

## **GENETIC AND ELECTRONIC MEDICAL RECORDS TO PREDICT OUTCOMES IN HEART FAILURE PATIENTS: BRIDGING BRAZILIAN AND UNITED KINGDOM GENETIC EPIDEMIOLOGY IN HEART FAILURE PATIENTS BRIDGING BRAZILIAN AND UNITED KINGDOM GENETIC EPIDEMIOLOGY IN HEART FAILURE**

Studies adopting electronic medical records (EMR) and genomic information are becoming widespread. Through this new modality of research, it is possible to study how genetic variants influence susceptibility towards chronic conditions and can improve patient care. Both Brazil and UK are developing projects towards using this information to predict different outcomes in heart failure patients. Our aim is to develop a collaborative project using Brazilian heart failure patients with genome-wide data already available, conduct genome-wide association studies (GWAS) for derivation of target hits associated with heart failure-related phenotypes and use UK-based cohort studies to validate the hits disclosed. Methods: patients between 18 and 80 years old with heart failure diagnosis of different etiologies and left ventricular ejection fraction < 50%, with already generated GWAS data will be eligible for enrollment on the study. GWAS analysis will be conducted using as dependent variables, etiology, left ventricular ejection fraction and combined incidence of cardiovascular outcomes (all-cause mortality, cardiovascular mortality, hospitalization for worsening heart failure and current medication use). The discovery phase will use data on 1,000 Brazilian patients. We will investigate the effects of multiple data imputation algorithms (using 1000 genomes data with or without Brazilian genomes). Main hits will be tested against available UK-cohort studies in a second-stage analysis. Expected Results: to create a UK-Brazil working group focused on the development and implementation of algorithms for validation and application of medical routines using genetic information for heart failure management. Moreover, to build capacity of young researchers, to do a pilot study of plasma or serum samples on metabolomics with metabolon US platform and with a proteomics platform and 10 show proof of concept with Brazilian GWAs data using Brazilian sequencing data for imputation and the impact of population stratification on known genetic hits for a well-established trait available in the Brazilian cohort.

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### ABOUT THE PROJECT

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