[S2-2] [4/18/2005(Mon) 10:00-10:30/Gumungo Hall A]

Proteomic Approach for Discovering The Drug Targets and Biomarkers of Diseases

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High throughput –omics including genomics, proteomics and metabolomics have been applied significantly to several fields of biomedical researches during recent several years. Genomics enabled rapid accumulation of information from complex biological systems. The complete DNA sequence is now known for many organism and the informational database obtained from genome sequencing projects has provide the base for the specification of proteome - the protein complement of genome. Genomic functions can be inferred from the analysis of gene structure and gene expression profiles because proteins are the functional molecules of an organism. Integrated technologies including protein separation, identification, characterization and information manage system are essential to analyze the proteins in complex cellular matrix. Proteomics, combined with separation technology and mass spectrometry, makes it possible to dissect and characterize the individual parts of various disease model system by investigating the protein expression profiles, post-translational modifications and protein-protein interaction changes in various cellular systems. This can be applied for the early detection of disease as a biomarker and for the validation of target proteins of therapeutic drugs.

Systemic analysis of proteomic changes in various disease states has been applied to understand the molecular changes of diseases. Availability will advance new technologies that improve sensitivity and peptide coverage. The progress of novel analytical technologies that are rapidly emerging, offer a great potential for determining the biomarker of diseases and drug targets.

This presentation will focus on the strategies of proteome analysis using sample preparation, 2-dimensional gel electrophoresis, processing of protein spots and identification of proteins and posttranslational modifications and protein-protein interactions by peptide fingerprinting using MALDI-TOF-MS and amino acid sequencing with nanoLC-ESI-q-TOF tandem MS. In this work, we applied this technology for the determination of differentially expressed proteins, post-translational modifications and protein-protein interactions in various cancer models: angiogenesis and metastasis.

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