Published on *NHLBI Trans-Omics for Precision Medicine* (https://topmed.nhlbi.nih.gov)

TMF: Deciphering rare non-coding lipid associations using whole genome sequencing meta- analysis

Principal Investigator: Margaret Sunitha Selvaraj, PhD

Project Title: Deciphering rare non-coding lipid associations using whole genome sequencing metaanalysis

Abstract: High blood lipids are heritable risk factors for cardiovascular diseases, the leading cause of death worldwide. Recent genome wide association studies (GWAS) have identified hundreds of loci associated to blood lipid levels. Meta-analysis of these individual cohorts from multiple-ancestral groups has paved way to the identification of unexplored loci, improved fine mapping of functional variants and increased understanding of polygenic contributions. However, GWAS are robust for common variants discovery, whereas the rare variants, especially rare non-coding variants across the genome are not well studied. Whole genome sequencing (WGS) data provides a platform to study rare non-coding variants, but the difference in sample sizes between meta-analyzed array-genotype GWAS with 1.65 M individuals and whole genome sequencing studies camouflages the contribution of rare non-coding variation to blood lipid levels. Therefore, to gain maximum insights from WGS datasets, here we propose to conduct meta-analysis using whole genome data from TOPMed (Freeze10) and UK Biobank (UKB) for plasma lipid phenotypes. We intend to use state-of-the-art statistical framework to meta-analyze WGS data and replicate the findings in independent samples. Finally, we plan to carry out fine mapping of associated rare variant sets to add knowledge to the association of these variants and plasma lipids.

PI:	Margaret Sunitha Selvaraj
Award Type:	TOPMed Fellowship
Start Year:	2022

Source URL (modified on 06/29/2023 - 11:26am):https://topmed.nhlbi.nih.gov/awards/15741