Abstract

TITLE: The Role of the University of Colorado Human Cardiac Tissue Bank (UC-HCTB) in the Transomics for Precision Medicine (TOPMed) Program

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ABSTRACT BODY:

Purpose of Study: Tissue specific biorespositories are expensive yet valuable entities that enable critical biological studies of human diseased tissue. The University of Colorado Human Cardiac Tissue Bank (UC-HCTB) was established over 30 years ago to collect human cardiac samples. The extensive UC-HCTB has joined the Transomics for Precision Medicine (TOPMed) study sponsored by the NIH-NHLBI. TOPMed aims to sequence the entire genome, transcriptome, and proteome of human samples to establish a robust, publicly-available dataset for biological discovery and hypothesis testing of NHLBI focused diseases, akin to the established Cancer Genome Atlas (https://cancergenome.nih.gov/). Here, we present the study design of the HC-HCTB TOPMed collaboration and present early 'omic' data related to human heart failure genomics.

Methods Used: 1078 human heart samples from the IRB-approved UC-HCTB are approved for submission. Tissue selection is from left ventricle samples harvested at the time of orthotopic heart transplantation or implantation of a left ventricular assist device (LVAD). Whole genome and transcriptome sequencing will be done in phase one of the project.

Summary of Results: The UC-HCTB contains tissue from 1,343 unique patients. Of these patients, 860 have complete clinical and demographic data on age, sex, race, year of transplant, and diagnosis. The 860 samples include 591 (69.7%) failing and 269 (31.3%) non-failing hearts. Common diagnoses include: ischemic cardiomyopathy (26.7%), idiopathic dilated cardiomyopathy (22.7%), familial cardiomyopathy (4.3%), and retransplant (3.8%). The failing and non-failing samples are 21.7% and 52.8% female respectively. The racial distribution among the failing hearts is 77.5% White, 9.6% Black, 9.1% Hispanic, and 2.4% Asian.

Conclusions: Initial studies include DNA and RNA sequencing; subsequent, planned studies include metabolomic and proteomic analysis. We present data on the analyses of disease versus control states and within-disease, subgroup analyses. Additional, planned analyses will include studying gender and racial differences in gene expression.