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| **eMERGE Network: Manuscript Concept Sheet** | | | **m** |
| **Reference Number**  *(to be assigned by CC)* | NT413.2 | |  |
| **Submission Date** | 01/13/2022 | |  |
| **Project Title** | Genomic Variance of Type 2 Diabetes Mellitus in African Americans | |  |
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| **All Other Authors** | UAB: Marguerite (Ryan) Irvin; Hemant Tiwari; Nita A. Limdi; Amit Patki  MGH: Elizabeth W. Karlson; Tian Ge; James B. Meigs  Other eMERGE investigators interested in the project | |  |
| **Sites Participating** | UAB, Mass General Brigham, and any other eMERGE sites that want to participate | |  |
| **Background / Significance** | Diabetes refers to a heterogeneous group of metabolic and health conditions characterized by glucose dysregulation and defects in insulin secretion and/or insulin action(1). Chronic hyperglycemia has been associated with long-term damage, dysfunction, and failure of several organs, including the kidneys, heart, and blood vessels(2), and is a major risk factor for cardiovascular disease, particularly coronary heart disease and stroke(3). In the United States, type 2 diabetes (T2D) is the most common form, which constitutes 90-95% of cases (1). T2D is more often associated with increased age (4); however, the T2D epidemic can largely be attributed to a worldwide increase in obesity(5).  It is well established that T2D clusters in families and the risk of developing T2D depends on both genetic and environmental factors. In the Framingham Heart Study, having a first degree relative conferred 3.4 times increased risk of T2D compared to the general population, which increased to a 6.1 times increase if both parents were affected (6). The genetic nature of the disease is supported by stronger heritability in monozygotic twins compared to dizygotic twins in previous studies (7-10). A 2005 study demonstrated that family history, together with a BMI ≥30 kg/m2 and fasting plasma glucose ≥5.5 mmol/L, is associated with a significantly increased risk of T2D compared to those with one or two risk factors (hazard ratio (HR) (95% CI) 3.7 (2.3-6.1), p<0.0001)(11). Furthermore, African Americans (AAs) tend to have higher mortality rates and a higher risk of T2D complications compared to individuals of European descent, where AAs are at least twice as likely to die due to T2D (12, 13).  Narrow-sense heritability is the proportion of phenotypic variance due to additive genetic variation. Traditionally, heritability has been estimated from family-based studies, which have suggested for many complex traits that much of the phenotypic variance is due to additive genetic variance(14, 15). However, these family-based heritability estimates may be biased by factors shared by close relatives, such as non-additive genetic and common environmental effects(15). Previous heritability estimates of T2D and related clinical traits (e.g. fasting glucose, fasting insulin) have varied between 25-80%, depending on the study and follow-up periods, but have been calculated predominately in individuals of European ancestry (2, 16-19).  Genetic correlations are genome-wide aggregate effects of causal variants affecting related traits. In the past, genetic correlations between complex traits were estimated from pedigree studies, but estimates from family designs can also be confounded by shared environmental factors. Statistical methods that used GWAS based on linear mixed models to obtain unbiased estimates of the genetic correlation between pairs of quantitative or binary traits, are now the standard to give insight into genetic correlation (20). Previous studies have used these approaches to estimate the genetic correlation between chronic cardiometabolic diseases and traits in large samples of EAs. For instance, the joint risk of T2D and hypertension was evaluated in the Wellcome Trust Case Control Consortium (positive correlation ~0.31; SE 0.14; *p*=0.024)(21). Similar estimates have not been reported among AAs.  In the present study, we seek to capture the T2D variance associated with genetic variation from >28,000 AA participants in the Reasons for Geographic and Racial Differences in Stroke (REGARDS) study, the Genetics of Hypertension Associated Treatments (GenHAT) study, the Warfarin Pharmacogenomics Cohort (WPC) and the electronic medical records and genomics network phase III (eMERGE III), making the proposed study the largest study to estimate T2D heritability in AAs. | |  |
| **Outline of Project** | UAB will lead narrow-sense heritability analyses for 28,784 individuals of African ancestry across the REGARDS study (2,683 T2D cases and 6,066 controls), the GenHAT study (2,776 T2D cases and 4,132 controls), the WPC (300 T2D cases and 355 controls), and eMERGE III (2,688 T2D cases and 9,784 controls). We will compare these estimates to those we calculate in the subset of individuals of European descent from the REGARDS study (310 T2D cases, 1,237 controls) and the WPC (325 cases, 659 controls). We will also evaluate the bivariate genetic correlation between T2D and a cluster of related cardiometabolic traits (CKD, HTN, Obesity).  First, we will harmonize the T2D definition across all AA datasets, using T2D ICD codes, a single measurement of glucose (fasting glucose ≥ 126 mg/dL or non-fasting glucose ≥ 200 mg/dL) or use of any glucose-lowering medications.  Second, we will utilize two heritability estimating toolkits: the genome-wide complex trait analysis (GCTA) (22) and LDAK (23), to estimate the genetic component of phenotypic variance that is explained by the additive genetic effects using the available TOPMed imputed genetic variants.  We will compare our heritability estimates to previously published estimates in European populations, as well as in our REGARDS/WPC European dataset.  Lastly, we will explore the GCTA toolkit to conduct bivariate genome-based restricted maximum likelihood (GREML) to estimate the genetic correlation between T2D and 1.) BMI, 2.) hypertension, and 3.) chronic kidney disease using eMERGE data where cohort sample size allows. | |  |
| **Desired Data - Common Variables\***  *(Available from the CC)* | Demographics  ICD9/10 codes  CPT codes  Phecodes  BMI | Common Variable Labs  Common Variable Meds  Other: Case/Control status on Phase I and Phase II phenotypes |  |
| **Other Desired Data *(Available from participating sites)*** | *Please specifically list out any data elements that participating sites would collect or extract from clinical or other sources for this project (i.e. not common variables above)* | |  |
| **Desired Genetic Data** | eMERGE I-III Merged set (HRC imputed, GWAS)  eMERGE PGx/PGRNseq data set  eMERGEseq data set (Phase III)  eMERGE Whole Genome sequencing data set  eMERGE Exome chip data set  eMERGE Whole Exome sequencing data set  Other (not listed above): | |  |
| **Does project pertain to an existing eMERGE Phenotype?** | Yes, if so please list: Type 2 Diabetes Mellitus  No | |  |
| **Planned Statistical Analyses** | Using GCTA Toolkit to estimate heritability using imputed genetic variants:   1. Construct a genomic relationship matrix (GRM) within the GCTA toolkit, as previously described (15, 22). 2. Detect cryptic relatedness among participants. Remove individuals at relatedness values > 0.025. 3. Generate top 10 principal components using EIGENSTRAT (24) to account for genetic ancestry in mixed models (for use as covariates). 4. Estimate narrow-sense heritability using mixed models, where T2D phenotypic covariance between any two individuals in a study will be modeled as a function of the genomic relatedness of the individual. We will include age, sex and genetic ancestry covariates as fixed effects.   Generate heritability estimates using LDAK using imputed genetic variants:   1. Calculate kinship matrix for each study 2. Estimate the heritability contributed by each kinship matrix using the restricted maximum likelihood (REML) or phenotype-correlation, genotype-correlation (PCGC) regression (while REML is generally preferred because it produces the most precise estimates of heritability, i.e. the smallest standard deviation, it is more computationally intensive and makes more assumptions, i.e. the effect sizes are Gaussian, when compared to PCGC. Therefore, PCGC produces less-biased estimates for binary traits)(23, 25). We will adjust for age, sex, and genetic ancestry.   Investigate the genetic correlation between T2D and comorbid traits:   1. Using bivariate-GREML in GCTA, we will calculate the genetic correlation of T2D and BMI, hypertension, and chronic kidney disease in the eMERGE AA dataset. | |  |
| **Ethical Considerations** | N/A | |  |
| **Target Journal** | PLoS Genetics | |  |
| **Milestones**  *(This section should include the key dates for completion of project, including approval, project duration, draft completion, and submission.)* | * 01/2022: Perform narrow-sense heritability estimates for T2D on eMERGE III * 01/2022: Perform a combined, narrow-sense heritability estimate for T2D on participants from eMERGE III, GenHAT, WPC, and REGARDS. * 02/2022: Perform genetic correlation analyses * 02/2022: Manuscript draft completion * 03/2022: Manuscript draft submission | |  |

**\*Common Variables available across all datasets:**

* Demographics: sex, year of birth, a decade of birth, race, ethnicity
* Codes: (repeated values & age at the event): ICD9/10, CPT, Phecodes
* BMI: (repeated value & age at the event) height, weight, BMI, for potential sensitivity analyses
* HTN: (repeated value & age at event): SBP, DBP, HTN case-control status
* CKD: (repeated value & age at event): eGFR, albuminuria
* Medications: (medication name, repeated, & age at event) Blood pressure medications for adjustment to baseline blood pressure values
* Other: Case/Control status on Phase I and Phase II phenotype: only on GWAS dataset participants

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