**Title: Whole Genome Sequencing data from the Wellderley study identifies rare variants in genes associated with diabetes and cardiomyopathy**

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**Abstract:** The impact of type 2 diabetes (T2D) and cardiovascular diseases on the global health burden is increasing at a rapid pace due to changes in lifestyle and behavior. It is estimated that diabetes and cardiac diseases will affect more than 10% of the global population by 2030. Understanding diabetes, and complications associated with diabetes at a molecular level can lead to the development of new therapies and biomarkers for early detection and prevention of the disease. We took a genomic approach to this problem and analyzed the publicly available whole genome sequence data (WGS) of 454 healthy elderly Caucasian individuals (Median Age 85 years) from the Wellderly study (Scripps Translational Science Institute). We analyzed genes known to be causative/predictive of diabetes (T2D, neonatal and MODY) and cardiovascular diseases and analyzed the prevalence of rare variants in this population. From over 240 genes analyzed, there were surprisingly few mutated genes in the diabetic pathway. We detected known pathological variant in the HNF1a gene in 6% of the individuals. Interestingly a significant fraction of the Wellderly individuals has mutations in genes associated with cardiac function. Out of the 181 genes analyzed, we identified mutations in 172 genes in this population. A significant finding of this study is the discovery of a rare variant in Nebulin (NEB) present in 60% of the individuals in this cohort. NEB is a multifunctional protein that binds and stabilizes actin allowing thin filaments to reach mature length. Mutations in NEB are associated with recessive nemaline myopathy. Understanding whether the Nebulin variant discovered in this study plays a protective role in preserving muscle function during aging can provide important insights into cardiac diseases that arise as a result of loss of muscle function.

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