Is Heritability of Telomere Length Modified by Lifecourse Socioeconomic Status?

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Telomere length is a widely used marker of biological aging and is strongly associated with an increased risk of morbidity and premature mortality. Recently, there has been evidence for an association between socioeconomic status (SES) and telomere length, particularly with measures of education and childhood SES. Individual differences in telomere length are also influenced by genetic factors, with heritability estimates from twin and sibling studies ranging from 34 to 82%. Yet unknown is the additive heritability due to *measured* genes for telomere length and to what extent it is modified by SES. The aim of this study is to provide the first estimates of molecular-based heritability of telomere length by using a multi-ethnic, nationally-representative cohort of over 5,000 older adults (mean age 66.9 yrs) and to examine whether heritability varies by lifecourse SES. Telomere length, genotype, and survey data are linked from the Health and Retirement Study. Telomere length was measured by quantitative PCR on DNA from saliva samples. Genotyping of common and rare variants was obtained using the Illumina HumanOmni2.5 BeadChip and HumanExome Beadchip v1.1. SES in childhood, educational attainment, income and wealth in adulthood collected prior to and concurrent with telomere length assessment, and cumulative lifecourse SES measures are investigated. Using genome-wide complex trait analysis (GCTA), we estimate the variance in telomere length explained by the additive effects of all measured single nucleotide polymorphisms and rare functional variants in unrelated individuals separately by ethnic group and controlling for population structure. We then examine whether SES measures modify these estimates of molecular-based heritability. Understanding the interaction between SES-related disadvantage and genome-wide data will help to elucidate the pathway by which SES-related health disparities emerge.