COMPARATIVE PATHWAY ANALYSIS OF AGING ASSOCIATED GENES IN HUMANS AND MODEL ORGANISMS

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A great deal of research over the past few decades has been devoted to the study of aging in humans and model organisms. Despite the steadily increasing foundation of research, very little is known about its biological mechanisms. Many genes have been implicated in the process of aging, largely through the use of model organisms, such as C. elegans, D. melanogaster, and M. musculus. Although these genes shed light on the aging process, the vast majority do not translate to other model organisms, and even fewer to humans. A few putative genes found to affect aging have been indentified in humans, but much remains to be discovered. In this study, we compared two gene sets associated with aging, GenAge (human-related genes), and AnAge (aging genes in animal models), in order to determine if the gene sets from different organisms carried any functional similarities. Comparisons were performed using gene ontology and ingenuity pathway analysis. Additionally, each gene set was used to train Endeavour to see if common genes were predicted from the gene sets. The results show commonalities between animal models and humans and may provide a mechanism for inferring the appropriate aging genes in humans.