Abstract Information

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Participation :	symposium
Title of the Symposium :	Neuroimmune dysfunction and mental health outcomes: advances in immunopsychiatry in Africa
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Title :	Genetic risk for depression among Continental Africans: establishing a genetic database for depression in Africa

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Abstract : Depression is a significant global health issue, with genetic factors playing role in its etiology. Current genetic research on depression largely includes African Americans and Africans in Western countries, excluding continental Africans. This gap limits understanding of gene-environment interactions unique to Africa, perpetuating health disparities as indigenous Africans may miss out on tailored treatments. Our study addresses this gap by creating a genetic database for depression in Africa. The database combines data from four cohorts: (i) MRC/UVRI & LSHTM Uganda Research Unit's general population cohort (GPC, n=10,560), (ii) the NeuroGAP study (n=7,073), (iii) Malawi Epidemiology & Interventions Research Unit (MEIRU, n=1,700), and (iv) DepGenAfrica (n=14,000). The GPC is on-going and has so far enrolled 4,200 participants, assessing depression with the MINI (version 7.0.2) and to sequence participants? DNA using the blended genome-exome (BGE) technology. Preliminary data from 1,066 participants show a 23.3% lifetime depression prevalence. NeuroGAP is complete and has MDD and BGE sequence data on 7,073 participants (360 MDD cases) across Uganda, Kenya, Ethiopia, and South Africa. MEIRU includes genetic and depression data on 1,700 participants from Malawi. DepGenAfrica aims to recruit 10,000 cases and 4,000 controls across Nigeria, Malawi, and Ethiopia, using PHQ-9 for MDD assessment and 4x

whole-genome sequencing. Collectively, this database will encompass ~33K participants (~11K cases). The database will be used to investigate genetic risk factors for depression in continental Africa through genome-wide association study (GWAS) followed by post-GWAS analyses, develop a machine learning model for prediction and test causal inferences to MDD using Mendelian randomisation. Portability of genetic markers and polygenic risk scores across diverse ethnic backgrounds will also be investigated. This groundbreaking study has potential to illuminate the genetic underpinnings of depression within African populations, potentially uncovering novel loci and elucidating the transferability of genetic risk factors. Preliminary GWAS analysis among 1,000 participants from GPC has identified four novel single nucleotide polymorphisms associated with depression, of which one (rs1513848, near FHOD3 gene) has been replicated in a large GWAS study from the Psychiatric Genomics Consortium. Depression genetic research in Africa has potential to enhance global discovery and will potentially add to global efforts