

# Gerald Mboowa, Ph.D.

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

## Personal Statement

My scientific background has given me extensive experience in the genomics of infectious diseases. Briefly, as an investigator, I have worked on four research projects three of which are through 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) Cholera genomic surveillance in Africa (<https://bit.ly/3ZzVJWX>) while the fourth one is from the European and Developing Countries Clinical Trials Partnership (EDCTP) that is looking at pathogen detection in HIV-infected children with non-malarial febrile illnesses using metagenomic sequencing (<https://bit.ly/3KNjH9y>). 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 more than 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://bit.ly/3kyL5gk>) 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>). 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 an 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 and 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>). 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 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://ipg.africacdc.org/>) 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/>). 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.

## **Positions and Employment**

2021 - 2023 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**

2023 - Section Editor for the Journal of Public Health in Africa  
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)  
2021 - Microbiology Society  
2020 - African Association for Research and Control of Anti-Microbial Resistance "AAAMR"  
2020 - The Public Health Alliance for Genomic Epidemiology (PHA4GE)  
2019 - 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 - Member, Genetics Society of America (GSA)  
2019 - Associate Editor, BMC Infectious Diseases  
2018 - Member, African Society of Human Genetics (AfSHG)  
2017 - 2018 Member, B3Africa, 'Bridging Biobanking and Biomedical Research across Europe and Africa'  
2017 - Member, Global Alliance for Genomics and Health (GA4GH)  
2017 - Member, International Society for Computational Biology (ISCB) & African Society for Bioinformatics and Computational Biology (ASBCB)  
2016 - Member, Makerere University/UVRI Infection, and Immunity Research  
2014 - 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 Human Genetics  
2011 - 2012 Graduate study scholarship for MSc in Immunology & Clinical Microbiology, Muljibhai Madhvani Foundation  
2005 - 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/dr-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 39/55 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/3MB1Fcz>). 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. The strategic objective is to democratize the use of next-generation sequencing of pathogens on the African continent for timely public health action. One major barrier is access to fast and reliable internet. This grant supports installation and initial access to Starlink satellite internet in Africa CDC network of laboratories in countries where Starlink access is available and will measure success against genomics-specific and general KPIs. Improved internet connectivity at these laboratories will provide benefits beyond genomics including communication and collaborative projects in Data Science, AI, Machine learning, & Tele-medicine.,
- 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://aureus.procc.fiocruz.br/>).
- 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 recently 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.

- 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/37jtPYF>).
- I am very passionate about promoting applications of bioinformatics & genomics in Africa over the last five years and below are my selected sessions. Here is a compilation of some of the training workshops I have organized;
  - <https://twitter.com/GeraldGmboowa/status/1453017514926092292>
  - <https://bit.ly/34Wbuji>
  - <https://bit.ly/37jtPYF>
  - <https://bit.ly/3tUyA2n>
  - <https://bit.ly/34Dh3Dn>
  - <https://twitter.com/TheHackbio/status/1369568305913139202>
  - <https://twitter.com/THRiVEDELTA/status/1357261630795632640>
  - <https://twitter.com/IDIMakerere/status/1339100073817468930>
  - <https://twitter.com/GeraldGmboowa/status/1037740890834518016>
  - <https://twitter.com/GeraldGmboowa/status/1143898015905849350>
  - <https://twitter.com/GeraldGmboowa/status/1161214294467534848>
  - <https://twitter.com/kanyerezi30/status/1192734017268920320>
  - <https://twitter.com/GeraldGmboowa/status/1529052494776639488>
  - <https://twitter.com/AfricaCDC/status/1502951963385905160>
  - <https://mobile.twitter.com/GeraldGmboowa/status/1105813862195122177>

## Publications

1. 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](#)
2. Aruhomukama, D., Sserwadda, I., & **Mboowa, G.** (2019). Investigating colistin drug resistance: The role of high-throughput sequencing and bioinformatics. *F1000Research*, 8. [PMID: 31354944](#)
3. **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](#)
4. **Mboowa, G.**, Mwesigwa, S., Katagiriya, 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](#)
5. **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](#)
6. 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](#)
7. Sserwadda, I., Lukege, 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](#)



8. 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](#)
9. 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](#)
10. 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](#)
11. 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](#)
12. 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](#)
13. 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](#)
14. 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](#)
15. **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](#)
16. **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](#)
17. Wamala, D., Asiiimwe, 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](#)
18. 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](#)
19. Asiiimwe, 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](#)
20. 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](#)
21. 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](#)

22. **Mboowa, G.**, (2020). Current and emerging diagnostic tests available for the novel COVID-19 global pandemic. *AAS Open Res* 2020, 3:4. [PMID: 32537561](#)
23. 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](#)
24. 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](#)
25. **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
26. **Mboowa, G.** (2014). Tuberculosis and Genetics of Sub-Saharan Africa Human Population. *J Mycobac Dis*, 4(164), 2161-1068
27. **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
28. **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](#)
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30. 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
31. 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
32. **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](#).
33. 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](#)
34. 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](#)
35. 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](#)

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37. **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](#).
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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>)

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64. **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](#)
65. Adrian Muwonge, Carys J Redman-White, Kathrin Loosli, Vesa Qarkaxhija, Tim Nicholas Lee, **Gerald Mboowa**, Bryan A Wee. A digital One Health framework to integrate data for public health decision-making. *International Journal of Infectious Diseases (IJID) One Health*, 2023
66. Benson R. Kideny, Gerald Mboowa, Ivan Sserwadda, Stephen Kanyerezi, Esther Nakafu, Inyasi Lawrence Akaro, Baraka Mkinze, Moses L. Joloba, Jeremiah Seni. Whole genome-based characterization of extended-spectrum  $\beta$ -lactamase-producing *Enterobacter cloacae* from orthopedic patients and environment of a tertiary referral hospital in Tanzania. **Journal of New Microbes and New Infections, 2023**
67. Gerald Mboowa; Sofonias Kifle Tessema; Nicaise Ndembu; Yenew Kebede; Jean Kaseya. Africa in the era of pathogen genomics: unlocking data barriers. **Cell, 2023**
68. The first report of a multi-drug resistant-hypervirulent ST307 clone from genomic surveillance of extended-spectrum beta-lactamase-producing *Klebsiella pneumoniae* species complex in East Africa. **Nature Scientific Reports, 2023**
69. Fahad Muwanda, Hakim Sendagire, Gerald Mboowa, David Patrick Kateete, Beatrice Achan, Ezekiel Mupere, Hussein Mukasa Kafeero and Bernard Ssentalo Bagaya. African children 15 to 17 years of age demonstrate significantly reduced hepatitis B vaccine sero-protection rates: evidence from a systematic review and meta-analysis **Nature Scientific Reports, 2023**
70. Mike Nsubuga, Ronald Galiwango, Daudi Jjingo, Gerald Mboowa. Machine-learning generalizability in prediction of antimicrobial resistance in *E. coli*: a case study in Uganda. **BMC Genomics 2023**
71. Stephen Tukwasibwe, Shreeya Garg, Thomas Katairo, Victor Asua, Asimwe Brian Kagurutsi, Gerald Mboowa, David Giesbrecht, Gerald Tumusiime, Julius Businge<sup>6</sup>, David Alula, Julius Kasozi<sup>7</sup>, Ibrahim Wadembere, Emmanuel Arinaitwe, Joaniter I. Nankabirwa, Samuel L. Nsoby<sup>2</sup>, Moses R. Kamya, Bryan Greenhouse<sup>4</sup>, Grant Dorsey, Jeffrey A. Bailey, Jessica Briggs, Melissa Conrad, and Philip J. Rosenthal. Varied prevalence of antimalarial drug resistance markers in different populations of newly arrived refugees in Uganda. **Lancet Infectious Diseases, 2023**
72. Stephen Kanyerezi, Ivan Sserwadda, Aloysius Ssemaganda, Julius Seruyange, Alisen Ayitewala, Hellen Oundo, Wilson Tenywa, Brian Kagurusi, Godwin Tusabe, Stacy Were, Isaac Ssewanyana, Susan Nabadda, Maria Magdalene Namaganda, **Gerald Mboowa**. HIV-DRIVES: HIV Drug Resistance Identification, Variant Evaluation, & Surveillance Pipeline. **Microbial genomics, 2023**

## Grants and research support

### 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 - *Chol*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: **\$3,817,937.00** (<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/3Izex9R>)

**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, The 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: **\$100,000** (<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** (<https://bit.ly/31BjQIF>)

## 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. Editorial Board Member, BMC Genomics Journal (<https://bit.ly/3L9XJ2F>)
2. Guest editor for Bacteriophages against multi-drug resistant bacteria; *BMC Infectious Diseases* Journal (<https://www.biomedcentral.com/collections/bamrb>)
3. Associate editor at BMC Infectious Diseases Journal (<https://bit.ly/3qpTghF>)
4. 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
5. Editorial Board of antimicrobial resistance (specialty section of Frontiers in Tropical Diseases).
6. 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/3QzylLI>)
7. Academic Editor: Global Health, Epidemiology and Genomics Journal (<https://bit.ly/3eE3zfs>)

## Work Experience

### Current Position and Responsibilities/Activities

April 2021 – to date: Science Implementation Expert, Africa Centres for Disease Control and Prevention (<https://africacdc.org/>)

### 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>)

## Post-Doctoral Fellow

The African Centre of Excellence in Bioinformatics and Data-Intensive Sciences, Uganda (<https://ace.ac.ug/>)

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 – to date

### 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), Xpert MTB/Rif, BACTEC™ MGIT 960™
- 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), 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' project
- 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 24<sup>th</sup>, 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 11<sup>th</sup> 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 9<sup>th</sup> UCSF - East Africa collaborative scientific symposium at the Infectious Diseases Institute, Mulago, January 20<sup>th</sup>, 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 14<sup>th</sup>, 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 11<sup>th</sup> - 14<sup>th</sup>, 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. **Moses Njagi Mwaniki**, (2021). MSc in Bioinformatics, Pwani University, exploring virus sequence diversity using genome graphs
2. **Esther Nakafu**, (2021). MSc in Molecular Biology, Makerere University. Molecular characterization of carbapenem-resistant *Acinetobacter baumannii* clinical isolates from Mulago Hospital orthopedic ward
3. **Fredrick Kakembo**, (2020). MSc in Bioinformatics, Makerere University. Breast cancer-predisposing genetic variants from 50 Kenyan patients using Whole-exome sequencing
4. **Eric Gathirwa**, (2020). MSc in Bioinformatics, Makerere University. Functional characterization of lignocellulosic biomass degradation microbes from the black soldier fly larval gut microbiome
5. **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
6. **Shahiid Kiyaga**, (2020). MSc in Bioinformatics, Makerere University. Comparative genomics and antibiotic-resistant determinants profile of clinical *Pseudomonas aeruginosa* isolates from Kenya
7. **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
8. **Maria Namaganda** (2020). MSc in Bioinformatics, Makerere University. Low Abundance Drug Resistant Variant Patterns Among Hiv-1 Patients with Virological Failure in Uganda
9. **Baker Lwasampijja**, (2020). MSc in Bioinformatics, Makerere University. Using deep learning to predict the function of lipopeptide antibiotics from their structure
10. **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.
11. **Isaac Omara**, (2020). MSc in Bioinformatics, Makerere University. Genetic diversity of Bundibugyo Ebolavirus from Uganda and the Democratic Republic of the Congo.
12. **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*.
13. **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.
14. **Mary Nantongo**, (2019). MSc Immunology and Clinical Microbiology. Molecular diversity of HIV-1 among Long- Term Non-progressors attending MJAP-ISS clinic in Mulago
15. **Sharon Amanyanya**, (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

16. **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. **Judith Nanyondo**, (2023). Makerere University, Ph.D. in Public Health. Molecular Epidemiology of Multiple Drug Resistant Organisms (MDROs) in patients diagnosed with Maternal Sepsis in Uganda: Supervisor
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: External Examiner
4. **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: External Examiner
5. **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
6. **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
7. **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
8. **Owalla Tonny**, (2020). Makerere University, Ph.D. in Biomedical Sciences. Genome-wide association studies and polygenic risk prediction models of psychological distress among participants of African ancestry attending the NeuroGap study: 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 20<sup>th</sup>, 2019 at Makerere University College of Health Sciences (<https://bit.ly/3jshnGh>)
5. Antimicrobial Resistance: Next-Generation Sequencing & Bioinformatics. Host-Pathogen Interaction Workshop, March 21<sup>st</sup>, 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 13<sup>th</sup> to 17<sup>th</sup> 2015 (<https://bit.ly/2FThk8Z>)
5. Bioinformatics Mentorship Programs (Computational and Molecular Epidemiology Training in TB and HIV in Uganda)
6. Media contributions
  - a) COG-Train Newsletter - February 2022 (<https://bit.ly/3B75CQu>)
  - b) Wellcome Connecting Science - first of its kind global Covid-19 genomics training program launches (<http://bit.ly/3Ye9n0N>)
  - c) Why HIV NGS? (<https://bit.ly/34Wbuji>)
  - d) New funding set to transform data science research and innovation (<https://go.nature.com/3CuUyLD>)
  - e) Africa's struggle with inadequate COVID-19 testing, May 01<sup>st</sup>, 2020 (<https://bit.ly/31CpsSP>)
  - f) COVID-19 Breath Test Trial Set for June, June 15<sup>th</sup>, 2020 (<https://bit.ly/3mitozU>)
  - g) Nigerian scientists have developed a Covid-19 vaccine candidate but need funding for human trials October 2<sup>nd</sup>, 2020 (<https://bit.ly/3dTcMf7>)
  - h) Researcher studies how long it takes for HIV positive person to develop AIDS (<https://bit.ly/2HAW9cD>)
  - i) The world could learn a lot from how Africa is handling Covid-19 (<https://bit.ly/3qKa7gi>)
  - j) The African feat against Covid-19 (<https://bit.ly/384pmFT>)
  - k) Africans begin to take the reins of research into their own genomes (<https://bit.ly/3CmkHwq>)
  - l) Two Nigerian laboratories have taken big steps to boost genetics medicine in Africa (<https://bit.ly/37XTvH2>)
  - m) Ugandan researcher takes 2020 Anglophone Young Investigators Award (<http://bit.ly/34KDMu7>) & (<http://bit.ly/3ruDcuo>)
  - n) Why Africa doesn't have its own Covid-19 vaccine (<https://bit.ly/3wSpCDU>)
  - o) The trouble with Tuberculosis (<https://bit.ly/3Hw2TCx>)
  - p) A new US-led malaria initiative has African scientists calling for the “decolonization” of donor funding (<https://bit.ly/3nlZDld>)
  - q) Presentation during the World Health Summit Africa Regional Meeting: WS 03 - COVID-19 Variants on Jun 28, 2021 (<https://bit.ly/3oyCt9>)
  - r) Drivers of antimicrobial resistance in East Africa (<https://bit.ly/3z6y7OI>)
7. Community and public engagement activities
  - a) Diaries of SARS-CoV-2 Genomics Training – Webinar (<https://bit.ly/3QznoSm>)
  - b) Expert advice for future pandemics via COG-Train (<https://www.youtube.com/watch?v=sxNhMwCgIlg>)
  - c) What can we do better for the pandemics that may come? (<https://bit.ly/3RsXmIrl>)
  - d) Webinar “Africa PGI Multi-pathogen data management & sharing platform (<https://bit.ly/3GXWqAH>)
  - e) Session moderator for Pathogen Genomics to control diseases during the African Society for Laboratory Medicine (ASLM) 2021 Virtual Conference. Wednesday 17 November 2021
  - f) Virtual conference on antimicrobial resistance (AMR) research organized by Nottingham Trent University (NTU), UK on Current Topics in Microbiology on Friday 25<sup>th</sup> September 2020 from 11.00 am to 1.00 pm (<https://bit.ly/34nqunF>)

- g) Dissemination of AMR Policy brief (<https://bit.ly/3o6kJnn> | <https://bit.ly/3u23Hu5>)
- h) 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 27<sup>th</sup> February 2020.
- i) I conducted two antimicrobial resistance awareness seminars at Kyambogo University on Thursday 13<sup>th</sup> February 2020 and Saturday 15<sup>th</sup> February 2020
- j) I conducted an antimicrobial resistance awareness seminar at the School of Public Health, Makerere University on Tuesday 12<sup>th</sup> February 2020 (<https://bit.ly/3ogZuOp>)
- k) Lung Health: Metagenomics, Next-Generation Sequencing & Bioinformatics. The day of Lung Science, March 20<sup>th</sup>, 2019, at Makerere University College of Health Sciences (<https://bit.ly/3mgnWh2>)
- l) I carried out a community engagement exercise in Timuna SSS Nakaseke on February 11<sup>th</sup>, 2020. During this sensitized secondary school students on HIV/AIDS acquisition, transmission, and treatment. This was funded by THRIVE Research Enrichment: Community and Public Engagement project
- m) 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/>)
- n) Biosafety COVID-19 training for COVID-19 testing at Makerere University (<https://bit.ly/2Tj94SD>)
- o) 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>)
- p) Genes can determine the years a person living with HIV will take to develop AIDS if not on treatment (<https://bit.ly/3bv3HsE>)
- q) Active Rotary Member at Kampala rotary club contributing to improving rural water and sanitation projects in Mukono District, Uganda
- r) Grant Writing mini workshop focusing on successes and failures of grant applications September 15<sup>th</sup>, 2020 (<https://bit.ly/37zxhN5> | <https://bit.ly/34nyV27> | <https://bit.ly/38Gpcsl>)

## **Referees**

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