Epigenetic Age and Depressive Symptoms in African American Women with Cardiometabolic Conditions
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OBJECTIVES/GOALS: To examine the relationship between epigenetic age acceleration (EAA) and depressive symptoms in a cohort of African American women (AAW) with cardiometabolic conditions (CMC) including hypertension, diabetes, obesity; and to explore clinical phenotypes of depressive symptoms in this population.

METHODS/STUDY POPULATION: This secondary analysis utilized genomic and longitudinal clinical data from AAW in the InterGEN cohort (n = 250). EWAS data was used to estimate EAA based on the Horvath method, which incorporates the DNA methylation statuses at 353 specific CpG sites and regresses this epigenetic age on chronological age to determine EAA. Pearson’s correlations and linear regression will be used to examine the relationship between EAA and depressive symptoms and a linear mixed model will investigate this relationship over four time points during a two-year period. Clinical phenotyping of depressive symptoms will be explored using a cluster analysis.

RESULTS/ANTICIPATED RESULTS: Analysis is underway and will be complete by the time of presentation. We hypothesize that higher EAA will associate with higher depressive symptoms and poorer trajectories over time. We expect that this relationship may be mediated by the presence of CMCs. Exploratory analysis of clinical phenotyping is expected to provide descriptive evidence with respect to specific depressive symptoms or clusters which are most associated with EAA and CMCs. These results will address several gaps. To our knowledge, this is the first study to examine the relationship of EAA and depressive symptoms considering the role of CMC, in a historically understudied population with disproportionate risk.

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European Ancestry as a Risk Factor for Atrial Fibrillation in Puerto Rican Hispanics
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OBJECTIVES/GOALS: Atrial fibrillation (AF) not only is the most common sustained cardiac arrhythmia in clinical practice placing patients at increased risk for thromboembolic events. Hispanics despite having a higher risk factor burden for developing AF have a lower overall incidence and prevalence of AF when compared to Non-Hispanic Whites (NHW). European ancestry in the African American population was found to be an independent predictor for developing AF. Consequently, we have decided to evaluate if European ancestry is an independent risk factor for Puerto Rican Hispanics (PRH) METHODS/STUDY POPULATION: This project is a secondary analysis of a Puerto Rican population sample (n = 250) from ThePharmacogenetics of Warfarin in Puerto Ricans Study and A Genomic Approach for Clopidogrel in Caribbean Hispanics; and 1000Genome Project to establish a control group of healthy PRH population. We will evaluate the presence of 111 known single nucleotide polymorphisms (SNP) associated with AF Europeans and determine the frequency in PRH population sample. Using admixture informatic markers (AIM) analysis will determine the percentage of admixture. Statistical analysis will include the use of Pearson Product-Moment Coefficient correlation analysis and multivariate regression.

RESULTS/ANTICIPATED RESULTS: We anticipate that higher-frequency of AF associated European SNPs and overall higher percentage of European admixture will be associated with atrial fibrillation in PRH patients.

DISCUSSION/SIGNIFICANCE OF IMPACT: The expected outcomes for this study are to identify the frequency of known genetic loci associated with AF Europeans and validate their use PRH population for machine learning risk factor models.