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The Semi-automated Quantification Approach of The Activated Microglia in a Mouse Model of Alzheimer's Disease

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Alzheimer's disease (AD), the most common aging-related neurodegenerative memory disease, is characterized by amyloid beta plaques and tau tangles. Recently Sharpin mutations have been identified as Alzheimer's disease-related factors in Asian populations as a result of Genome-wide association studies (GWAS). SHARPIN is a component of the LUBAC complex which conjugates linear polyubiquitin chains and plays a key role in NF-kappa-B activation and regulation of inflammation. It is proposed that targeting those SHARPIN mutants may offer a new approach for treating Alzheimer's disease by modulating neuroinflammation and addressing synaptic dysfunction. Microglia are the main immune cells in the nervous system and are known to play a crucial role in neuronal damage and neurodegenerative diseases. Specifically, the activation of microglia has been observed in the cerebral cortex and hippocampus of Alzheimer's disease patients. This activation of microglia can be distinguished by their morphological changes or cell surface antigen expression, but analyzing these within tissue requires significant time and effort. Recently, many studies suggested automated image processing techniques for the massive quantification of microglia. In this study, we aimed to modify one of this machine learning based-method to improve the accuracy and quality of the automated analysis of microglia in the batch image processing and analysis stages. Then, we performed automated analysis of microglia in an AD mouse model to distinguish the AD-related modification of microglia compared to wild-type. Our revised machine learning system allowed us to analyze microglia in the AD mouse model in a more objective and efficient manner, and we applied it to the SHARPIN mutant mouse model to define the role of Sharpin in microglia regulation in AD.

Keyword : Alzheimer's disease, SHARPIN, microglia

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