

https://dspace.org/

Retaining African networks is urgent for global health

J Serwanga; Chinedu Ugwu; Ines Vigan-Womas; Jinal Bhiman; Peter K Quashie ...

https://hdl.handle.net/10539/49050
WOS

Downloaded from a DSpace repository. https://dspace.org/

CellPress
OPEN ACCESS

Trends in
Microbiology

Science & Society

Retaining African networks is urgent for global health

Jinal N. Bhiman[1,2], Jennifer Serwanga[3,4], Chinedu A. Ugwu[5,6], Ines Vigan-Womas[7,8], Peter K. Quashie[9], Jayanta Bhattacharya[10,11], Charles Sande[12], Adriana Bonomo[13], Fatu Badiane Markey[14], Gordon A. Awandare[9], Pramod Kumar Garg[11], Pontiano Kaleebu[3,4], Christian Happi[5,6], Ashton Rennergarbe[15], Colleen Woods[15], Jacqueline Kirchner[15], Anastazia Older Aguilar[15], Karen Makar[15], Penny L. Moore[1,2,16,17,*], and the GIISER network[18]

The Global Immunology and Immune Sequencing for Epidemic Response (GIISER) network, established in 2021, exemplifies the power of South–South collaboration in pandemic preparedness and response. Emerging from the COVID-19 crisis, GIISER integrated genomic surveillance, immunology, and capacity building across African, Asian, and South American sites, enabling rapid detection and characterization of SARS-CoV-2 variants. Through technology transfer, standardized protocols, and coordinated training, GIISER informed public health policy, advanced monoclonal antibody discovery, and strengthened local expertise. As COVID-19 research subsides and in the context of profound funding constraints, GIISER's scientific successes highlight the urgent need to sustain and expand regional networks to address current and future infectious disease threats, while championing diversity and scientific leadership in low- and middle-income countries (LMICs).

Introduction

The unprecedented speed of COVID-19 vaccine development, driven by global scientific unity, transparency, and innovation saved countless lives and highlighted the need for worldwide surveillance to track variants with immune escape potential. The GIISER network, a South–South initiative was therefore founded in 2021 to support epidemic preparedness, immune monitoring, and rapid response to future threats. The reemergence of Mpox clade Ia and Ib in multiple countries, and the spread of influenza H5N1 clade 2.3.4.4b virus, linked to 30% human fatality, among cattle in the USA reinforced the need for these networks. With 57 virological outbreaks reported in Africa in January 2025 alone, continued investment in infectious disease science remains essential.

Creation of an immunology-focused network during the COVID-19 pandemic

Early in the COVID-19 pandemic, genomic surveillance investments enabled the detection of emerging SARS-CoV-2 variants in Africa. The early successes of South African scientists in characterizing the Beta variant inspired the Gates Foundation Global Health Discovery Collaboratory (GHDC, https://ghdiscoverycollaboratory.org/) to launch GIISER, which integrated pathogen genomic surveillance, clinical epidemiology and local immunology, building infrastructure to rapidly assess emerging pathogens proximal to where they were detected. Through two closed calls, seven African, one South American, and one Asian GIISER sites were selected, based on their in-house capabilities and their role in the identification and/or characterization of SARS-CoV-2 variants (Figure 1A).

GIISER's impact during the COVID-19 pandemic

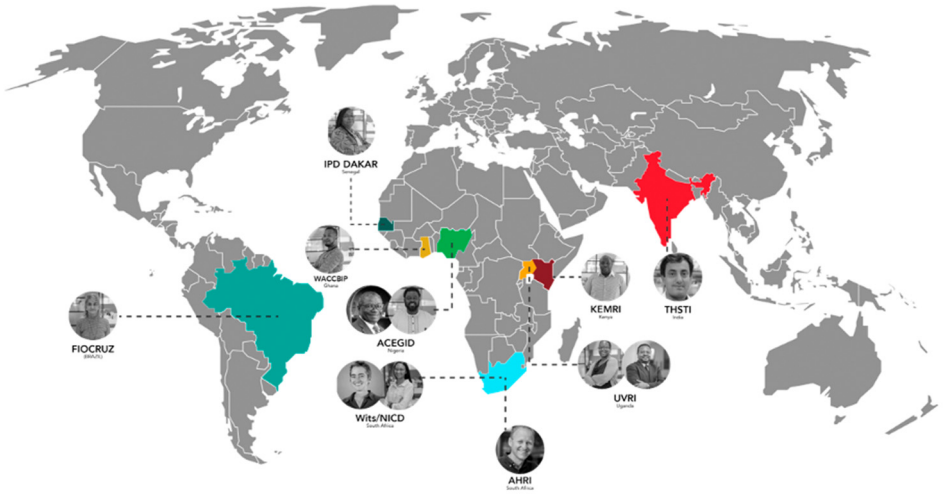
GIISER sites operated through standardized protocols, data sharing frameworks and coordinated intra-network training. Technology transfers from GHDC Collaboratory Platforms at the Massachusetts Institute of Technology and Nexelis, and laboratories at the US National Institutes of Health Vaccine Research Center (US-NIH VRC), strengthened the network with B cell repertoire analysis platforms, vesicular stomatitis virus (VSV)-based pseudovirus neutralization assays and rapid monoclonal antibody (mAb) isolation. Training and technology transfers at the height of the pandemic were virtual, but as travel restrictions eased, these became in-person. Challenges in establishing the network were typical of many African sites and networks, including administrative under-staffing, logistics in procurement, shipping, acquisition of permits and infrastructural shortcomings. Sharing of reagents within the network alleviated some procurement challenges, and extremely active engagement by GIISER country leads using informal real-time communication tools, supported by a network coordinator, enabled the network to navigate these challenges. GIISER data informed policy through local incident management teams, communication with global partners and pre-print releases, resulting in 52 publications (Figure 2). We now highlight major contributions from each site.

GIISER Brazil (Fundação Oswaldo Cruz (Fiocruz, Brazil)) advanced understanding of SARS-CoV-2 evolution, infectivity, replication, and immune escape in Brazil and

characterized the Gamma VOC. The team developed a low-cost method for selecting human-specific mAbs from single B cell sorting [1], and structural biology modeling enabled the identification of broadly reactive antibodies now being produced for further development.

The West African Centre for Cell Biology of Infectious Pathogens (WACCBIP), **GIISER Ghana**, contributed >70% of the country's SARS-CoV-2 sequences and led Africa's first population-level sero-epidemiology study on COVID-19 exposure. While the Noguchi Memorial Institute

(A)



(B)

	Brazil	Ghana	India	Kenya	Nigeria	Senegal	South Africa	Uganda
CEPI CL			Yes			Yes		Yes
CoViNet	Yes		Yes			Yes	Yes	Yes
EPSILON		Yes		Yes	Yes		Yes	
PRICOS				Yes				
Commercial partners		Yes	Yes		Yes	Yes		Yes
Expanded focus	Cancer	HIV-1, HIV-2, zoonotic viruses	RSV, Nipah	RSV, CMV, coronaviruses	Lassa, Mpox, preeclampsia, zoonotic viruses, CCHF	Dengue, Zika, Chikungunya, Ebola, Mpox, CCHF	RSV, CMV, Ebola, zoonotic viruses	Ebola, Rift Valley Fever, Mpox

Trends in Microbiology

Figure 1. Geographical distribution of the Global Immunology and Immune Sequencing for Epidemic Response (GIISER) sites and expansion of GIISER activities post the COVID-19 pandemic. (A) The GIISER network represents a South–South collaborative with sites in South America, Asia, and Africa. Adriana Bonomo leads GIISER-Brazil (teal), Ines Vigan-Womas leads GIISER-Senegal (dark green), Peter Quashie leads GIISER-Ghana (mustard), Chinedu Ugwu and Christian Happi lead GIISER-Nigeria (light green), Jennifer Serwanga and Pontiano Kaleebu lead GIISER-Uganda (orange), Charles Sande leads GIISER-Kenya (maroon), Penny Moore, Alex Sigal, and Jinal Bhiman lead GIISER-South Africa (cyan), and Jayanta Bhattacharya leads GIISER-India (red). (B) The GIISER network has expanded into other areas of infectious disease post the COVID-19 pandemic, including Crimean-Congo hemorrhagic fever (CCHF), cytomegalovirus (CMV) and respiratory syncytial virus (RSV). GIISER has concurrently been involved in additional networks, including the Coalition for Epidemic Preparedness Innovations (CEPI) Centralized Laboratory Network; the World Health Organization's Coronavirus Network (CoViNet); the Science for Africa, Pandemic Sciences Institute and Mastercard Foundation's Epidemic Science Leadership and Innovation Networks (EPSILON); and the Platform for Rapid Immunological Characterization of SARS-CoV-2 variants in Kenya and the East African Region (PRICOS). In addition, multiple GIISER sites now have commercial partners who will accelerate development of their academic outputs for commercialization.

for Medical Research (NMIMR) led the national SARS-CoV-2 testing to support the Ghana Health Service, GIISER Ghana performed molecular and sero-epidemiological surveillance and host immune profiling. Sequencing index cases confirmed local transmission and viral evolution, while serosurveys across Ghana and West Africa revealed large-scale asymptomatic infections, especially with Delta and Omicron [2,3]. WACCBIP and NMIMR deposited >95% of Ghana's SARS-CoV-2 sequences and performed sequencing for several neighboring countries.

GIISER India (Translational Health Science and Technology Institute, (THSTI)) characterized the Delta VOC and subsequently applied existing mAb discovery platforms, initially developed for Nipah and HIV, to isolate anti- SARS-CoV-2 mAbs [4]. The team also assessed ChAdOx1-S and BBV152 vaccine effectiveness in India [5].

Kenya Medical Research Institute Wellcome Trust Research Programme (KEMRI-WTRP), **GIISER Kenya**, brought a strong history of genomic and immunological research on respiratory viruses with pandemic potential and contributed to the 2014 Ebola response. GIISER Kenya were the first to identify two novel variants; namely FY.4, which spread globally and a novel Beta-like variant that contained Omicron and Delta-associated mutations [6].

GIISER Nigeria (African Centre of Excellence for Genomics of Infectious Diseases, ACEGID), generated Africa's first SARS-CoV-2 whole genome and supported 26 African countries in genomic surveillance as a SARS-CoV-2 continental reference laboratory [7]. GIISER Nigeria provided the first description of natural and vaccine-induced immune responses from SARS-CoV-2 survivors and vaccinated individuals in Nigeria [8]. The team supported the Nigerian Centre for Disease Control and Prevention with training in serological assays and shared real-time immunological data which guided the government's outbreak response.

GIISER Senegal within the Institut Pasteur de Dakar (IPD), leveraged its expertise in infectious diseases, genomics, immunology, diagnostics, and public health, to serve as an Africa CDC regional SARS-CoV-2 genomic surveillance hub, supporting 17 other African countries. GIISER Senegal generated the first national-level SARS-CoV-2 seroprevalence data in 2020. As a regional hub for the Africa CDC Pathogen Genomics Initiative (ACDC-PGI) and the GISAID platform, IPD provided training and technical support in genomic surveillance, enabling real-time monitoring of SARS-CoV-2 across Senegal and West Africa. The site also probed the relationship between pre-existing antibody immunity and COVID-19 outcomes in Senegal [9].

GIISER South Africa (African Health Research Institute (AHRI) and the University of the Witwatersrand/National Institute for Communicable Diseases (Wits/NICD)) provided the first evidence of SARS-CoV-2 immune escape, identifying the Beta and Omicron variants [10]. The team showed that humoral responses varied by infecting variant and that prolonged SARS-CoV-2 infection in people living with HIV could drive the emergence of novel variants [11]. Lastly, GIISER-SA assessed infection-induced neutralizing antibodies as correlates of protection against Delta and Omicron infections, highlighting

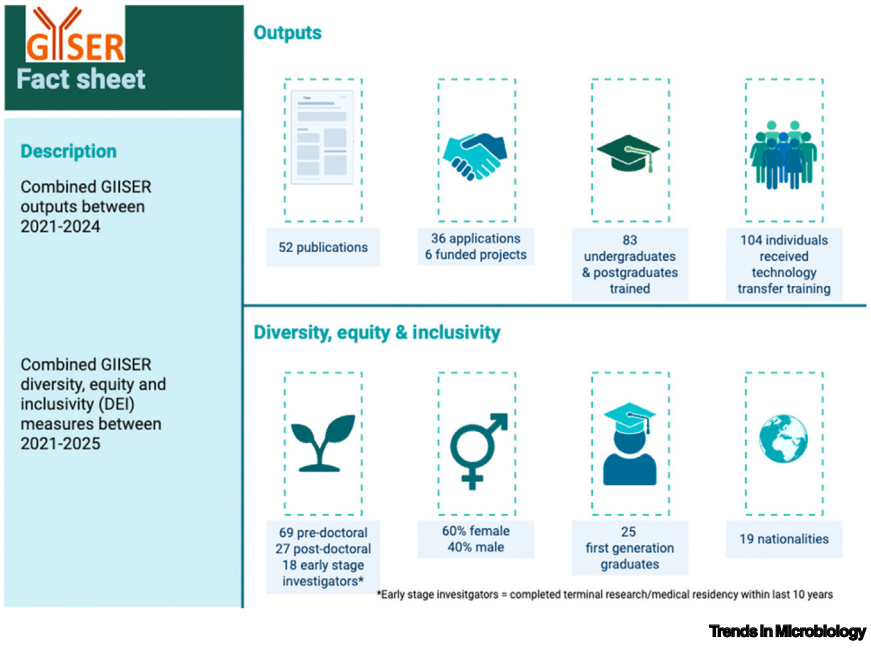


Figure 2. Global Immunology and Immune Sequencing for Epidemic Response (GIISER) fact sheet between 2021 and 2024/2025. GIISER sites, representing 19 nationalities, have collectively published 52 journal articles, submitted 36 collaborative grant applications (with a 17% success rate) and trained 83 undergraduates/postgraduates and 104 individuals in advanced immunological techniques. The GIISER network is inclusive and diverse, with 60% of individuals being female, 96 early career researchers, 18 investigators within 10 years of completing their terminal research or medical residency, and at least 25 first-generation college or graduate individuals.

the limited contribution of serum antibodies in this context [12].

The Uganda Virus Research Institute (UVRI), **GIISER Uganda**, was Uganda's SARS-CoV-2 reference laboratory and a regional SARS-CoV-2 reference laboratory for Africa CDC and WHO. GIISER Uganda defined pre-pandemic cross-reactivity and antibody responses to SARS-CoV-2 infection and vaccines deployed in Uganda [13–15]. Preliminary mAb discovery efforts have identified promising candidates currently undergoing functional characterization.

GIISER sustainability beyond SARS-CoV-2

As the threat of SARS-CoV-2 receded, and amidst existential funding threats resulting from changes in the US administration, the GIISER network has pivoted to other funding sources and regional viral risks: respiratory syncytial virus (RSV), cytomegalovirus (CMV), dengue, zika, chikungunya, Mpox, Lassa, Ebola, Marburg, rift valley fever (RFV), Nipah, and Crimean–Congo hemorrhagic fever (CCHF). GIISER South Africa, Ghana, Uganda, Nigeria, and Kenya obtained Wellcome Trust funding for pan-coronavirus mAb isolation, to support local vaccine development. GIISER Uganda isolated mAbs for Ebola Sudan, Ebola Bundibugyo, and Marburg during the 2022 Ebola Sudan outbreak, and GIISER South Africa is developing Ebola diagnostics. GIISER Nigeria is isolating mAbs of therapeutic and diagnostic potential for Lassa fever. With CEPI–Wellcome funding, GIISER Uganda is defining immune correlates of protection for Marburg vaccines and monitoring Ebola Sudan, Marburg, and Mpox clade Ib. GIISER Ghana and South Africa are testing novel HIV antibodies for therapeutics and prevention. Finally, a collaborative GIISER proposal was funded through the Epidemic Science Leadership and Innovation Networks (EPSILONs) call to screen bats for viruses with pandemic potential. GIISER's links to the CEPI Centralized Laboratory Network, also supports responses to Mpox and Marburg in South Sudan, Burundi, Rwanda, and the Democratic Republic of Congo. In parallel, WHO's Coronavirus Network (CoViNet) sites are coordinating training to strengthen diagnostics and immunology in 17 African countries, ensuring that regional COVID-19 expertise informs WHO policy. Lastly, GIISER partnered with the Science for Africa (SFA) Foundation, to strengthen readiness for clinical trials, and enhance African scientific leadership.

Securing the future of GIISER by embracing diversity, inclusivity, equity, and excellence

LMIC science is challenged by talent retention in constrained environments, however GIISER champions local training to reduce 'brain drain'. Talent stems from all walks of life and in Africa, those paths are often unconventional, but bring valuable perspectives. GIISER embraces people from all backgrounds, genders, and regions, with members from 19 African, Asian, and South American countries, including several first-generation graduate students. Female researchers make up 40–82% of each GIISER team. The work of 95 GIISER graduate students and postdoctoral fellows has strengthened local scientific expertise. Additionally, more than 39 staff learned and applied advanced immunology techniques through GIISER activities (Figure 2). These advances in regional capacity building are seeding the next generation of GIISER leaders with globally scarce skills, and the potential to expand the network's footprint with additional sites (Figure 2).

Conclusions

GIISER demonstrated the transformative power of collaboration, innovation, and investment in immunological research across LMICs. By integrating advanced immunological tools, enhancing regional expertise, and catalyzing South–South partnerships, GIISER bolstered pandemic preparedness and, with other networks, redefined the role of LMICs in global health. This network made groundbreaking discoveries, while empowering local scientists. Especially now, in an environment of reduced focus on infectious diseases and reduced funding for such science, GIISER's success underscores the importance of continued investment in regional networks to address current and emerging infectious threats.

Acknowledgments

We would like to acknowledge all staff, students and fellows who have supported the GIISER network through their dedication, initiative and passion. Additional acknowledgement to Ryan Mwakwi, SFA Foundation, for graphical designs. We thank the Nexelis team, especially Luc Gagnon and Philipa Levesque-Damphousse; Alex Shalek and his SCAP team; Daniel Douek, Amy Ransier, Tim Johnston and the RATP-Ig teams for the exceptional training. The GIISER network was established and is funded by the Gates Foundation (INV-030570 to P.L.M. and J.N.B.; INV-030776 to I.V.-W.; INV-036304 to C.H. and C.U.; INV-036307 to G.A. and P.K.Q.; INV-036308 to C.S.; INV-036306 to P.K. and J.S.; INV-030591 to A.B.; INV-030592 to P.K.G. and J.B.).

Declaration of interests

The authors have no interests to declare.

[1]SAMRC Antibody Immunity Research Unit, School of Pathology, University of the Witwatersrand, Johannesburg, South Africa
[2]National Institute for Communicable Diseases of the National Health Laboratory Services, Johannesburg, South Africa
[3]Viral Pathogens Theme, Medical Research Council, Uganda Virus Research Institute and London School of Hygiene and Tropical Medicine, Uganda Research Unit, Entebbe, Uganda.
[4]Department of Immunology, Uganda Virus Research Institute, Entebbe, Uganda
[5]Africa Centre of Excellence for Genomics of Infectious Diseases (ACEGID) Redeemer's University Ede, Nigeria
[6]Department of Biological Sciences, Redeemer's University Ede, Nigeria
[7]Institut Pasteur de Dakar, Immunophysiopathology and Infectious Diseases Department, Dakar, Senegal
[8]Pasteur Network, Institut Pasteur, Paris, France
[9]The West African Centre for Cell Biology of Infectious Pathogens (WACCBIP), College of Basic and Applied Sciences, University of Ghana
[10]Center for Virus Research, Vaccine & Therapeutics, BRIC-Translational Health Science & Technology Institute, NCR Biotech Science Cluster, Department of Biotechnology, Faridabad, Haryana 121001, India
[11]BRIC-Translational Health Science & Technology Institute, NCR Biotech Science Cluster, Faridabad, Haryana-121001, India
[12]KEMRI-Wellcome Trust Research Programme, Kllifi, Kenya
[13]Laboratory on Thymus Research,IOC, FIOCRUZ, Brazil

[14]Science for Africa Foundation, Nairobi, Kenya
[15]The Gates Foundation, Seattle, Washington, USA
[16]Centre for the AIDS Programme of Research in South Africa, Durban, South Africa
[17]Wits Infectious Diseases and Oncology Research Institute, Faculty of Health Sciences, University of the Witwatersrand, Johannesburg, South Africa
[18]Dale Kitchin, Gerald Kevin Oluka, Laban Kato, Jackson Sembera, Joseph Katende Ssebwana, Johnson C. Okoli, Philomena Eromon, Israel Ajayi, Ifeoluwa Bejide, Jolly Adole, Rokhaya Faye, Adji Astou Mbow, Irene Amoakoh Owusu, Kesego Tapela, Prince Adom Nartey, Alberta Serwaa, Suprit Deshpande, Pallavi Kshetrapal, Tripti Shrivastava, Sweety Samal, Shailendra Mani, Sankar Bhattacharya, Gaurav Batra, Sreevatsan Raghavan, Rajesh Pandey, Sheetal Gandotra, Maureen Mburu, Elijah Gicheru, Suelen M. Perobelli, Paola C. Resende, Marilda M. Siqueira, Elisa C. Pereira, Luciana Jesus da Costa, Marcela Sabino Cunha, Aline Albuquerque, Andre M Vale, Liza Fellicore, Marie Henriette Dior Ndione, Ndongo Dia, Moussa Moise Diagne, Cheikh Loucoubar.Affiliations: Dale Kitchin, SAMRC Antibody Immunity Research Unit, School of Pathology, University of the Witwatersrand, Johannesburg, South Africa and National Institute for Communicable Diseases of the National Health Laboratory Services, Johannesburg, South Africa; Gerald Kevin Oluka, Viral Pathogens Theme, Medical Research Council, Uganda Virus Research Institute and London School of Hygiene and Tropical Medicine, Uganda Research Unit, Entebbe, Uganda and Department of Immunology, Uganda Virus Research Institute, Entebbe, Uganda; Laban Kato, Viral Pathogens Theme, Medical Research Council, Uganda Virus Research Institute and London School of Hygiene and Tropical Medicine, Uganda Research Unit, Entebbe, Uganda and Department of Immunology, Uganda Virus Research Institute, Entebbe, Uganda; Jackson Sembera, Viral Pathogens Theme, Medical Research Council, Uganda Virus Research Institute and London School of Hygiene and Tropical Medicine, Uganda Research Unit, Entebbe, Uganda and Department of Immunology, Uganda Virus Research Institute, Entebbe, Uganda; Joseph Katende Ssebwana, Viral Pathogens Theme, Medical Research Council, Uganda Virus Research Institute and London School of Hygiene and Tropical Medicine, Uganda Research Unit, Entebbe, Uganda and Department of Immunology, Uganda Virus Research Institute, Entebbe, Uganda; Johnson C. Okoli, Africa Centre of Excellence for Genomics of Infectious Diseases (ACEGID) Redeemer's University Ede Nigeria; Philomena Eromon, Africa Centre of Excellence for Genomics of Infectious Diseases (ACEGID) Redeemer's University Ede Nigeria; Israel Ajayi, Africa Centre of Excellence for Genomics of Infectious Diseases (ACEGID) Redeemer's University Ede Nigeria and Department of Biological Sciences, Redeemer's University Ede, Nigeria; Ifeoluwa Bejide, Africa Centre of Excellence for Genomics of Infectious Diseases (ACEGID) Redeemer's University Ede Nigeria and Department of Biological Sciences, Redeemer's University Ede, Nigeria; Jolly Adole, Africa Centre of Excellence for Genomics of Infectious Diseases (ACEGID) Redeemer's University Ede Nigeria and Department of Biological Sciences, Redeemer's University Ede, Nigeria; Rokhaya Faye, Institut Pasteur de Dakar, Immunophysiopathology and Infectious Diseases Department, Dakar, Senegal; Adji Astou Mbow, Institut Pasteur de Dakar, Immunophysiopathology and Infectious Diseases Department, Dakar, Senegal; Irene Amoakoh Owusu, The West African Centre for Cell Biology of Infectious Pathogens (WACCBIP), College of Basic and Applied Sciences, University of Ghana; Kesego Tapela, The West African Centre for Cell Biology of Infectious Pathogens (WACCBIP), College of Basic and Applied Sciences, University of Ghana; Prince Adom Nartey, The West African Centre for Cell Biology of Infectious Pathogens (WACCBIP), College of Basic and Applied Sciences, University of Ghana; Alberta Serwaa, The West African Centre for Cell Biology of Infectious Pathogens (WACCBIP), College of Basic and Applied Sciences, University of Ghana; Suprit Deshpande, Center for Virus Research, Vaccine & Therapeutics, BRIC-Translational Health Science & Technology Institute, NCR Biotech Science Cluster, Department of Biotechnology, Faridabad, Haryana 121001, India and BRIC-Translational Health Science & Technology Institute, NCR Biotech Science Cluster, Faridabad, Haryana-121001, India; Pallavi Kshetrapal, Center for Virus Research, Vaccine & Therapeutics, BRIC-Translational Health Science & Technology Institute, NCR Biotech Science Cluster, Department of Biotechnology, Faridabad, Haryana 121001, India and BRIC-Translational Health Science & Technology Institute, NCR Biotech Science Cluster, Faridabad, Haryana-121001, India; Tripti Shrivastava, Center for Virus Research, Vaccine & Therapeutics, BRIC-Translational Health Science & Technology Institute, NCR Biotech Science Cluster, Department of Biotechnology, Faridabad, Haryana 121001, India and BRIC-Translational Health Science & Technology Institute, NCR Biotech Science Cluster, Faridabad, Haryana-121001, India; Sweety Samal, Center for Virus Research, Vaccine & Therapeutics, BRIC-Translational Health Science & Technology Institute, NCR Biotech Science Cluster, Department of Biotechnology, Faridabad, Haryana 121001, India and BRIC-Translational Health Science & Technology Institute, NCR Biotech Science Cluster, Faridabad, Haryana-121001, India; Shailendra Mani, Center for Virus Research, Vaccine & Therapeutics, BRIC-Translational Health Science & Technology Institute, NCR Biotech Science Cluster, Department of Biotechnology, Faridabad, Haryana 121001, India and BRIC-Translational Health Science & Technology Institute, NCR Biotech Science Cluster, Faridabad, Haryana-121001, India; Sankar Bhattacharya, Center for Virus Research, Vaccine & Therapeutics, BRIC-Translational Health Science & Technology Institute, NCR Biotech Science Cluster, Department of Biotechnology, Faridabad, Haryana 121001, India and BRIC-Translational Health Science & Technology Institute, NCR Biotech Science Cluster, Faridabad, Haryana-121001, India; Gaurav Batra, Center for Virus Research, Vaccine & Therapeutics, BRIC-Translational Health Science & Technology Institute, NCR Biotech Science Cluster, Department of Biotechnology, Faridabad, Haryana 121001, India and BRIC-Translational Health Science & Technology Institute, NCR Biotech Science Cluster, Faridabad, Haryana-121001, India; Sreevatsan Raghavan, Center for Virus Research, Vaccine & Therapeutics, BRIC-Translational Health Science & Technology Institute, NCR Biotech Science Cluster, Department of Biotechnology, Faridabad, Haryana 121001, India; Rajesh Pandey, CSIR-Institute of Genomics and Integrative Biology, New Delhi, India; Sheetal Gandotra, CSIR-Institute of Genomics and Integrative Biology, New Delhi, India; Maureen Mburu, KEMRI-Wellcome Trust Research Programme, Kllifi, Kenya; Elijah Gicheru, KEMRI-Wellcome Trust Research Programme, Kllifi, Kenya; Suelen M. Perobelli, Laboratory on Thymus Research,IOC, FIOCRUZ, Brazil and Universidade Veiga de Almeida, Rio de Janeiro, Brazil; Paola C. Resende, Laboratory of Respiratory Viruses, Exanthematous, Enteroviruses and Viral Emergencies, IOC, FIOCRUZ, Brazil; Marilda M. Siqueira, Laboratory of Respiratory Viruses, Exanthematous, Enteroviruses and Viral Emergencies, IOC, FIOCRUZ, Brazil; Elisa C. Pereira, Laboratory of Respiratory Viruses, Exanthematous, Enteroviruses and Viral Emergencies, IOC, FIOCRUZ, Brazil; Luciana Jesus da Costa, Laboratory of Genetics and Immunology of Viral Infections,IMPG, Universidade Federal do Rio de Janeiro; Marcela Sabino Cunha, Laboratory of Genetics and Immunology of Viral Infections, IMPG, Universidade Federal do Rio de Janeiro; Aline Albuquerque, FIOCRUZ Ceará; Andre M Vale, Laboratory of Lymphocyte Biology, IBFCGF, Federal University of Rio de Janeiro; Liza Fellicore, Universidade Federal de Minas Gerais, Minas Gerais, Brazil; Marie Henriette Dior Ndione, Institut Pasteur de Dakar, Virology Department, Dakar, Senegal; Ndongo Dia, Institut Pasteur de Dakar, Virology Department, Dakar, Senegal; Moussa Moise Diagne, Institut Pasteur de Dakar, Virology Department, Dakar, Senegal; Cheikh Loucoubar, Institut Pasteur de Dakar, Epidemiology, Clinical Research and Data Sciences Department, Dakar, Senegal

*Correspondence:
pennym@nicd.ac.za (P.L. Moore)

https://doi.org/10.1016/j.tim.2025.07.002

© 2025 The Authors. Published by Elsevier Ltd. This is an open access article under the CC BY-NC-ND license (http://creativecommons.org/licenses/by-nc-nd/4.0/).

References

1. Conde, L. *et al.* (2025) Comprehensive analysis of the human SARS-CoV-2 memory B cell repertoire in low-resource settings. *medRxiv*, 2025.2001.2014.25320505. https://doi.org/10.1101/2025.01.14.25320505
2. Tapela, K. *et al.* (2024) Cellular immune response to SARS-CoV-2 and clinical presentation in individuals exposed to endemic malaria. *Cell Rep.* 43, 114533
3. Sandi, J.D. *et al.* (2024) Upper airway epithelial tissue transcriptome analysis reveals immune signatures associated with COVID-19 severity in Ghanaians. *J Immunol Res* 2024, 6668017
4. Hingankar, N. *et al.* (2022) A combination of potently neutralizing monoclonal antibodies isolated from an Indian convalescent donor protects against the SARS-CoV-2 Delta variant. *PLoS Pathog.* 18, e1010465
5. Medigeshi, G.R. *et al.* (2022) Sub-optimal neutralisation of omicron (B.1.1.529) variant by antibodies induced by vaccine alone or SARS-CoV-2 Infection plus vaccine (hybrid immunity) post 6-months. *EBioMedicine* 78, 103938
6. Lugano, D. *et al.* (2024) Evaluation of population immunity against SARS-CoV-2 variants, EG.5.1, FY.4, BA.2.86, JN.1, JN.1.4, and KP.3.1.1 using samples from two health demographic surveillance systems in Kenya. *BMC Infect. Dis.* 24, 1474
7. Ihekweazu, C. *et al.* (2020) First African SARS-CoV-2 genome sequence from Nigerian COVID-19 case. https://virological.org/t/first-african-sars-cov2-genome-sequence-from-nigerian-covid19-case/421
8. Ugwu, C.A. *et al.* (2024) Immunological insights into COVID-19 in Southern Nigeria. *Front. Immunol.* 15, 1305586
9. Faye, R. *et al.* (2025) Differential association of SARS-CoV-2 IgG responses with anti-OC43 IgG in a Senegalese cohort. *bioRxiv*, 2025.2004.2007.647508. https://doi.org/10.1101/2025.04.07.647508
10. Wibmer, C.K. *et al.* (2021) SARS-CoV-2 501Y.V2 escapes neutralization by South African COVID-19 donor plasma. *Nat. Med.* 27, 622–625
11. Cele, S. *et al.* (2022) SARS-CoV-2 prolonged infection during advanced HIV disease evolves extensive immune escape. *Cell Host Microbe* 30, 154–162 e155
12. Sun, K. *et al.* (2024) SARS-CoV-2 correlates of protection from infection against variants of concern. *Nat. Med.* 30, 2805–2812
13. Serwanga, J. *et al.* (2023) Rapid, early, and potent Spike-directed IgG, IgM, and IgA distinguish asymptomatic from mildly symptomatic COVID-19 in Uganda, with IgG persisting for 28 months. *Front. Immunol.* 14, 1152522
14. Oluka, G.K. *et al.* (2025) Long-term immune consequences of initial SARS-CoV-2 A.23.1 exposure: a longitudinal study of antibody responses and cross-neutralization in a Ugandan cohort. *Vaccines (Basel)* 13. https://doi.org/10.3390/vaccines13020143
15. Serwanga, J. *et al.* (2024) Persistent and robust antibody responses to ChAdOx1-S Oxford-AstraZeneca (ChAdOx1-S, Covishield) SARS-CoV-2 vaccine observed in Ugandans across varied baseline immune profiles. *PLoS One* 19, e0303113