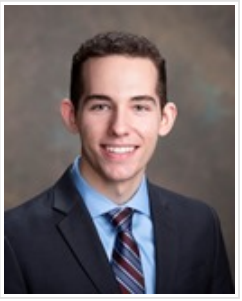
Genome-wide Association Study of Telomere Length and Disease Associated Genetic Variants



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Background: Genome-wide association studies (GWASs) have been successful in establishing associations among different single-nucleotide polymorphisms (SNPs) and many complex traits. Telomeres are repetitive DNA sequences located at the ends of chromosomes that function to protect against genomic instability. It is widely known that telomere length decreases with age, which contributes to cellular senescence. Evidence indicates that telomere length may be positively correlated with healthy living and is inversely correlated with the presence of several age-related diseases, including cancer, cardiovascular disease, obesity, diabetes, and chronic pain. This study aims to expand the associations among telomere length and SNPs related to disease states with a large number of study participants, which could help further elucidate the etiology of human diseases, improve diagnostic abilities, and direct future studies regarding disease treatment.

Methods: DNA samples from the Personalized Medicine Research Project (PMRP) and BioVU biobank (includes >85,000 patients) were processed to determine the relative average telomere length (raTL) using a standard quantitative polymerase chain reaction (PCR) assay. RaTL was linked with genomic data, and a GWAS was performed to determine associations among telomere length and genetic variants.

Results: Preliminary data indicates significant associations among raTL and genetic variants already known to be linked with telomere length, including SNPs within genes RTEL, TERC, TERT, and OBFC1. Suggestive associations have also been identified in 20 additional loci and may be validated as more data is processed.

Conclusions: This study has confirmed genetic variants previously associated with telomere length. Additional data is being processed that will help strengthen the power of these associations and identify novel genetic variants associated with telomere length. Future studies will utilize data gathered here to improve polygenetic risk scores that may help us predict disease.