Proteomic Profiling of Aging Hippocampus from a Postmortem Human Brain Bank

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Abstract: Hippocampus is one of the most critically affected regions in aged human brain. However, aging-related changes in protein profile in the human hippocampus have not been well described, especially for the Chinese population. We performed a proteomic study in the postmortem human hippocampus from the Human Brain Bank in Chinese Academy of Medical Sciences and Peking Union Medical College. A total of 16 human brains were used and divided to 4 aging groups: 20-50, 50-70, 70-90, and over 90 (n=4 each). None of the donors were diagnosed with neurodegenerative diseases before death according to their medical history. TMT-labeled quantitative protein profiling methods were applied and the results identified 4582 proteins, among which 99 proteins were upregulated and 42 proteins were downregulated during the aging process. Bioinformatics analysis revealed a numbers of proteins involved in the cytoskeletal or electron transport chain were significantly changed in aged hippocampus as compared to the younger groups. However, proteins highly associated with AD such as APP and tau showed no significant change in aged brains. Some of the proteins significantly changed during the aging process were verified by western blot. This study demonstrated the feasibility of research based on a standardized human brain bank in China. Our results indicated a series of changes in proteomic profile in aged human hippocampus that may relate to the normal aging process and potentially against age-related neurodegenerative disorders.

Key words: aging, human brain bank, brain proteomics, hippocampus