

1284-P: Genetic and Lifestyle Associations with Cardiometabolic Traits and Diabetes Risk Factors in Ethnically Diverse Africans

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Abstract

African ancestry populations are underrepresented in human genetic studies, which leaves a knowledge gap about genetic and environmental risk factors for metabolic disease which can bias healthcare treatment. To alleviate these shortcomings, we conducted a series of genome-wide association studies of cardiometabolic traits in a diverse sampling of ~2,500 (max sample size) ethnically and geographically diverse Africans from populations practicing agriculturalist, hunter-gatherer, and pastoralist subsistence strategies. This study includes the Fulani pastoralists who have a relatively high incidence of adult-onset diabetes, despite having a low average body mass index (BMI). All individuals in the present study are sampled from rural populations that have relatively homogeneous lifestyles and diet within a community. This unique aspect to the study cohort allows for within- and between- group comparisons to identify trait variation attributable to genetics vs. lifestyle variation. Subjects were genotyped on a new African-focused SNP array from the Human Heredity and Health in Africa (H3 Africa) consortium. Genome-wide data was imputed based on a panel of African whole-genome sequences and data from the 1000 genomes project, resulting in a total of million variants for trait association analysis. Genetic associations were tested for BMI, blood pressure, and blood biomarkers of cardiometabolic health. We checked for replication of genotype/phenotype associations by comparison to large non-African cohorts studied for the same traits. We find that most associations identified in non-African populations do not replicate in the Africans. However, we identified a number of novel loci associated with cardiometabolic traits in the African populations. This study has important implications for identifying genetic risk factors that may play a role in metabolic disease in individuals of African ancestry. Funded by ADA Pathway award 1-19-VSN-02.