**The impact of aging specific differentially expressed genes on immuno-pathological regulations**

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ABSTRACT

Aging is defined as an increase in failure (mortality) rate that is irreversible and in biological mechanisms leading to progressive functional decline and increased risk for disease and death. By profiling gene expression levels, we intend to study aging with the pathological regulations of myeloid malignancies. We characterized aging at the gene expression level using GSE32719 data set publicly available at gene expression omnibus (GEO) and ArrayExpress. Using Biobase, GEOquery, doMC, and Limma packages, top 579 genes that shows up and down regulation (p < 0.05 and fold change > 2.5) out of which 117 genes were chosen in the intersection of gene ontology (GO) analysis. Similar to previous research, the increase in hematopoietic stem cell population and functional decline in age-related hematopoietic pathologies have contributed significantly. Our results further enabled identification of candidate genes that are associated with aging such as negative regulation of cellular process such protein modification and protein phosphorylation processes. A majority of the top GO genes encoded proteins function intracellularly and also provide insights into plasma membrane. Gene expression profile with GO enrichment further reveals a metabolic process of the immunopathological basis of aging that are associated with several signaling cascades which plays an important role of the family of ATP-binding cassette (ABC) transporters.

BACKGROUND

The process of aging is characterized by a degeneration in the maintenance of homeostatic processes with advancing time, leading to functional decline in a variety of organ and tissue systems and increased risk for many diseases (cardiovascular, several types of cancer, metabolic and neurological diseases) and ultimately death (Fraga et al. 2007). Aging decreases an organism’s ability to handle environmental and physiological disturbance which also another cause that increases the vulnerability to death (Rodero et al., 2007).

It is important to identify and characterize the genetic and environmental factors (smoking, environmental pollution) that modulate longevity in order to understand the basic mechanism of aging. The complex aging process and wide variability between individuals limited the identification of factors affecting aging (Rodero 2007).

To date, several theories have been proposed which provided beneficial insights to understand the physiological changes during the aging process (Tosato et al., 2007). The notable ones are immunologic, inflammation, free radical and mitochondrial.

To date several hundred genes have been found to associated with aging.

MATERIALS AND METHODS