Proteomic Approach to Aging Research

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Abstract

The aging process is multifactorial and results from the combined effects of inherited(genetic) and acquired factors including life style, food habits, physical activity, and diseases. That give rise to the various approaches in aging. We are trying to study biological changes with aging. In detail we are focused on gene and protein function accompanied by normal or abnormal aging process, especially our efforts are aimed at revealing the functional relationship of proteins in aging as a final product of gene. We expect that proteomic approach to the study of protein function involved in aging should give us variety of integrated data to understand biological changes of long lived lives.

We have applied expression proteomics to rat liver bred in dietary restriction or in at libitum to elucidate the effects of food habit on aging. Expression proteomics shows us protein profile in a selected tissue or cells as a whole and gives us the information about protein expression level, posttranslational modification and degenerative modification of expressed proteins. Comparative analysis of young and old rat liver by two dimensional gels shows that gene expression of several proteins was down regulated in old rats and some protein expression level is increased with aging. Dietary restriction slows down these changes of gene expression and in some proteins there's no difference in protein expression level at same ages in comparison with rats bred in at libitum.

About forty protein was identified by peptide mass fingerprint with MALDI-TOF and rest of the protein of interest is in the course of identification. Also we are trying to make mitochondrial and cytosolic proteom reference map.

These suborganelle proteom map will gives us the information about low abundance proteins and cellular localization of proteins.

Proteomics is a growing methodology to study biological system. High throughput qualitative and qualitative aspect of this approach will gives us large amount of integrated information and speed up our understanding about biological system