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Network level analysis of Aging and Alzheimer's disease

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Abstract

Alzheimer's disease (AD) is a neurodegenerative disorder affecting the memory and cognitive functions in the aged population. The hallmarks of AD include accumulation of amyloid plaques, and neurofibrillary tangles (NFT) in the brain, and neuroinflammation leading to synaptic dysfunction, alterations in energy metabolism and apoptosis. Although genomic studies on AD have been performed extensively, the molecular mechanism of disease progression is still not clear. One possible reason might be the interaction of age and disease in the progression of AD.

To understand the contribution of aging and disease in the progression of AD, we adopted the network level approach to analyze the transcriptomic data obtained from the human postmortem brain tissues. We have performed gene co-expression network analysis and Knowledge-based (Integrated-PPI) network analysis involving 3 groups: young (<50 years), aged (>70 years) and AD (>70 years with AD). Co-expression network analysis identified modules/processes related to the phenotype (aging and disease). Both aging and disease are associated with increase in inflammation and its related processes involving the activation of microglia and reactive astrocytes. The significant differences in aging and disease are related to cytoskeleton remodelling, loss of synaptic transmission and oxidative phosphorylation. Further, the expression data was integrated with PPI network and various graph theoretical network measures were computed. Using edge betweenness network measure; we identified the significant unstable/active subnetworks and their hub genes. This study identifies the molecular mechanism that protects the aging brain from AD and that makes it susceptible to AD.

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