Proteomic Study of Aging Using Drosophila Model

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Aging is the gradual change in the structure and function of various organs that leads to an increased mortality. However, aging is a complex biological phenomenon influenced by various biochemical interactions. The biological process that causes aging is complex and remains poorly understood at the bimolecular level. In a previous study, cDNA microarrays has been introduced to aging analysis. To further realize aging in protein level, we used 2-DE PAGE approach combined with MALDI-TOF/TOF MS and LC-MS/MS to identify differently expressed proteins between control and longevous life span *drosophila*. The results showed that 45 protein spots with different expression presents in head proteome, and 32 different expressed spots with up-regulation presents in longeveous group. In body proteome, 19 significantly different expressed spots were detected and 17 protein spots were increased in the longevious group. Most differently expressed proteins of the longevous group were higher than control group. These proteins were classified by Gene Ontology in biological process to have generation of precursor metabolites and energy, oxidation reduction, tricarboxylic acid cycle, protein folding, oxidative phosphorylation, mitotic spindle organization, alcohol biosynthetic process and pyruvate metabolic process.

The differentially expressed proteins between normal and long lifespan *drosophila* can provide a comprehensive study to assist in uncovering anti-aging mechanism. The comparative proteomics could also provide novel markers for anti-aging.

Keywords:

Aging / *Drosophila* / 2-DE PAGE / MALDI-TOF/TOF / LC-MS/MS / Gene Ontology

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