

Yusuph Mavura

Yusuph Mavura, MS.

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SKILLS:

Areas of expertise: Exome/Genome sequence data analysis, clinical/mendelian genetics, genetic epidemiology and complex disease genetics, population genetics, statistical genetics, RNASeq data analysis, causal inference using observational data, general epidemiology and study design, grant writing, technical writing.

Programming: Python, Bash Scripting, R, Stata, Perl.

Languages: English and Kiswahili

EDUCATION:

Ph.D.	University of California, San Francisco Epidemiology and Translational Science <i>Thesis Advisor:</i> Neil Risch, PhD	San Francisco, CA Expected, Dec 2024
M.S.	Georgia Institute of Technology Bioinformatics	Atlanta, GA Dec 2018
B.S.	Jomo Kenyatta University of Agriculture and Technology Biochemistry and Molecular Biology	Nairobi, Kenya Jun 2016

RESEARCH AND TECHNICAL EXPERIENCE:

University of California San Francisco <i>PhD Researcher</i>	Sep 2019 – Present
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- Junior Principal investigator and project lead: Assessed Diagnostic Yield from Genome and Exome Sequencing in ancestrally diverse prenatal, neonatal intensive care unit (NICU), pediatric patients suspected mendelian disorders in various healthcare settings in the NHGRI Clinical Sequencing Evidence Generating research (CSER) Phase II program, involving multiple centers and collaborators across the US.
- Principal investigator: Assessing Clinical Utility of Polygenic Risk Scores in Ancestrally Diverse Real-World Cohorts.
- Research assistant: Assessing association between genetic ancestry Diagnostic Yield from Exome Sequencing in ancestrally diverse newborns with suspected metabolic disorders in the Newborn Sequencing (NBSeqNext) program, UCSF.
- Project lead: Investigating the role of environmental and genetic factors in the effectiveness of antihypertensive drug therapy in ancestrally diverse individuals using AllofUS data.
- Research assistant/rotation student: Pleiotropy in cancer in a pan-cancer, cross-tissue transcriptome-wide association study (TWAS) using UKBiobank and Genetic Epidemiology research on Aging (GERA) cohort.
- Project lead in a collaborative study of the genomic rearrangement landscape of localized prostate cancer samples of Nigerian men of African descent.

Yusuph Mavura

National institutes of Health (NIH), Bethesda, MD

June 2018 – August 2018

Intern

- Conducted a Genome-Wide Association study (GWAS) which identified multiple new risk loci for pancreatic cancer in East Asian populations

Georgia Institute of technology, Atlanta, GA

August 2017 – December 2018

Master's Researcher

- Analysis of mutations in cancer driver genes in matched primary, metastatic and recurrent ovarian cancer whole-exome sequencing samples (WES)

SELECT PUBLICATIONS:

Mavura Y, Song H, Xie J, Tamayo P, Mohammed A, Lawal AT, Bello A, Ibrahim S, Faruk M, Huang FW. Transcriptomic profiling and genomic rearrangement landscape of Nigerian prostate cancer. *Prostate*. 2023 Jan 4;. doi: 10.1002/pros.24471. [Epub ahead of print] PubMed PMID: 36598071.

Kamran SC, Xie J, Cheung ATM, **Mavura MY**, Song H, Palapattu EL, Madej J, Gusev A, Van Allen EM, Huang FW. Tumor Mutations Across Racial Groups in a Real-World Data Registry. *JCO Precis Oncol*. 2021 Nov;5:1654-1658. doi: 10.1200/PO.21.00340. PMID: 34994651.

Oni-Orisan A, **Mavura Y**, Banda Y, Thornton TA, Sebro R. Embracing Genetic Diversity to Improve Black Health. *N Engl J Med*. 2021 Mar 25;384(12):1163-1167. doi: 10.1056/NEJMms2031080. Epub 2021 Feb 10. PMID: 33567186.

Mavura MY, Huang FW. How Cancer Risk SNPs May Contribute to Prostate Cancer Disparities. *Cancer Res*. 2021 Jul 15;81(14):3764-3765. doi: 10.1158/0008-5472.CAN-21-1146. PMID: 34266915.

Yusuph Mavura, Nuriye Sahin-Hodoglugil, Ugur Hodoglugil, Mark Kvale, Pierre-Marie Martin, Jessica Van Ziffle, W. Patrick Devine, Sara L. Ackerman, Barbara A Koenig, Pui-Yan Kwok, Mary E. Norton, Anne Slavotinek, Neil Risch. Diagnostic Yield of Exome Sequencing in a Diverse Pediatric and Prenatal Population is not Associated with Genetic Ancestry. *medRxiv*. Published online May 24, 2023:2023.05.19.23290066. doi:10.1101/2023.05.19.23290066. *In Press at npj Genomic Medicine*.

Yusuph Mavura, David Crosslin, Kathleen DM Ferar, John Greally, Lucia Hindorff, Gail P Jarvik, Sara Kalla, Barbara A Koenig, Mark Kvale, Pui-Yan Kwok, Mary Norton, Sharon E. Plon, Bradford C. Powell, Anne Slavotinek, Michelle L Thompson, Alice B Popejoy, Eimear E. Kenny, Neil Risch. Diagnostic yield of genome and exome sequencing in the ancestrally diverse CSER Phase II consortium is not associated with genetic ancestry in a variety of clinical settings. *In preparation*.

References available upon request