

Position: Bioinformatics scientist
Email: [gmboowa@gmail.com](mailto:gamboowa@gmail.com)
Website: <https://gmboowa.github.io/>

Twitter: @GeraldGmboowa
Google Scholar: <https://bit.ly/3D6l28e>
ORCID: <https://orcid.org/0000-0001-8445-9414>

INSTITUTION AND LOCATION	DEGREE	END DATE	FIELD OF STUDY
University of Washington	-	10/2021	Leadership & Management in
University of Washington	-	09/2021	Health
AMR-SORT-IT WHO-AFRO, Uganda	Fellowship	06/2021	Project Management in Global
Makerere University, Kampala, Uganda	PhD	08/2019	Health
University of Cambridge, Cambridge, the UK	Fellowship	01/2018	Operational Research in Africa
Baylor College of Medicine, Houston, Texas	Fellowship	12/2016	Genomics & Bioinformatics
Makerere University, Kampala, Uganda	MSc	01/2014	Bioinformatics
Makerere University, Kampala, Uganda	BSc	01/2009	Genomics, Genetics & Bioinformatics
			Immunology & Clinical Microbiology
			Biomedical Laboratory Technology

Personal Statement

My scientific background has given me extensive experience in the genomics of infectious diseases. Briefly, as an investigator on different research projects including Bill & Melinda Gates Foundation (BMGF)-funded research grants entitled; (i) understanding transmission dynamics and acquisition of antimicrobial resistance at referral hospitals and community settings in East Africa (<https://bit.ly/3D5E1OU>), (ii) piloting the use of rapid RT-qPCR assay for surveillance of known SARS-CoV-2 variants of concern in Africa (<https://gates.ly/3vOmOsY>), (iii) *Vibrio cholerae*, *Escherichia coli* and *Klebsiella pneumoniae* genomic surveillance in Africa (<https://bit.ly/3ZzVJWX>) and the European and Developing Countries Clinical Trials Partnership (EDCTP) funded project that is looking at pathogen detection in HIV-infected children with non-malarial febrile illnesses using metagenomic sequencing (<https://bit.ly/3iZfioF>). Over the past 15 years, I have been involved in both research and academia. One of my professional achievements has been working with colleagues at Makerere University in Uganda to introduce Fogarty/NIH-funded bioinformatics graduate training programs to support genomics, bioinformatics, and research capacity in Africa. Beyond these programs, I have organized several training programs in Africa involving over 800 graduate students and researchers in bioinformatics & genomics including mentorships (<https://bit.ly/3AYJRBn>), UC Berkeley's Center for Emerging and Neglected Diseases and the Alliance for Global Health and Science (<https://bit.ly/3igJ9VI>), H3ABioNet, Makerere University (<https://bit.ly/33dTyNI>), the Wellcome Advanced Courses (<https://bit.ly/3i9OI8B>), and Africa CDC (https://youtu.be/YpQFH_ZtA4E) among others. I have also recently worked to establish data science graduate training through Makerere University Data Science Research Training (MakDARTA) to strengthen evidence-based health innovation, intervention, and policy (<https://bit.ly/3HofeZx>). In this grant, we have applied machine learning to identify antimicrobial resistance determinants from genomic sequence data (<https://bit.ly/3xdiWVo>). My career has involved a lot of wet laboratory work. I specifically worked with World Health Organization Risk Groups 2, 3 & 4 pathogens as a laboratory technologist, biosafety officer, and supervisor of a Biosafety Level-3 (BSL-3) research and diagnostic laboratory at Makerere University (<https://bit.ly/3Kg5IRk>). However, this has over time transitioned to applying bioinformatics tools to analyze pathogen genome sequence data generated from exploring microbiological questions, particularly those pertaining to pathogen typing, genomic characterization, surveillance, virulence determinants, and deciphering antimicrobial resistance (resistome) while specifically working with drug-resistant *Mycobacterium tuberculosis*, HIV drug resistance, *Brucella spp*, *Acinetobacter baumannii*, *Klebsiella pneumoniae*, *Neisseria gonorrhoeae*, *Vibrio cholerae*, SARS-CoV-2, and Ebola. My team developed two automated & highly scalable assembly, annotation, and higher-level analyses microbial bioinformatics pipeline for genomic sequence data - rMAP: Rapid microbial analysis, profiling pipeline, and visualization (<https://bit.ly/36g809L>). This tool has features such as per isolate quality/adaptor clipping, assembly,

scaffolding, comprehensive annotation, taxonomic classification, multi-locus sequence typing, known antibiotic resistance detection via comprehensive reference databases, virulence factor detection, reference mapping, and novel resistance gene profiling. This tool finally creates results in standard bioinformatics file formats as well as HTML reports (<https://bit.ly/3m9C0ZN>). This work also received a travel scholarship from the BMGF. It was presented during the American Society for Microbiology (ASM) Conference on Rapid Applied Microbial Next-Generation Sequencing and Bioinformatics Pipelines 2020 (<https://bit.ly/346lyCW>). We have published this tool in the *Microbial Genomics Journal* (<https://bit.ly/3uPC745>). The second tool for profiling HIV drug resistance is called HIVDRIVES (<https://bit.ly/3PDpfHX>). I also won the Young Investigators Award – 2020 from the African Association for Research and Control of Antimicrobial Resistance "AAAMR" and BioMérieux, Inc (<https://bit.ly/3SAbd9G>). My other scientific contributions have resulted in the authorship of over 70 peer-reviewed manuscripts (<https://bit.ly/3LrA2kC>) while working with local, regional, continental as well as international collaborators. I am a bioinformatics scientist at the African Center of Excellence in Bioinformatics and Data-Intensive Sciences (<https://ace.ac.ug/about/staff/>). I am an external visiting examiner for Pwani University (Kenya), the Catholic University of Allied Health Sciences (Tanzania), and the University of KwaZulu-Natal (South Africa). Recently, I have participated in SARS-CoV-2 whole-genome sequencing and analysis for Africa CDC's pathogen genomics program (<https://africacdc.org/people/gerald-mboowa/>) as a Bioinformatics Implementation Science Expert leading pathogen bioinformatics and data visualization (<https://nextstrain.org/groups/africa-cdc/>). Furthermore, under this role, I have promoted bioinformatics and genome sequencing as well as coordinated equipping National Public Health Institutes with computing infrastructure in Africa and supported the development of a continental pathogen genomic data platform (<https://bit.ly/46sJUFp> & <https://apaportal.sanbi.ac.za/> & https://www.youtube.com/watch?v=YpQFh_ZtA4E). I have also promoted genomic data sharing & coordinated the analysis and publication of 100,000 SARS-CoV-2 genomes from 53/55 African countries (<https://bit.ly/3DucASq>) involving over 400 researchers and more than 200 institutions in Africa. Beyond this, I have contributed to the Sequence Read Archive (SRA) of the National Center for Biotechnology Information (NCBI) pathogen genomes from several organisms (<https://bit.ly/3Qs0aQH>).

Positions and Employment

- 2021 - 2024 Implementation Science Expert - Bioinformatics at Africa CDC | African Union (AU), Addis Ababa
- 2020 - 2021 Post-doctoral Fellow, NIH Fogarty training grant in HIV and Co-infections | D43-TW009771-06
- 2019 - Bioinformatics Scientist, the African Center of Excellence in Bioinformatics and Data-Intensive Sciences
- 2018 - Research Fellow, Makerere University
- 2017 - 2019 Tutor of Pre-Doctoral Students, Makerere University
- 2017 - 2018 Project Coordinator, B3Africa – Bridging Biobanking & Biomedical Research Across Europe & Africa
- 2017 - 2018 Project Coordinator - H3BioNet Program, Introduction to Bioinformatics (IBT) - online beginner's & intermediate Bioinformatics Courses, Makerere University
- 2012 - 2014 Laboratory Supervisor, Mycobacteriology (BSL-3) Laboratory, Makerere University, Kampala
- 2011 - 2014 Lecturer, International Health Sciences University, Kampala
- 2008 - 2012 Laboratory Technologist, Infectious Diseases Institute, Makerere University
- 2007 - 2009 Tutor, Nsambya School of Laboratory Technicians, Kampala

Other Experience and Professional Memberships

- 2024 - Wellcome Trust committee member for Infectious Diseases
- 2023 - Editorial Board Member, BMC Genomics & BMC Infectious Diseases Journals
- 2023 - Editor for Frontiers in Public Health Journal
- 2021 - Expert Reviewer for Africa Research Excellence Fund – AREF
- 2021 - Member, Wellcome Trust Surveillance and Epidemiology of Drug-Resistant Infections Consortium (SEDRIC)

- 2021 - Africa Task Force for Novel Coronavirus (AfTCOR), Africa CDC
- 2021 - EDCTP HIV Technical Working Group
- 2021 - African Society for Laboratory Medicine (ASLM)
- 2020 - Microbiology Society
- 2020 - African Association for Research and Control of Anti-Microbial Resistance "AAAMR"
- 2019 - The Public Health Alliance for Genomic Epidemiology (PHA4GE)
Member, African Centers of Excellence in Bioinformatics (ACE), a consortium of research and training centers facilitated by the NIH's National Institute of Allergy and Infectious Diseases
- 2019 - Diseases
- 2018 - Member, Genetics Society of America (GSA)
- 2017 - Associate Editor, BMC Infectious Diseases
- 2018 - Member, African Society of Human Genetics (AfSHG)
- 2017 - Member, B3Africa, 'Bridging Biobanking and Biomedical Research across Europe and Africa'
- 2017 - Member, Global Alliance for Genomics and Health (GA4GH)
Member, International Society for Computational Biology (ISCB) & African Society for Bioinformatics and Computational Biology (ASBCB)
- 2016 - Bioinformatics and Computational Biology (ASBCB)
- 2014 - Member, Makerere University/UVRI Infection, and Immunity Research
Member, Human Heredity and Health in Africa (H3Africa)

Honors

- 2023 - Emerging Leader of the Human Heredity and Health in Africa (H3Africa) Consortium
- 2020 - African Association for Research & Control of Anti-Microbial Resistance (AAAMR)
Anglophone Young Investigators Award 2020
- 2017 - Travel award - NYU Abu Dhabi Institute Statistical Genetics Conference, African Society of
- 2011 - Human Genetics
- 2012 - Graduate study scholarship for MSc in Immunology & Clinical Microbiology, Muljibhai
- 2005 - Madhvani Foundation
- 2008 - Undergraduate degree study scholarship, Makerere University, the Government of Uganda

Contribution to Science & Public Health

- As a Bioinformatics Implementation Science Expert at Africa CDC (<https://africacdc.org/people/gerald-mboowa/>) leading pathogen bioinformatics and data visualization (<https://nextstrain.org/groups/africa-cdc/>), I have participated in capacity building of SARS-CoV-2 whole-genome sequencing and analysis for Africa CDC's pathogen genomics program. Furthermore, under this role, I have promoted bioinformatics and genome sequencing as well as coordinated equipping National Public Health Institutes (NPHIs) with computing infrastructure in Africa and supported the development of a continental pathogen genomic data platform (<https://www.nature.com/articles/s41591-023-02266-y>). I have also coordinated the analysis and publication of 100,000 SARS-CoV-2 genomes from 53/55 African countries (<https://bit.ly/3DucASq>) involving over 400 researchers & more than 200 institutions in Africa. At least 40/55 African Union Member States have functional NGS platforms in their NPHIs by 2023 compared to 7 countries in 2019. Beyond short courses, I also pioneered the Pathogen Genomics & Bioinformatics fellowship program at Africa CDC which is oversubscribed and offers intermediate training throughout Africa (<http://bit.ly/3md2BL9> & <http://bit.ly/3MB1Fez>). I'm also supporting the satellite-based internet to improve genomic data sharing in Africa, a project under Africa CDC (<https://bit.ly/3RpZOLQ>). The aim is to attempt to address the limitations of poor internet connectivity and bandwidth within Africa. Unleashing the power of next-generation sequencing to safeguard public health across Africa is our paramount mission. Yet, a formidable hurdle stands in our path: the lack of swift and dependable internet access. This grant aims to shatter this barrier by facilitating the deployment of Starlink satellite internet within the Africa CDC's network of laboratories, wherever Starlink service is accessible. Our success will be gauged by specific metrics tailored to genomics and overall performance indicators. By enhancing internet connectivity in these vital hubs, we paved the way for seamless communication and transformative collaborations in Data Science, AI,

Machine Learning, and Tele-medicine. Together, we forge a brighter future for healthcare innovation in Africa.

- Our work on the first report of Whole-genome analysis of extensively drug-resistant *Mycobacterium tuberculosis* clinical isolates with Bedaquiline, Linezolid, and Clofazimine resistance from Uganda contributed additional data on drug resistance World Health Organization (WHO) catalog of mutations in *M. tuberculosis* complex & their association with drug resistance to new anti-TB drugs (<https://bit.ly/3ywsvgK>). This work has demonstrated the utility of next-generation sequencing (NGS) in the surveillance of acquired resistance in drug-resistant tuberculosis cases in low-income settings like Uganda. The WHO has now operationalized targeted next-generation sequencing for routine diagnosis of drug-resistant TB (<https://www.who.int/publications/i/item/9789240076372>)
- We developed rMAP (<https://bit.ly/36g809L>); a thorough easy-to-use resistome profiling bioinformatics pipeline for ESKAPE (*Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and *Enterobacter* species) pathogens using Illumina Whole-genome sequencing (WGS) paired-end reads. The impact of this tool so far has been a grant from PHA4GE grant to promote sustainable development in bioinformatics to support public health. This was awarded to Ivan Sserwadda the first author of this manuscript. This work has also motivated a group in Brazil to develop a web-based tool for the analysis of AMR from sequence reads called CABGen: Clinical Applied Bacterial Genomics Analysis System(<https://cabgen.fiocruz.br/en>).
- HIV Drug Resistance Bioinformatics Analysis Pipeline (HIV-DRIVES - HIV Drug Resistance Identification, Variant Evaluation, & Surveillance). Briefly, the global prevalence of resistance to the non-nucleoside reverse transcriptase inhibitors drug class emphasizes the need to fast-track the transition to the newer Dolutegravir-based regimens. To stop HIV drug resistance (HIVDR), different global stakeholders must do the following; (1) promote the availability of optimal medicines to treat HIV infections, (2) support retention in care and optimal adherence to antiretroviral therapy (ART), and increase access and use of viral load testing to know if HIV treatment is working, and (3) rapidly switch regimens in cases of confirmed treatment failure (<https://www.who.int/news-room/fact-sheets/detail/hiv-drug-resistance>) and (4) importantly, access to Next-Generation Sequencing (NGS) for HIVDR characterization and comprehensive profiling. COVID-19 catapulted routine NGS in many national public health laboratories in Africa (40 reference laboratories in Africa having NGS platforms) and this investment is poised to support genomic activities in different disease programs including HIV. A number of countries embracing NGS-HIVDR are facing the challenge of bioinformatics analysis and interpretation of the data for patient management. Our work on the impact of NGS on HIVDR testing among patients experiencing virological failure at the time of therapy switching in Uganda has demonstrated the role of NGS HIVDR testing. This work has great implications for HIV management in Africa, especially at a time when many countries are switching to Dolutegravir-containing regimens as the preferred first- & second-line ART regimens. Our work emphasizes that NGS HIVDR testing offers more comprehensive HIVDR than Sanger. We recommend the application of NGS HIVDR testing especially in individuals with viral non-suppression, including regimen switch if indicated to achieve favorable treatment outcomes. I followed up this work with a blog (<https://bit.ly/34Wbuji>) & a publication by Maria Namaganda in F1000Research 2022 titled NGS reveals low-abundance HIV-1 drug resistance mutations among patients experiencing virological failure at the time of therapy switching in Uganda (<https://bit.ly/3A6K8Eg>). The above work has led to the development of the HIV-DRIVES bioinformatics pipeline by our team (<https://github.com/MicroBioGenoHub/HIV-DRIVES>), an NGS-HIVDR bioinformatics pipeline has been developed and validated by our team using Illumina short-reads (<https://bit.ly/4bNdVRV>). We followed this work with a blog (<https://bit.ly/3SjEkQf>) on implementation of next-generation sequencing-based HIV drug resistance testing: enhancing antiretroviral treatment monitoring and public health outcomes.
- Knowledge exchange & mentoring: Beyond conventional indicators such as mentorship and training, I have promoted knowledge exchange among international researchers through social media posts which have led to collaborative networks. I work with other professionals to promote diversity and careers in science to young people through engaging talks, webinars, presentations to school children, & hands-on

science activities. This helps to inform students' career choices. I have also engaged and promoted my works through creative social media posts (<https://twitter.com/GeraldGmboowa>) that aim to demonstrate the role of bioinformatics and genomics such as (<https://bit.ly/47YhV0P> and <https://bit.ly/3w2Pu4l>)

Selected Publications

1. Nsubuga M, Galiwango R, Jjingo D, **Mboowa G**. Generalizability of machine learning in predicting antimicrobial resistance in *E. coli*: a multi-country case study in Africa. *BMC Genomics*. 2024 Mar 18;25(1):287. doi: 10.1186/s12864-024-10214-4. PMID: 38500034.
2. **Mboowa G**, Sserwadda I, Kanyerezi S, Tukwasibwe S, Kidenya B. The dawn of a cure for sickle cell disease through CRISPR-based treatment: A critical test of equity in public health genomics. *Ann Hum Genet*. 2024 Mar 22. doi: 10.1111/ahg.12558. PMID: 38517013.
3. Aruhomukama, D., Najjuka, C. F., Kajumbula, H., Okee, M., **Mboowa, G.**, Sserwadda, I., ... & Kateete, D. P. (2019). *bla* VIM-and *bla* OXA-mediated carbapenem resistance among *Acinetobacter baumannii* and *Pseudomonas aeruginosa* isolates from the Mulago hospital intensive care unit in Kampala, Uganda. *BMC infectious diseases*, 19(1), 853. PMID: 31619192
4. Aruhomukama, D., Sserwadda, I., & **Mboowa, G**. (2019). Investigating colistin drug resistance: The role of high-throughput sequencing and bioinformatics. *F1000Research*, 8. PMID: 31354944
5. **Mboowa, G.**, & Sserwadda, I. (2019). Role of genomics literacy in reducing the burden of common genetic diseases in Africa. *Molecular genetics & genomic medicine*, e776. PMID: 31131548
6. **Mboowa, G.**, Mwesigwa, S., Katagirya, E., Retshabile, G., Mlotshwa, B. C., Williams, L., ... & Kintu, B. N. (2018). The Collaborative African Genomics Network (CAfGEN): Applying Genomic technologies to probe host factors important to the progression of HIV and HIV-tuberculosis infection in sub-Saharan Africa. *AAS open research*, 1. PMID: 30714022
7. **Mboowa, G.**, Sserwadda, I., Amujal, M., & Namatovu, N. (2018). Human Genomic Loci Important in Common Infectious Diseases: Role of High-Throughput Sequencing and Genome-Wide Association Studies. *Canadian Journal of Infectious Diseases and Medical Microbiology*, 2018. PMID: 29755620
8. Retshabile, G., Mlotshwa, B. C., Williams, L., Mwesigwa, S., **Mboowa, G.**, Huang, Z., ... & Wayengera, M. (2018). Whole-Exome Sequencing Reveals Uncaptured Variation and Distinct Ancestry in the Southern African Population of Botswana. *The American Journal of Human Genetics*, 102(5), 731-743. PMID: 29706352
9. Sserwadda, I., Lukenge, M., Mwambi, B., **Mboowa, G.**, Walusimbi, A., & Segujja, F. (2018). Microbial contaminants isolated from items and work surfaces in the post-operative ward at Kawolo general hospital, Uganda. *BMC infectious diseases*, 18(1), 68. PMID: 29409447
10. Mlotshwa, B. C., Mwesigwa, S., **Mboowa, G.**, Williams, L., Retshabile, G., Kekitiinwa, A., ... & Mardon, G. (2017). The collaborative African genomics network training program: a trainee perspective on training the next generation of African scientists. *Genetics in Medicine*, 19(7), 826. PMID: 28383545

11. Erume, J., Roesel, K., Dione, M. M., Ejobi, F., **Mboowa, G.**, Kungu, J. M., ... & Elschner, M. (2016). Serological and molecular investigation for brucellosis in swine in selected districts of Uganda. *Tropical animal health and production*, 48(6), 1147-1155. [PMID: 27142028](#)
12. Jones-López, E. C., White, L. F., Kirenga, B., Mumbowa, F., Ssebidandi, M., Moine, S., **Mboowa, G.** & Thornton, C. S. (2015). Cough aerosol cultures of *Mycobacterium tuberculosis*: insights on TST/IGRA discordance and transmission dynamics. *PloS one*, 10(9), e0138358. [PMID: 26394149](#)
13. Ssengooba, W., Cobelens, F. G., Nakiyingi, L., **Mboowa, G.**, Armstrong, D. T., Manabe, Y. C., ... & De Jong, B. C. (2015). High genotypic discordance of concurrent *Mycobacterium tuberculosis* isolates from sputum and blood of HIV-infected individuals. *PloS one*, 10(7), e0132581. [PMID: 26176604](#)
14. Mugizi, D. R., Muradrasoli, S., Boqvist, S., Erume, J., Nasinyama, G. W., Waiswa, C., **Mboowa, G.** & Magnusson, U. (2015). Isolation and molecular characterization of Brucella isolates in cattle milk in Uganda. *BioMed research international*, 2015. [PMID: 25793204](#)
15. Dharan, N. J., Amisano, D., **Mboowa, G.**, Ssengooba, W., Blakemore, R., Kubiak, R. W., ... & Ellner, J. J. (2015). Improving the sensitivity of the Xpert MTB/RIF assay on sputum pellets by decreasing the amount of added sample reagent: a laboratory and clinical evaluation. *Journal of clinical microbiology*, 53(4), 1258-1263. [PMID: 25653410](#)
16. Ssengooba, W., Gelderbloem, S. J., **Mboowa, G.**, Wajja, A., Namaganda, C., Musoke, P., ... & Joloba, M. L. (2015). Feasibility of establishing a biosafety level 3 tuberculosis culture laboratory of acceptable quality standards in a resource-limited setting: an experience from Uganda. *Health research policy and systems*, 13(1), 4. [PMID: 25589057](#)
17. **Mboowa, G.**, Namaganda, C., & Ssengooba, W. (2014). Rifampicin resistance mutations in the 81 bp RRDR of *rpoB* gene in *Mycobacterium tuberculosis* clinical isolates using Xpert® MTB/RIF in Kampala, Uganda: a retrospective study. *BMC infectious diseases*, 14(1), 481. [PMID: 25190040](#)
18. **Mboowa, G.** (2014). Genetics of sub-Saharan African human population: implications for HIV/AIDS, tuberculosis, and malaria. *International journal of evolutionary biology*, 2014. [PMID: 25202468](#)
19. Wamala, D., Asiimwe, B., Kigozi, E., **Mboowa, G.**, Joloba, M., & Kallenius, G. (2014). Clinico-pathological features of tuberculosis due to *Mycobacterium tuberculosis* Uganda genotype in patients with tuberculous lymphadenitis: a cross-sectional study. *BMC clinical pathology*, 14(1), 14. [PMID: 24690344](#)
20. Lee, J., Armstrong, D. T., Ssengooba, W., Park, J. A., Yu, Y., Mumbowa, F., **Mboowa, G.**, & Chien, G. (2014). Sensititre MYCOTB MIC plate for testing *Mycobacterium tuberculosis* susceptibility to first- and second-line drugs. *Antimicrobial agents and chemotherapy*, 58(1), 11-18. [PMID: 24100497](#)
21. Asiimwe, B. B., Bagyenzi, G. B., Ssengooba, W., Mumbowa, F., **Mboowa, G.**, Wajja, A., ... & Joloba, M. L. (2013). Species and genotypic diversity of non-tuberculous mycobacteria isolated from children investigated for pulmonary tuberculosis in rural Uganda. *BMC infectious diseases*, 13(1), 88. [PMID: 23413873](#)
22. Jones-López, E. C., Namugga, O., Mumbowa, F., Ssebidandi, M., Mbabazi, O., Moine, S., ... & **Mboowa, G.** (2013). Cough aerosols of *Mycobacterium tuberculosis* predict new infection. A household contact study. *American journal of respiratory and critical care medicine*, 187(9), 1007-1015. [PMID: 23306539](#)

23. Ssengooba, W., Kateete, D. P., Wajja, A., Bugumirwa, E., **Mboowa, G.**, Namaganda, C., ... & Waako, J. (2012). An early morning sputum sample is necessary for the diagnosis of pulmonary tuberculosis, even with more sensitive techniques: a prospective cohort study among adolescent TB suspects in Uganda. *Tuberculosis research and treatment*, 2012. [PMID: 23304491](#)
24. **Mboowa, G.**, (2020). Current and emerging diagnostic tests available for the novel COVID-19 global pandemic. *AAS Open Res* 2020, 3:4. [PMID: 32537561](#)
25. Naluyange, R., **Mboowa, G.**, Komakech, K., Semugenze, D., Kateete, D. P., & Ssengooba, W. (2020). High prevalence of phenotypic pyrazinamide resistance and its association with *pncA* gene mutations in *Mycobacterium tuberculosis* isolates from Uganda. *Plos one*, 15(5), e0232543. [PMID: 32413052](#)
26. Amanya, S.B., Nyiro, B., Waswa, F., **Mboowa, G.**, et al. (2020). Variations in *Trim5a* and *Cyclophilin A* genes among HIV-1 elite controllers and non-controllers in Uganda: a laboratory-based cross-sectional study. *Retrovirology* 17, 19 (2020). [PMID: 32631377](#)
27. **Mboowa, G.**, & Inda, D. A. (2015). Seroprevalence of Syphilis among Human Immunodeficiency Virus Positive Individuals Attending Immune Suppressed Syndrome Clinic at International Hospital Kampala, Uganda. *International STD Research & Reviews*, 84-90
28. **Mboowa, G.** (2014). Tuberculosis and Genetics of Sub-Saharan Africa Human Population. *J Mycobac Dis*, 4(164), 2161-1068
29. **Mboowa, G.**, Ocheng, F., Okeng, A., & Bwanga, F. (2014). Periodontopathogenic bacterial species among patients with periodontal diseases at Mulago Hospital Dental Clinic in Kampala, Uganda: A cross-section study. *Journal of Dentistry and Oral Hygiene*, 6(6), 58-63
30. **Mboowa G**, Musoke D, Bulafu D, Aruhomukama D. Face-Masking, an Acceptable Protective Measure against COVID-19 in Ugandan High-Risk Groups. *Am J Trop Med Hyg*. Published online 2020. doi:<https://doi.org/10.4269/ajtmh.20-1174>. [PMID: 33319741](#)
31. **Mboowa G**, Sserwadda I, Aruhomukama D, (2020). Genomics and bioinformatics capacity in Africa: no continent is left behind. *Genome*. 0(0): 1-11. <https://doi.org/10.1139/gen-2020-0013>. [PMID: 33433259](#)
32. Aruhomukama D, Sserwadda I, **Mboowa G.** (2019). Whole-genome sequence analysis of *Vibrio cholerae* from three outbreaks in Uganda, 2014-2016. *F1000Research*, 8(1340), 1340
33. Aruhomukama D, Sserwadda I, **Mboowa G.** Whole-genome sequence analysis reveals the evolution of antimicrobial resistance in a Ugandan colistin-resistant *Acinetobacter baumannii*. *bioRxiv* 2020.06.18.159236
34. **Mboowa G**, Semugenze D, Nakabuye H, Bulafu D, Aruhomukama D. Efficacy of Face Masks Used in Uganda: A Laboratory-Based Inquiry during the COVID-19 Pandemic. *Am J Trop Med Hyg*. 2021 Mar 16:tpmd210030. doi: 10.4269/ajtmh.21-0030. [PMID: 33724922](#).
35. Mwesigwa S, Lesedi W, Gaone R, Katagirya E, **Mboowa G**, Mlotshwa B, Kyobe S, Kateete D, Wampande E, Wayengera M, Mpoloka S, Mirembe A, Kasvosve I, Koketso M, Kisitu G, Kekitiinwa A, Anabwani G, Joloba ML, Matovu E, Mulindwa J, Noyes H, Botha G, Brown C, Mardon G, Matshaba M, Collaborative African Genomics Network (CAfGEN) of H3Africa, and TrypanoGEN Research

Group of H3Africa. Unmapped exome reads implicate a role for Anelloviridae in childhood HIV-1 long-term non-progression. *npj Genom. Med.* 6, 24 (2021). [PMID: 33741997](#)

36. Seni J, Akaro IL, Mkinze B, Kashinje Z, Benard M, **Mboowa G**, Aruhomukama D, Sserwadda I, Joloba ML, Mshana SE, Kidenya BR. Gastrointestinal Tract Colonization Rate of Extended-Spectrum Beta-Lactamase-Producing Gram-Negative Bacteria and Associated Factors Among Orthopaedic Patients in a Tertiary Hospital in Tanzania: Implications for Infection Prevention. *Infect Drug Resist.* 2021;14:1733-1745. [PMID: 34007192](#)
37. Sserwadda I, **Mboowa G** 2021. rMAP: the Rapid Microbial Analysis Pipeline for ESKAPE bacterial group whole-genome sequence data. *Microbial Genomics.* 7(6):000583. doi:10.1099/mgen.0.000583. [PMID: 34110280](#)
38. **Mboowa G**, Aruhomukama D, Sserwadda I, Kitutu EF, Davtyan H, Owiti P, Kamau ME, Enbiale W, Reid A, Bulafu D, Kisukye J, Lubwama M, Kajumbula H. Increasing Antimicrobial Resistance in Surgical Wards at Mulago National Referral Hospital, Uganda, 2014-2018 - Cause for Concern? *Tropical Medicine and Infectious Disease* (2021). [PMID: 34069345](#)
39. **Mboowa G**, Sserwadda I, Bulafu D, Chaplain D, Wewedru I, Seni J, Kidenya B, Mshana S, Joloba M, Aruhomukama D. Transmission Dynamics of Antimicrobial Resistance at a National Referral Hospital in Uganda. *Am J Trop Med Hyg.* 2021 Jun 28:tpmd201522. doi: 10.4269/ajtmh.20-1522. [PMID: 34181567](#).
40. **Mboowa G**, Mwesigwa S, Kateete D et al. Whole-genome sequencing of SARS-CoV-2 in Uganda: implementation of the low-cost ARTIC protocol in resource-limited settings. *F1000Research* 2021, 10:598. [PMID: 34457243](#)
41. Nabisubi P, Kanyerezi S, Kebirungi G and **Mboowa G**. Knowledge and attitude of secondary school students in Nakaseke, Uganda towards HIV transmission and treatment. *AAS Open Res* 2021, 4:23. [PMID: 34458678](#)
42. Jjingo D, **Mboowa G**, Sserwadda I, Kakaire R, Kiberu D, Amujal M, Galiwango R, Kateete D, Joloba M, Whalen C. Bioinformatics Mentorship in a Resource Limited Setting. *Briefings in Bioinformatics* 2021. [PMID: 34591953](#)
43. Kabahita JM, Kabugo J, Kakooza F, Adam I, Guido O, Byabajungu H, Namutebi J, Namaganda MM, Lutaaya P, Otim J, Kakembo FE, Kanyerezi S, Nabisubi P, Sserwadda I, Kasule GW, Nakato H, Musisi K, Oola D, Joloba ML, **Mboowa G**. First report of whole-genome analysis of an extensively drug-resistant *Mycobacterium tuberculosis* clinical isolate with bedaquiline, linezolid and clofazimine resistance from Uganda. *Antimicrob Resist Infect Control.* 2022 May 12;11(1):68. doi: 10.1186/s13756-022-01101-2. [PMID: 35550202](#).
44. Omara EI, Kiwuwa MS, Balinandi S, Nyakarahuka I, Kiconco J, Kayiwa JT, **Mboowa G**, Jjingo D, Lutwama J. Genetic Diversity of Bundibugyo Ebolavirus from Uganda, and the Democratic Republic of Congo. *BioRxiv.* (2021)
45. Kiyaga, S., Kyany'a, C., Muraya, A., Smith, H.J., Mills, E.G., Kibet, C., **Mboowa, G.** and Musila, L., Genetic diversity, distribution, and genomic characterization of antibiotic resistance and virulence of clinical *Pseudomonas aeruginosa* strains in Kenya. *Frontiers in Microbiology*, p.699. [PMID: 35369511](#)

46. Tegally H, San JE, Cotten M, Moir M, Tegomoh B, **Mboowa G**, Nkengasong J, Wilkinson E. The evolving SARS-CoV-2 epidemic in Africa: Insights from rapidly expanding genomic surveillance. *Science*. 2022 Sep 15:eabq5358. doi: 10.1126/science.abq5358. [PMID: 36108049](#).
47. Happi C, Adetifa I, Mbala P, Njouom R, Nakoune E, Happi A, **Mboowa G** et al. (2022) Urgent need for a non-discriminatory and non-stigmatizing nomenclature for monkeypox virus. *PLoS Biol* 20(8): e3001769. [PMID: 35998195](#)
48. Perier, C., Nasinghe, E., Charles, I., Ssetaba, L. J., Ahyong, V., Bangs, D., **Mboowa G**,... & Schaletzky, J. (2022). Workshop-based learning and networking: a scalable model for research capacity strengthening in low-and middle-income countries. *Global Health Action*, 15(1), 2062175. [PMID: 35730550](#)
49. Achan, B., **Mboowa, G.**, Kwizera, R., Kateete, D. P., Kajumbula, H., & Bongomin, F. (2022). Medical Mycology dissertation topics require prioritization among Postgraduate Microbiology trainees of Makerere University, Uganda. *IJID Regions*, 3, 261-264. [PMID: 35755461](#)
50. Namaganda MM, Sendagire H, Kateete DP, Kigozi E, Nsubuga LM, Katabazi AF, Kabahita JM, Kakembo FE, Kanyerezi S, Castelnuovo B, Kambugu A, Ssewanyana I, Okirya C, Nabadda S, Joloba M, **Mboowa G**. Next-generation sequencing (NGS) reveals low-abundance HIV-1 drug resistance mutations among patients experiencing virological failure at the time of therapy switching in Uganda. *F1000Research* 2022, 11:901
51. Mutayoba BK, Hoelscher M, Heinrich N, Joloba ML, Lyamuya E, Kilale AM, Range SN, Ngowi BJ, Ntinginya NE, Mfaume SM, Wilfred A, Doulla B, Lyimo J, Kisonga R, Kingalu A, Kabahita JM, Guido O, Kabugo J, Adam I, Luutu M, Namaganda MM, Namutebi J, Kasule GW, Nakato H, Byabajungu H, Lutaaya P, Musisi K, Oola D, **Mboowa G** & Pletschette M. Phylogenetic lineages of tuberculosis isolates and their association with patient demographics in Tanzania. *BMC Genomics*. 2022;23(1):561. doi:10.1186/s12864-022-08791-3. [PMID: 35931954](#)
52. Kalanzi D, Mayanja-Kizza H, Nakanjako D, Semitala F, **Mboowa G**, Mbabali M, Kigozi E, Katabazi FA, Sserwadda I, Kateete DP, Achan B, Sewankambo NK, Muwonge A. Microbial characteristics of dental caries in HIV positive individuals. *Front Oral Health*. 2022 Sep 21;3:1004930. doi: 10.3389/froh.2022.1004930. [PMID: 36211252](#)
53. Nakku-Joloba, E., **Mboowa, G.**, Ssengooba, W., Kiyimba, A., Kigozi, E., Baluku, H., ... & Kateete, D. P. (2022). Prevalence and antimicrobial resistance profiles of *Neisseria gonorrhea* and *Chlamydia trachomatis* isolated from individuals attending STD clinics in Kampala, Uganda. *African Health Sciences*, 22(3), 62-71. [PMID: 36910377](#)
54. Kakooza F, Kiggundu R, **Mboowa G**, Kateete PD, Nsangi OT, Kabahita JM, Ssentalo Bagaya B, Golparian D and Unemo M (2023) Antimicrobial susceptibility surveillance and antimicrobial resistance in *Neisseria gonorrhoeae* in Africa from 2001 to 2020: A mini-review. *Front. Microbiol*. 14:1148817. [PMID: 37089569](#)
55. Kariuki EG, Kibet C, Paredes JC, **Mboowa G**, Mwaura O, Njogu J, Masiga D, Bugg TH and Tanga CM (2023) Metatranscriptomic analysis of the gut microbiome of black soldier fly larvae reared on lignocellulose-rich fiber diets unveils key lignocellulolytic enzymes. *Front. Microbiol*. 14:1120224. [PMID: 37180276](#)

56. Tukwasibwe, S., **Mboowa, G.**, Sserwadda, I. et al. Impact of high human genetic diversity in Africa on immunogenicity and efficacy of RTS,S/AS01 vaccine. *Immunogenetics* (2023). [PMID: 37084013](#)
57. Nabweyambo S, Kanyerezi S, Petterson JH, Katabazi FA, Ssekagiri A, Mwesigwa S, **Mboowa G**, Nakazzi F, Keesiga A, Adroma M, Bwanga F, McGovern N, Sande OJ, Nakimuli A. No association of a Vascular endothelial growth factor A (VEGFA) gene polymorphism with pre-eclampsia among pregnant women in Uganda. *BMC Genomics*. 2023 Mar 20;24(1):132. [PMID: 36941544](#).
58. Megan E. Carey, M. E., Dyson, Z. A., Argimón, S., Cerdeira, L., Yeats, C., Aanensen, D., **Mboowa, G.**, Baker, S., Tessema, S. K., Smith, A. M., Okeke, I. N., & Holt, K. E. (2023). Unlocking the Potential of Genomic Data to Inform Typhoid Fever Control Policy: Supportive Resources for Genomic Data Generation, Analysis, and Visualization. *Open Forum Infectious Diseases*, 10, S38-S46. [PMID: 37274533](#).
59. Christoffels A, **Mboowa G**, van Heusden P, et al. A pan-African pathogen genomics data sharing platform to support disease outbreaks. *Nat Med* 2023; 1–4. [PMID: 37161068](#)
60. Susan Nabadda Isaac Ssewanyana, Alisen Ayitewala, Aloysious Ssemaganda, Stephen Kanyerezi, Ivan Sserwadda, Pimundu Godfrey, Sofonias Tessema, **Gerald Mboowa**, Placide Mbala-Kingebeni, Dorcas Waruguru Wanjohi, Jean-Jacques Muyembe, Adrienne Amuri-Aziza, Jean Claude Makangara, Gradi Luakanda, Andrew Rambaut, Kakooza Francis. Preliminary analysis of selected Sudan Ebola Virus isolates from the 2022 Uganda outbreak. (<http://bit.ly/3YdVVdj>)
61. Sisay A, Tshiabuila D, van Wyk S, Tesfaye A, **Mboowa G**, Oyola SO, Tesema SK, Baxter C, Martin D, Lessells R, Tegally H, Moir M, Giandhari J, Pillay S, Singh L, Ramphal Y, Maharaj A, Pillay Y, Maharaj A, Naidoo Y, Ramphal U, Chabuka L, Wilkinson E, de Oliveira T, Desta AF, San JE. Molecular Epidemiology and Diversity of SARS-CoV-2 in Ethiopia, 2020–2022. *Genes*. 2023; 14(3):705. [PMID: 36980977](#)
62. Nyiro, B., Amany, S.B., Bayiyana, A, Wasswa F, Nabulime E, Kayongo A, Nankya I, **Mboowa G. et al.** Reduced CCR5 expression among Uganda HIV controllers. *Retrovirology* 20, 8 (2023). [PMID: 37231494](#)
63. Mpanga Kasonde, Joseph Mutale, Nchimunya Siabenzu, Otridah Kapona, Kunda Musonda, Roma Chilengi, Peter Mwansa, Frazer Mtine, Stephen Kanyerezi, Ivan Sserwadda, Sofonias Tessema, **Gerald Mboowa**. Genomic analysis of selected *Vibrio cholerae* isolates from the 2023 Cholera outbreak in Zambia: A use-case for integration of whole-genome sequencing in cholera outbreak response (<https://bit.ly/3O4gsPb>)
64. Sserwadda I, Kidenya BR, Akaro IL, Mkinze B, Mshana SE, Hashim SO, Isoe E, Seni J, Joloba ML, **Mboowa G**. Unraveling virulence determinants in extended-spectrum beta-lactamase-producing *Escherichia coli* from East Africa using whole-genome sequencing. *BMC Infect Dis* **23**, 587 (2023). [PMID: 37679664](#)
65. Kidenya BR, **Mboowa G**, Sserwadda I, Kanyerezi S, Nakafu E, Akaro IL, Mkinze B, Joloba ML, Seni J, Virulence genes and plasmid replicon profiles of selected β -Lactamases producing *Acinetobacter baumannii* from orthopedic patients and environment in a tertiary referral hospital in Tanzania, East Africa, *J Hosp Infect*. 2023. [PMID: 37729952](#)

66. **Mboowa G**. Reviewing the journey to the clinical application of bacteriophages to treat multi-drug-resistant bacteria. *BMC Infect Dis* 23, 654 (2023). [PMID: 37789281](#)
67. Carys J Redman-White, Kathrin Loosli, Vesa Qarkaxhija, Tim Nicholas Lee, **Gerald Mboowa**, Bryan A Wee and Adrian Muwonge, A Digital One Health framework to integrate data for public health decision-making, *IJID One Health*, (2023) doi:<https://doi.org/10.1016/j.ijidoh.2023.100012>
68. Muwanda F, Sendagire H, **Mboowa G**, Kateete DP, Achan B, Mupere E, Kafeero HM, Bagaya BS. A systematic review reveals that African children of 15-17 years demonstrate low hepatitis B vaccine seroprotection rates. *Sci Rep*. 2023 Dec 13;13(1):22182. doi: 10.1038/s41598-023-49674-1. [PMID: 38092870](#)
69. Djamal Hachim-Abdoulaye, Adrienne Amuri-Aziza, Gradi Luakanda-Ndelemo, Akil Bandali-Prince, Houlkeurbe Ngam-Daita, Anouar Mahamat-Moustaph, Emmanuel Lokilo-Lofiko, Dorcas Waruguru-Wanjohi, Eddy Kinganda-Lusamaki, Jean-Claude Makangara-Cigolo, Jean-Jacques Muyembe-Tamfum, **Gerald Mboowa**, Placide Mbala-Kingebeni, Oumar Ouchar-Mahamat, Tony Wawina-Bokalanga. First outbreak of Dengue virus fever in Chad, 2023 (<https://virological.org/t/first-outbreak-of-dengue-virus-fever-in-chad-2023/954>)
70. Obame-Nkoghe J, Agossou AE, **Mboowa G**, Kamgang B, Caminade C, Duke DC, Githeko AK, Ogega OM, Engone Elloué N, Sarr FB, Nkoghe D, Kengne P, Ndam NT, Paupy C, Bockarie M, Voua Otomo P. Climate-influenced vector-borne diseases in Africa: a call to empower the next generation of African researchers for sustainable solutions. *Infect Dis Poverty*. 2024 Mar 14;13(1):26. doi: 10.1186/s40249-024-01193-5. [PMID: 38486340](#)
71. **Mboowa G** (2024). Table 3. Various pathogens have been sequenced by institutions within and outside Africa, with the data accessible through the Sequence Read Archive (SRA) of the NCBI from multiple African countries. *figshare*. Dataset. <https://doi.org/10.6084/m9.figshare.25574040.v1>
72. **Mboowa G**, Kakooza F, Egesa M, Tukwasibwe S, Kanyerezi S, Sserwadda I, R Kidenya B, Kabahita JM, Namaganda MM, Nsubuga M, Nabisubi P, Ayitewala A, Kebirungi G, Nakafu E, Akwii NP. The rise of pathogen genomics in Africa. *F1000Res*. 2024 Sep 4;13:468. doi: 10.12688/f1000research.147114.2. [PMID: 39464779](#).
73. Benson M, Turyamuhika L, Mwesigwa A, Nalumaga PP, Kabajulizi I, Njovu IK, Mwebesa E, Luggya T, Ocheng F, Kateete DP, Itabangi H, **Mboowa G**, Sande OJ, Achan B. Distribution and antifungal susceptibility profile of oropharyngeal *Candida* species isolated from people living with HIV in the era of universal test and treat policy in Uganda. *Ther Adv Infect Dis*. 2024 May 28;11:20499361241255261. doi: 10.1177/20499361241255261. [PMID: 38812710](#).
74. Ndiaye M, Ndiaye M, Kane M, Balde D, Sankhé S, Mbanne M, Diop SMS, Ahmad U, **Mboowa G**, Sagne SN, Cisse M, Dia N, Sall AA, Faye O, Fall G, Faye O, Weidmann M, Diagne MM, Dieng I. CDC Triplex diagnostic assay underperforms in detection of circulating Chikungunya West African genotype. *J Clin Microbiol*. 2024 Jul 16;62(7):e0040524. doi: 10.1128/jcm.00405-24. Epub 2024 Jun 13. [PMID: 38869270](#).
75. Ndembu N, **Mboowa G**, Tessema SK, Tebeje YK, Kaseya J. The pandemic agreement: an African perspective. *Nature*. 2024 Jul;631(8021):505. doi: 10.1038/d41586-024-02317-5. [PMID: 39014037](#).
76. Kanyerezi S, Nabisubi P, Kebirungi G,... **Mboowa G** et al. Metagenomics insights into the microbial resistome and virulome composition of Kampala's wastewater [version 1; peer review: awaiting peer review]. *Open Res Africa* 2024, 7:8 (<https://doi.org/10.12688/openresafrika.15040.1>)

77. Sserwadda I, Kidenya BR, Akaro IL, Mkinze B, Mshana SE, Hashim SO, Isoe E, Seni J, Joloba ML, **Mboowa G**. Unraveling virulence determinants in extended-spectrum beta-lactamase-producing *Escherichia coli* from East Africa using whole-genome sequencing. *BMC Infect Dis* 23, 587 (2023). [PMID: 37679664](#)
78. Kidenya BR, **Mboowa G**, Sserwadda I, Kanyerezi S, Nakafu E, Akaro IL, Mkinze B, Joloba ML, Seni J, Virulence genes and plasmid replicon profiles of selected β -Lactamases producing *Acinetobacter baumannii* from orthopedic patients and environment in a tertiary referral hospital in Tanzania, East Africa, *J Hosp Infect*. 2023. [PMID: 37729952](#)
79. Kanyerezi S, Sserwadda I, Ssemaganda A, Seruyange J, Ayitewala A, Oundo HR, Tenywa W, Kagurusi BA, Tusabe G, Were S, Ssewanyana I, Nabadda S, Namaganda MM, **Mboowa G**. HIV-DRIVES: HIV drug resistance identification, variant evaluation, and surveillance pipeline. *Access Microbiol*. 2024 Jul 17;6(7):000815.v3. doi: 10.1099/acmi.0.000815.v3. [PMID: 39130735](#)
80. **Mboowa G**, Sserwadda I, Kanyerezi S, Tukwasibwe S, Kidenya B. The dawn of a cure for sickle cell disease through CRISPR-based treatment: A critical test of equity in public health genomics. *Ann Hum Genet*. 2024 Mar 22. doi: 10.1111/ahg.12558. Epub ahead of print. [PMID: 38517013](#).

Grants and research support

Muwonge, Adrian (PI)

Royal Society (RGS/R1/231137)

Piloting a digital one-health platform for AMR surveillance (Genopaths-Africa). The award aims to demonstrate and evaluate the feasibility and challenges of integrating One Health as a shared resource, to serve as catalyst for adopting digital One Health as a framework to support implementation of AMR national action plans

Role: Co-Investigator and amount awarded: \$88,000.00

Kateete, David (PI)

Award Number: U2RTW012116 Organization: Fogarty International Center

01/Sept/2021 - 30/August/2026

Harnessing Data Science for Health Discovery and Innovation in Africa (DS- I Africa) Research Training Program Fogarty International Research training award. Makerere University Data Science Research Training to Strengthen Evidence-based Health Innovation, Intervention and Policy (MAKDARTA) grant is awarded to my Ph.D. supervisor. I contributed to the writing and I'm currently one of the faculty on this grant. The grant's goal is to leverage the existing partnership between Makerere University and Johns Hopkins University to build a joint comprehensive Data Science Research Training program to Strengthen Evidence-Based Health Innovation, Intervention, and Policy in Uganda.

Role: Key personnel and amount awarded: **\$1,750,000** (<https://reporter.nih.gov/project-details/10490445>)

INV-061818 African Society for Laboratory Medicine (ASLM) & Africa Centers for Disease Control and Prevention (Africa CDC)

01/September/2023 - 30/September/2025

The Bill and Melinda Gates Foundation grant to pilot the use of High-Speed Internet Access for Public Health Genomics in Africa

Role: Co-Investigator and amount awarded: **\$255,642** (<https://bit.ly/3RpZOLQ>)

Sub-grant promoting sustainable development in bioinformatics to support public health

PHA4GE/2021-01

Sserwadda, Ivan (PI)

01/March/2022 - 31/March/2023

This grant is awarded to my graduate trainee to undertake whole-genome sequencing analysis of pan-drug resistant bacterial isolates from Kampala

Role: Co-Investigator and the amount awarded: **\$20,000** (<https://bit.ly/3TTZNid>)

EDCTP - TMA2020CDF-3159 – PHICAMS | The Infectious Diseases Institute (IDI)

Mboowa, Gerald (PI)

01/November/2021 - 30/Oct/2024

Career development fellowship in poverty-related diseases and child and adolescent health – 2020. This grant is looking at pathogen detection in HIV-infected children and adolescents with non-malarial febrile illnesses using a metagenomic next-generation sequencing approach in Uganda.

Role: Principal Investigator and the amount awarded: **\$170,000** (<https://bit.ly/3iZfioF>)

INV-047157 Africa Public Health Foundation (APHF) & Africa Centers for Disease Control and Prevention (Africa CDC)

01/January/2023 - 31/December/2025

The Bill and Melinda Gates Foundation grant to Africa PGI - *Cho*/Gen: Cholera Genomics Consortium II. The goal is to support the generation of evidence to inform pre-emptive oral cholera vaccine use in Africa

Role: Co-Investigator and amount awarded: **\$4,995,205.00** (<https://bit.ly/3ZzVJWX>)

INV-036413 African Society for Laboratory Medicine (ASLM) & Africa Centers for Disease Control and Prevention (Africa CDC)

01/November/2021 - 31/July/2023

The Bill and Melinda Gates Foundation grant to enhance the organic development of a data-sharing platform for pathogen genomics

Role: Co-Investigator and amount awarded: **\$577,333** (<https://bit.ly/3IKlrR0> & <https://bit.ly/3xKGqOE> & <https://bit.ly/3lzex9R>)

INV-036379 African Society for Laboratory Medicine (ASLM) & Africa Centers for Disease Control and Prevention (Africa CDC)

01/October/2021 - 31/July/2022

The Bill and Melinda Gates Foundation grant to pilot the use of rapid commercial assays for surveillance of known SARS-CoV-2 variants of concern in Africa

Role: Co-Investigator and amount awarded: **\$562,000** (<https://gates.ly/3vOmOsY> & <https://bit.ly/3j0Mmze>)

GCA/AMR/rnd2/058, Bill and Melinda Gates | Makerere University

Mboowa, Gerald (PI)

01/June/2019 - 01/May/2021

New Approaches to Characterize the Global Burden of Antimicrobial Resistance. The goal of this grant was to understand transmission dynamics and acquisition of antimicrobial resistance at referral hospitals and community settings in East Africa using conventional microbiology and whole-genome sequencing

Role: Principal Investigator and the amount awarded: **\$100,000** (<https://bit.ly/3D5E1OU>)

Mboowa, Gerald (PI)

14/Dec/2020 - 01/August/2021

Validating rMAP: A new rapid microbial bioinformatics pipeline to characterize global burden antimicrobial resistance. This work is funded by the African Association for Research and Control of Anti-Microbial Resistance "AAAMR" under the Young Investigators Award – 2020

Role: Principal Investigator and the amount awarded: **\$13,000** (<https://bit.ly/3SAbd9G>)

Kanyerezi, Stephen (PI)

01/Dec/2020 - 01/August/2021

My graduate trainee was awarded a grant through the African Doctoral Dissertation Research Fellowship Program Policy, Practice, and Solutions: Research Fellowship Opportunities in Sanitation

and Fecal Waste Management in East Africa to characterize microbial diversity and resistome in urban sewage using shotgun metagenomics in Kampala, Uganda
Role: Co-Principal Investigator and amount awarded: **\$12,000**

Kiragga, Agnes (PI)

01/July/2020 - 01/December/2020

The Infectious Diseases Institute at Makerere University responded to COVID-19 global pandemic by awarding small a grant to our team to leverage Ugandan COVID-19 Social and Print Media Memes to Optimize Preventive Interventions

Role: Co-Investigator and amount awarded: **\$20,000**

MAK/DVCFA/151/20, MAK-RIF COVID-19

Mboowa, Gerald (PI)

25/July/2020 - 14/December/2020

In response to COVID-19 global pandemic, the government of Uganda awarded research funds to Makerere University to undertake research on COVID-19 prevention. I was awarded a sub-grant to assess knowledge, attitudes, perceptions, and skills toward the use of face masks through a community-level perspective in Uganda.

Role: Principal Investigator and the amount awarded: **\$18,000** (<https://rif.mak.ac.ug/list-of-projects-awarded-under-the-special-mak-rif-covid-19-call/>)

SORT-IT, World Health Organization

Mboowa, Gerald (PI)

25/August/2020 - 31/January/2021

Trends in the antimicrobial resistance profiles in the surgical wards at Mulago national referral hospital in Uganda. This Structured Operational Research and Training Initiative (SORT-IT) award sought to make low-income countries “data rich, information-rich and action rich” thereby contributing to improving health care delivery and outcomes.

Role: Principal Investigator and the amount awarded: **\$3,141** (<https://bit.ly/3ObHZeh>)

Mboowa, Gerald (PI)

01/July/2019 - 01/May/2021

THRiVE-Research Enrichment Community and Public Engagement for Enhanced Impact (RECPE) Project. This project looked at examining and understanding secondary school students' knowledge and attitude towards HIV acquisition, transmission, and treatment in Nakaseke district, Uganda

Role: Principal Investigator and the amount awarded: **\$10,000**

107742/Z/15/Z, Training Health Researchers into Vocational Excellence in East Africa (THRiVE)

Sewankambo, Nelson (PI)

30/May/2017 - 01/June/2020

Developing Excellence in Leadership, Training and Science Fellowship funded by the Wellcome Trust and UK's Department for International Development as part of the Developing Excellence in Leadership, Training and Science Initiative (DELTAS), which aimed to improve health in Africa through research driven by the most urgent regional challenges. The objective was to build a critical mass of local research capacity for African priorities

Role: Research fellow and amount awarded: **\$50,000** (<https://bit.ly/3rWh26a>)

U54-AI110398-01A1, The Collaborative African Genomics Network (CAfGEN)

Joloba, Moses (PI)

08/August/2014 - 31/December/2016

Genomics approaches to study gene/environment interactions for HIV/AIDS. The objective of this project was to create a collaborative, multi-disciplinary, multi-institutional, inter-, and intra-country network of African scientists, clinicians, and researchers using genomics approaches to study gene/environment interactions for HIV/AIDS, its co-morbidities, and other diseases among diverse pediatric African populations

Role: Research fellow and amount awarded: **\$100,000**

Academic programs taught at Makerere University since 2009

HMN 3104	Cell & Molecular Biology - BSc. Human Nutrition program
IMB 1302	Fundamental Genetics & Molecular Biology - MBChB & Biomedical Sciences programs
CYT 3201	Molecular Diagnostics - BSc. Cytotechnology program
BBi 3205	Principles of Molecular Cell Biology & Biotechnology – BSc. Biomedical Engineering program
BBi 4204	Introduction to Bioinformatics & Functional Genomics – BSc. Biomedical Engineering program
BLT 3205	Essentials of Bioinformatics & Computational Biology – BSc. Biomedical Laboratory Technology program
MIM 7104	Molecular Diagnostics (Introduction to Genomics) - MSc. Immunology & Clinical Microbiology program
MSB7103	Bio-Unix Scripting – MSc & PhD Bioinformatics programs
MSB7214	Systems Biology - MSc & PhD Bioinformatics programs
PAT 8101	Genetics – MMED Pathology program

Other Roles

1. The African Population Cohort Consortium (APCC) Omics workstream (<https://ce-apcc.org/collaborators/>)
2. Editorial Board Member, BMC Genomics Journal (<https://bit.ly/3L9XJ2F>)
3. Guest editor for Bacteriophages against multi-drug resistant bacteria; *BMC Infectious Diseases* Journal (<https://www.biomedcentral.com/collections/bamrb>)
4. Associate editor at BMC Infectious Diseases Journal (<https://bit.ly/3qpTghF>)
5. Section Editor Journal of Public Health in Africa (JPHiA) (<https://publichealthinafrica.org/index.php/jphia/pages/view/editorial-team>)
6. I am a reviewer for the following scientific journals; Nature Scientific Reports, PLOS One, PLOS Genetics, the American Journal of Tropical Medicine and Hygiene, PLOS Neglected Tropical Diseases, African Health Sciences, BMC Infectious Diseases, Expert Review of Molecular Diagnostics, F1000Research, BioMed Research International, Molecular Genetics & Genomic Medicine, Wellcome Open Research
7. Editorial Board of antimicrobial resistance (specialty section of Frontiers in Tropical Diseases).
8. Reviewing grants for the National Institute for Health Research (NIHR) Global Health Policy and Systems Research Programme; Grant #133307 - Global Health Research Unit on Genomic Surveillance of AMR (<https://bit.ly/3QzyrLI>)
9. Academic Editor: Global Health, Epidemiology and Genomics Journal (<https://bit.ly/3eE3zfs>)

Work Experience

Current Position and Responsibilities/Activities

April 2021: Science Implementation Expert, Africa Centres for Disease Control and Prevention (<https://africacdc.org/people/gerald-mboowa/>)

Tasks

- Coordinated data infrastructure for SARS-CoV-2 sequencing, analysis, and sharing.
- Participate in training and workforce development
- Coordinate grants to countries to support genomic surveillance
- Coordinate dissemination of program data through publications, webinars, seminars, and conferences
- Writing grants to support genomic surveillance and review of progress made by countries toward building genomic surveillance capacities
- Maintaining the Africa PGI SARS-CoV-2 data dashboard
- Coordinate development of the pan-African pathogen genomics data platform
- Providing technical support for bioinformatics and improving the bioinformatics computing capacity of National Public Health Institutions in Africa
- Coordination of 100K SARS-CoV-2 Africa genomes publication (<https://bit.ly/3DucASq>)
- Represent Africa CDC at external technical events, forums, and conferences

- Promote bioinformatics and pathogen genomics for public health decision-making
- Writing grants and review of progress made by countries towards building genomic surveillance capacities such as CholGen: Cholera Genomics Consortium II (<https://bit.ly/3ZzVJWX>), and Real-time pathogen genomics data sharing to enhance outbreak detection (<https://bit.ly/3IKlrR0>)

Principal Investigator

The African Centre of Excellence in Bioinformatics and Data-Intensive Sciences, Uganda

(<https://ace.ac.ug/about/staff/>)

Sept 2019 – March 2021

Tasks

- Research grant application and administration
- Lecturing both post-graduate and undergraduate courses
- Examining Makerere University students' thesis and supervising their research
- Mentoring students in bioinformatics and genomics
- Promote bioinformatics at Makerere University
- Conducting research and other activities such as supervision of students

Research consultant

The Infectious Diseases Institute, Makerere University, November 2021

Tasks

- Research grant application and administration
- Engage with researchers within the Makerere research community at large, to generate interest in leveraging facilities at the ACE e.g. including bioinformatics-supported research questions in their projects
- Participate and take the lead in the analysis of genomic data generated at the institute and its collaborators in collaboration with researchers and principal investigators.
- Propagate bioinformatics adoption within Makerere University scientific community through demonstration of its utility in modern science.
- Supervise and mentor junior staff, students, and visiting scientists and provide bioinformatics technical support to staff and scientists at IDI and the wider University community.
- Participate as an organizer and/or instructor of the center's training activities; short-term (workshops) and long-term (degree courses) in bioinformatics or data-intensive sciences.
- Organize internship placements for data science and bioinformatics students at IDI in a bid to generate research outputs e.g. scientific manuscripts from analysis of readily available datasets.
- Participate in scientific writing, dissemination, and presentation of research findings.

Research Assistant and Doctoral Fellow

Makerere University College of Health Sciences

January 2009 - August 2019

Tasks

- Perform laboratory experiments and research.
- Sample collection, processing for microbiological isolation, DNA extraction, Acid-fast bacilli smear, microscopy, use of liquid TB culture, drug susceptibility testing, Nucleic Acid Amplification Tests (NAATs), and Xpert MTB/Rif.
- Coordinating laboratory biosafety including maintaining routine medical records for personnel such as Chest X-ray and Mantoux tuberculin skin test (TST).
- Training of undergraduate university students in laboratory procedures.
- Data management and maintaining files for several projects on *M. tuberculosis*, *M. bovis*, *Mycobacterium avium paratuberculosis* (MAP), and Brucella.

Lecturer

Clarke International University (<https://ciu.ac.ug/>), June 2011– August 2014

Tasks

- Training of undergraduate university students.

- Teaching assistant to undergraduate students in Molecular biology, Immunology, and Microbiology.
- Planning teaching, including lectures, seminars/tutorials, and learning materials.
- Meeting students individually to discuss their progress.
- Checking and assessing students' academic work.
- Pursuing research.
- Interviewing potential new students

Tutor

Nsambya School of Laboratory Technicians October 2008 – July 2012

Tasks

- Training of students and conducting laboratory experiments.
- Supervision of students' projects.
- Mentoring of students.
- Examining students.

Selected Presentations

1. Building resilient bioinformatics ecosystems in Africa during the 20th H3Africa Consortium Meeting held in Cape Town, South Africa at the Cape Town International Convention Centre (<https://bit.ly/446SR5X>)
2. Developing pathogen genomic sequencing capacity in Africa during the 2022 Grand Challenges Annual Meeting in Brussels, Belgium (<https://bit.ly/3CX6x7A>)
3. A revised COVID-19 Testing Strategy to ensure Transitioning from Emergency Response to Integration into Routine Healthcare Services in Africa, Accra, Ghana: Nov 17, 2022 (<https://bit.ly/3PF7tVD>)
4. Driving the response to EIDs in LMICs with genomics and bioinformatics during the European Society of Clinical Microbiology and Infectious Diseases in Lisbon, Portugal from April 25, 2022 (<https://bit.ly/46A77Wj>)
5. Applications of bioinformatics presented during the host-pathogen Interactions and Basic bioinformatics annual workshop organized by the Uganda Society of Health Scientists (USHS) on May 24th, 2019, at Hotel Africana, Kampala, Uganda
6. An oral presentation titled Applications of Bioinformatics during the Host-pathogen Interactions and Basic Bioinformatics Annual Workshop organized by the University of Georgia, Case - Western Reserve University and Department of Medical Microbiology, Makerere University from March 21st – 25th, 2018
7. Role of genomic education in reducing the burden of common genetic diseases in Africa presented during the 11th H3Africa consortium meeting March 21 – 25, 2018 in Entebbe, Uganda, (Poster presentation)
8. Host genetic polymorphisms associated with malaria resistance in HIV-infected children: a retrospective study from sub-Saharan Africa presented at the International Society for Computational Biology (ISCB) – Africa Student Council on October 10, 2017

9. Functional host genetic loci associated with pediatric HIV/AIDS disease progression in sub-Saharan Africa at the International Society for Computational Biology (ISCB) and African Society for Bioinformatics and Computational Biology (ASBCB) at Entebbe, Uganda; October 12, 2017 (<https://bit.ly/3m7KpNg>)
10. Functional host genetic loci important in HIV/AIDS disease progression in Ugandan children presented during the 9th UCSF - East Africa collaborative scientific symposium at the Infectious Diseases Institute, Mulago, January 20th, 2017
11. Exome sequencing of HIV-infected sub-Saharan African children identifies genetic loci important to AIDS rapid progression presented at the Molecular & Human Genetics Retreat on Thursday, January 14th, 2016 at the Moody Gardens Hotel, Galveston, Texas
12. Novel Host Genetic loci important to rapid HIV/AIDS disease progression in Ugandan children presented at the Human Heredity & Health in Africa (H3Africa) meeting at National Institutes of Health (NIH), 9000 Rockville Pike, Bethesda, Maryland, (October 11th - 14th, 2015)

My Ph.D. Thesis

Functional host genetic loci important in pediatric HIV-disease progression in sub-Saharan Africa populations (<https://bit.ly/2XpiwsT>)

Selected supervised graduate students

1. **Esther Nakafu**, (2021). MSc in Molecular Biology, Makerere University. Molecular characterization of carbapenem-resistant *Acinetobacter baumannii* clinical isolates from Mulago Hospital orthopedic ward
2. **Fredrick Kakembo**, (2020). MSc in Bioinformatics, Makerere University. Breast cancer-predisposing genetic variants from 50 Kenyan patients using Whole-exome sequencing
3. **Eric Gathirwa**, (2020). MSc in Bioinformatics, Makerere University. Functional characterization of lignocellulosic biomass degradation microbes from the black soldier fly larval gut microbiome
4. **Jupiter Kabahita**, (2020). MSc in Bioinformatics, Makerere University. Use of whole-genome sequencing to determine the prevalence of resistance-associated variants (RAVs) to the newly approved anti-tb drugs: Delamanid, Pretonamid, Bedaquiline, Clofazimine linezolid
5. **Shahiid Kiyaga**, (2020). MSc in Bioinformatics, Makerere University. Comparative genomics and antibiotic-resistant determinants profile of clinical *Pseudomonas aeruginosa* isolates from Kenya
6. **Emmanuel Mande**, (2020). MSc in Bioinformatics, Makerere University. Molecular profile of drug resistance of *C. neoformans* isolated from patients with HIV-associated cryptococcal meningitis in Uganda
7. **Maria Namaganda** (2020). MSc in Bioinformatics, Makerere University. Low Abundance Drug Resistant Variant Patterns Among Hiv-1 Patients with Virological Failure in Uganda
8. **Baker Lwasampijja**, (2020). MSc in Bioinformatics, Makerere University. Using deep learning to predict the function of lipopeptide antibiotics from their structure
9. **Paul Mbavu**, (2020). MSc in Bioinformatics, Makerere University. Determining the functional capacity of the bacterial lung microbiome in Ugandan chronic obstructive pulmonary disease

(COPD) patients using shotgun metagenomics.

10. **Isaac Omara**, (2020). MSc in Bioinformatics, Makerere University. Genetic diversity of Bundibugyo Ebolavirus from Uganda and the Democratic Republic of the Congo.
11. **Eva Akurut**, (2020). MSc in Bioinformatics, Makerere University. Reverse vaccinology and molecular docking as a tool to identify potential vaccine candidates against drug-resistant *Mycobacterium tuberculosis* and *Mycobacterium bovis*.
12. **Resty Naluyange**, (2019). MSc Immunology & Clinical Microbiology, Makerere University. High prevalence of phenotypic pyrazinamide resistance and its association with *pncA* gene mutations in *Mycobacterium tuberculosis* isolates from Uganda.
13. **Mary Nantongo**, (2019). MSc Immunology and Clinical Microbiology. Molecular diversity of HIV-1 among Long- Term Non-progressors attending MJAP-ISS clinic in Mulago
14. **Sharon Amanya**, (2019). MSc Immunology and Clinical Microbiology, Makerere University. Variations in *Trim5 alpha* and *Cyclophilin A* genes among HIV-1 elite controllers and non-controllers in Uganda: a laboratory-based cross-sectional study
15. **Ivan Sserwadda**, (2018). MSc Bioinformatics, Pwani University, Kenya. Transmission Dynamics of Antimicrobial Resistance at a National Referral Hospital in East Africa

Selected examined and supervised Ph.D. students

1. **Kintu Christopher**, (2024). Makerere University, Ph.D. in Biomedical Sciences. The predictive utility of polygenic risk scores for chronic kidney disease: Examiner (<https://events.mak.ac.ug/events/2024/05/03/340>)
2. **Moses Okee**, (2023). Makerere University, Ph.D. in Biomedical Sciences. Molecular Epidemiology of Multiple Drug Resistant Organisms (MDROs) in patients diagnosed with Maternal Sepsis in Uganda: Supervisor
3. **San Emmanuel James**, (2021). University of KwaZulu-Natal, Durban, South Africa, Ph.D. in Computational Biology. Analysis and Visualization of the Transmission Dynamics, Evolution and Spread of SARS-CoV-2 in African Populations: Examiner
4. **Moses Njagi Mwaniki**, (2021). MSc in Bioinformatics, Pwani University, exploring virus sequence diversity using genome graphs: Examiner
5. **Ruth Nanjala**, (2021). MSc in Bioinformatics, Pwani University, evaluating the accuracy of genotype imputation in the major histocompatibility complex region in selected african populations: Examiner
6. **Stephen Tukwasibwe**, (2021). Makerere University, Ph.D. in Molecular and Biotechnology. Role of Killer-cell immunoglobulin-like receptors (KIR) and Human leukocyte antigens (*HLA*) in transmission and severity of malaria in Uganda: Examiner (<https://x.com/MUIIPlus/status/1379752268652756995>)
7. **John J O Mogaka**, (2020). University of KwaZulu-Natal, Durban, South Africa, Ph.D. in Health Sciences. Modeling critical factors influencing precision medicine implementation at the health systems level in resource-constrained settings: External Examiner
8. **Fahad Muwanda**, (2020). Makerere University, Ph.D. in Biomedical Sciences. Childhood responses to Hepatitis B Vaccine in Uganda: The Role of Human Leukocyte Antigen (*HLA*) and T-Cell Receptor (TCR) diversity: Supervisor
9. **Benson Musinguzi**, (2020). Makerere University, Ph.D. in Biomedical Sciences. Molecular and

phylogenetic characterization of Candida species causing oropharyngeal Candidiasis in HIV infected patients in Southwestern Uganda: Supervisor

Contribution to community service

Selected Invited scientific presentations made

1. The 20th H3Africa Consortium Meeting, 27 Feb 2023, Cape Town, South Africa; Presented, “Building resilient bioinformatics ecosystems in Africa (<https://bit.ly/3XrDGA3>)
2. Technical Workshop to establish Genomic Surveillance Network in the Eastern Mediterranean Region (EMR) for Emerging & Re-Emerging Infectious Diseases, 01 Feb 2023, Amman, Jordan; Presented, “Current genomic surveillance network in Africa: Successes & Challenges”
3. 32nd European Congress of Clinical Microbiology & Infectious Diseases, which took place in Lisbon, Portugal on April 25, 2022, | Meet-the-Expert Session: Driving the response to EIDs in LMICs with genomics and bioinformatics (<https://bit.ly/36UCe59>)
4. Lung Health: Metagenomics, Next-Generation Sequencing & Bioinformatics. The day of Lung Science, March 20th, 2019 at Makerere University College of Health Sciences (<https://bit.ly/3jshnGh>)
5. Antimicrobial Resistance: Next-Generation Sequencing & Bioinformatics. Host-Pathogen Interaction Workshop, March 21st, 2019, at Kolping Hotel, Kampala

Bioinformatics and Genomics Initiatives in Africa

1. Coordinated several bioinformatics trainings in Africa: NGS_2022, NGS_2021, Int_BT_2020, IBT_2020, IBT_2019, Int_BT_2019, IBT_2016
2. PHA4GE Bioinformatics Pipelines & Visualization Working Group developing bioinformatics solutions for SARS-CoV-2 genomic analysis (<https://bit.ly/3pltkEg>)
3. Bioinformatics Graduate Curriculum Development at Makerere University
4. Genomics and Bioinformatics workshops organized
 - a) Bioinformatics & Next Generation Sequencing Techniques Short Course, March 2018 (<https://bit.ly/33dTyNI>)
 - b) Alliance for Global Health and Science and Makerere University – 2017 and 2018 Summer Workshops (<https://bit.ly/3mk6Z5z> & <https://bit.ly/3igJ9VI>)
 - c) Host pathogens interactions and basic Bioinformatics a Global Infectious Diseases Research Program, April 13th to 17th 2015 (<https://bit.ly/2FThk8Z>)
5. Bioinformatics Mentorship Programs (Computational and Molecular Epidemiology Training in TB and HIV in Uganda)
6. News / Media contribution
 - a) Capacity-building on disease surveillance underway in Accra (<https://bit.ly/3vMfujH>)
 - b) COG-Train Newsletter - February 2022 (<https://bit.ly/3B75CQu>)
 - c) Wellcome Connecting Science - first of its kind global Covid-19 genomics training program launches (<http://bit.ly/3Ye9n0N>)
 - d) Why HIV NGS? (<https://bit.ly/34Wbujj>)
 - e) New funding set to transform data science research and innovation (<https://go.nature.com/3CuUyLD>)

- f) Africa's struggle with inadequate COVID-19 testing, May 01st, 2020 (<https://bit.ly/31CpsSP>)
- g) COVID-19 Breath Test Trial Set for June, June 15th, 2020 (<https://bit.ly/3mitozU>)
- h) Nigerian scientists have developed a Covid-19 vaccine candidate but need funding for human trials October 2nd, 2020 (<https://bit.ly/3dTcMf7>)
- i) Researcher studies how long it takes for HIV positive person to develop AIDS (<https://bit.ly/2HAW9cD>)
- j) The world could learn a lot from how Africa is handling Covid-19 (<https://bit.ly/3qKa7gi>)
- k) The African feat against Covid-19 (<https://bit.ly/384pmFT>)
- l) Africans begin to take the reins of research into their own genomes (<https://bit.ly/3CmkHwq>)
- m) Two Nigerian laboratories have taken big steps to boost genetics medicine in Africa (<https://bit.ly/37XTvH2>)
- n) Ugandan researcher takes 2020 Anglophone Young Investigators Award (<http://bit.ly/34KDMu7>) & (<http://bit.ly/3ruDcuo>)
- o) Why Africa doesn't have its own Covid-19 vaccine (<https://bit.ly/3wSpCDU>)
- p) The trouble with Tuberculosis (<https://bit.ly/3Hw2TCx>)
- q) A new US-led malaria initiative has African scientists calling for the "decolonization" of donor funding (<https://bit.ly/3nlZDld>)
- r) Presentation during the World Health Summit Africa Regional Meeting: WS 03 - COVID-19 Variants on Jun 28, 2021 (<https://bit.ly/3oyCtr9>)
- s) Drivers of antimicrobial resistance in East Africa (<https://bit.ly/3z6y7OI>)

7. Community and public engagement activities

- a) Africa Pathogen Data Management & Exchange Platform (https://www.youtube.com/watch?v=YpQFh_ZtA4E)
- b) Diaries of SARS-CoV-2 Genomics Training – Webinar (<https://bit.ly/3QznoSm>)
- c) Expert advice for future pandemics via COG-Train (<https://www.youtube.com/watch?v=sxNhMwCglg>)
- d) What can we do better for the pandemics that may come? (<https://bit.ly/3RsXmrl>)
- e) Webinar "Africa PGI Multi-pathogen data management & sharing platform" (<https://bit.ly/3GXWqAH>)
- f) Session moderator for Pathogen Genomics to Control Diseases during the African Society for Laboratory Medicine (ASLM) 2021 Virtual Conference. Wednesday 17 November 2021
- g) Virtual conference on antimicrobial resistance (AMR) research organized by Nottingham Trent University (NTU), UK on Current Topics in Microbiology on Friday 25th September 2020 from 11.00 am to 1.00 pm (<https://bit.ly/34nqnF>)
- h) Dissemination of AMR Policy brief (<https://bit.ly/3o6kJnn> | <https://bit.ly/3u23Hu5>)
- i) I presented a topic titled Understanding Transmission Dynamics and Acquisition of Antimicrobial Resistance at Referral Hospitals and Community settings in East Africa using Conventional Microbiology and Whole-Genome Sequencing" during the Infectious Diseases Institute (IDI) Research forum on Thursday 27th February 2020.
- j) I conducted two antimicrobial resistance awareness seminars at Kyambogo University on Thursday 13th February 2020 and Saturday 15th February 2020
- k) I conducted an antimicrobial resistance awareness seminar at the School of Public Health, Makerere University on Tuesday 12th February 2020 (<https://bit.ly/3ogZuOp>)
- l) Lung Health: Metagenomics, Next-Generation Sequencing & Bioinformatics. The day of Lung Science, March 20th, 2019, at Makerere University College of Health Sciences (<https://bit.ly/3mgnWh2>)
- m) I carried out a community engagement exercise in Timuna SSS Nakaseke on February 11th, 2020. During this sensitized secondary school students on HIV/AIDS acquisition, transmission, and treatment. This was funded by the THRiVE Research Enrichment: Community and Public Engagement project
- n) I have conducted a project called MASK_UG where we have sensitized people in police barracks, hospitals, and markets on how to use face masks to prevent COVID-19 transmission (<https://idi.mak.ac.ug/idi-science-fair/>)

- o) Biosafety COVID-19 training for COVID-19 testing at Makerere University (<https://bit.ly/2Tj94SD>)
- p) The Mérieux Foundation and the London School of Hygiene & Tropical Medicine (LSHTM) jointly organized a 2-hour webinar on September 15, 2021, at 3 pm (CET) on the Laboratory capacity strengthening for genomic sequencing in LMIC (<https://bit.ly/3wQcUWm> & <https://bit.ly/3oDqdWz>)
- q) Genes can determine the years a person living with HIV will take to develop AIDS if not on treatment (<https://bit.ly/3bv3HsE>)
- r) Active Rotary Member at Kampala Rotary Club contributing to improving rural water and sanitation projects in Mukono District, Uganda
- s) Grant Writing mini workshop focusing on successes and failures of grant applications September 15th, 2020 (<https://bit.ly/37zxhN5> | <https://bit.ly/34nyV27> | <https://bit.ly/38Gpcsl>)

Referees

1. Anthony Mukwaya, Ph.D.
Research Fellow in Ophthalmology
Massachusetts Eye and Ear Infirmary
Department of Ophthalmology
243 Charles St
Boston MA 02114
Email: anthonymukwaya@yahoo.com / amukwaya@meei.harvard.edu
2. Collins K. Tanui, Ph.D.
Principal Technical Officer Pathogen Genomics
Africa CDC | African Union
Emails: collinstonui@gmail.com / tanuic@africa-union.org
3. Alan Christoffels
Director of the South African National Bioinformatics Institute
Western Cape, Cape Town, South Africa
Email: alan@sanbi.ac.za