GAYLE SHERMAN



Healthcare workers affected by COVID-19 in a midwife obstetric unit in Johannesburg, South Africa

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African Journal of Midwifery and Women's Health

IMPACT FACTOR: n/a

BACKGROUND/AIMS

COVID-19 was first identified in China in December 2019 and was declared a pandemic in March 2020. South Africa reported its first case on 5 March 2020, and by December 2021, the country was battling a fourth wave of COVID-19 infections. This study assessed the impact of COVID-19 infections among healthcare workers in a midwives' obstetric unit in Soweto, South Africa, during the peak of the first wave.

METHODS

Healthcare workers from the unit who were infected with or affected by COVID-19 were interviewed. Data were collected on demographics, presenting symptoms, the need for hospital admission in those who tested positive and the perceived source of infection. Qualitative data were collected on perceptions of testing negative or positive and the impact of testing positive.

RESULTS

A total of 18 healthcare workers were interviewed, with the majority being midwives (61.1%), or advanced midwives (27.8%). Of the 15 included in quantitative analysis, 53% tested positive for COVID-19, with three (37.5%) requiring hospital admission, but there were no deaths. Of the staff who tested positive, 87.5% thought they became infected at work. None reported managing a patient with confirmed COVID-19. As a result of the high number of staff that tested positive for COVID-19 in the unit, there were staff shortages and anxiety about testing positive.

CONCLUSIONS

There was a high rate of COVID-19 infections in the unit, with the majority thought to have been acquired at work. This created anxiety among staff and had an impact on workload. The COVID-19 pandemic had a devastating impact on healthcare workers globally, and the effects are likely to be felt for years to come.

DR FAHIMA MOOSA

DR NICOLE WOLTER

Incidence and transmission dynamics of bordetella pertussis infection in rural and urban communities, South Africa, 2016–2018

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Emergency Infectious Diseases

IMPACT FACTOR: n/a

ABSTRACT

We conducted 3 prospective cohort studies (2016-2018), enrolling persons from 2 communities in South Africa. Nasopharyngeal swab specimens were collected twice a week from participants. Factors associated with Bordetella pertussis incidence, episode duration, and household transmission were determined by using Poisson regression, Weibull accelerated time-failure, and logistic regression hierarchical models, respectively. Among 1,684 participants, 118 episodes of infection were detected in 107 participants (incidence 0.21, 95% CI 0.17-0.25 infections/100 person-weeks). Children <5 years of age who had incomplete vaccination were more likely to have pertussis infection. Episode duration was longer for participants who had higher bacterial loads. Transmission was more likely to occur from male index case-patients and persons who had >7 days infection duration. In both communities, there was high incidence of B. pertussis infection and most cases were colonized.

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