Potential hippocampal genes and pathways involved in Alzheimer’s disease: a bioinformatic analysis


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ABSTRACT. Alzheimer’s disease (AD) is a neurodegenerative disorder and the most common cause of dementia in elderly people. Numerous studies have focused on the dysregulated genes in AD, but the pathogenesis is still unknown. In this study, we explored critical hippocampal genes and pathways that might potentially be involved in the pathogenesis of AD. Four transcriptome datasets for the hippocampus of patients with AD were downloaded from ArrayExpress, and the gene signature was identified by integrated analysis of multiple transcriptomes using novel genome-wide relative significance and genome-wide global significance models. A protein-protein interaction network was constructed, and five clusters were selected. The biological functions and pathways were identified by Gene Ontology and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment analysis. A total of 6994 genes were screened, and the top 300 genes were subjected to further analysis. Four significant KEGG pathways were identified, including oxidative phosphorylation and Parkinson’s...
disease, Huntington’s disease, and Alzheimer’s disease pathways. The hub network of cluster 1 with the highest average rank value was defined. The genes \( \text{NDUFB3, NDUFA9, NDUFV1, NDUFV2, NDUFS3, NDUFA10, COX7B, and UQCR1} \) were considered critical with high degree in cluster 1 as well as being shared by the four significant pathways. The oxidative phosphorylation process was also involved in the other three pathways and is considered to be relevant to energy-related AD pathology in the hippocampus. This research provides a perspective from which to explore critical genes and pathways for potential AD therapies.

**Key words:** Alzheimer’s disease; Hippocampus; Critical genes; Pathways