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Transcriptional analysis of human cardiac aging by chronological and biological age

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Aging, a major contributor to cardiac dysfunction, follows not only a biological program, but aging rate is also affected by lifestyle and environment. Cardiac aging and aging rate are not fully understood, particularly in humans. To improve this knowledge, RNA-seq data from left ventricular samples was analyzed. Hierarchical clustering showed that biological age marker *CDKN2A* better represented the transcriptome than the chronological age. *CDKN2A* expression was also significantly increased in cardiac-related deaths over non-cardiac deaths. By GSEA, the top 10 enriched gene ontology groups (GOs) in old individuals were all different between chronological and biological aging, with major differences in GOs related to gas transport and extracellular matrix organization. Instead, the top 10 enriched GOs in young individuals were identical. Cluster analysis identified gene groups with significant up/down-regulation over chrono/biological aging. Our results describe differences and similarities between human cardiac chrono/biological aging and highlight the relevance of considering biological age.

Keywords: Cardiac aging, Biological aging, Transcriptomics, Gene Set Enrichment Analysis