Laboratory of Protein Profiling and Functional Proteomics
Institute for Protein Research

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Mass spectrometry, which allows highly sensitive and rapid analysis, has been used to analyze amino acid sequences and post-translational modifications of various types of proteins. Recently, as protein and gene databases have been enriched, mass spectrometry has become a fundamental technology for proteomics research, which aims to elucidate various physiological phenomena by comprehensively analyzing the total expression of proteins in vivo. In our laboratory, we are developing chemical and analytical methods and instruments for primary structural analysis of peptides and proteins by mass spectrometry, as well as software for accurate analysis of mass spectra, and using them to identify physiologically important proteins and analyze the structures of post-translational modifications.

Development of chemical methods and software for protein primary structure analysis by mass spectrometry

In order to analyze the primary structure or identify proteins with trace amounts by mass spectrometry, we have developed the following methods: 1) amino acid sequence analysis using the stable isotope 18O, and its application for comparative quantition of proteins; 2) simultaneous analysis of multiple samples by gas phase chemical reaction apparatus; 3) software that can analyze peptide amino acid sequences based on MS/MS (SeqMS), protein identification support software (MS-Match), and software that can analyze complex isotope patterns (Isotopica). This project was achieved in collaboration with Center for Genetic Engineering & Biotechnology (Cuba). Currently, these software are available at http://www.protein.osaka-u.ac.jp/rcsfp/profiling.

Structural analysis of post-translational modifications of proteins by mass spectrometry

In 2006, we newly identified lipid modification essential for Wnt3a function (Fig. 1). We have revealed a unique lipid modification by phosphatidylethanol amine at the C terminus of Apg8 protein which is a key molecule involved with "Autophagy" (Fig. 2).

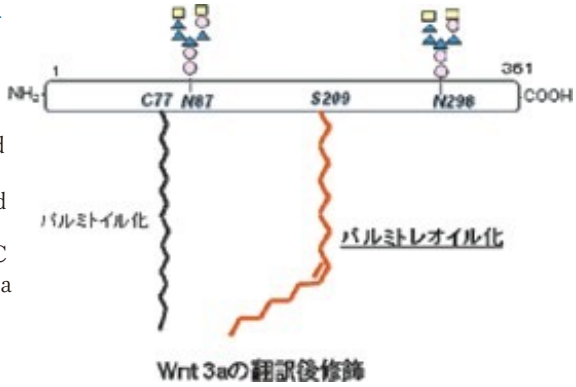

Figure 1. Novel lipid modification of Wnt protein (palmitoleoylation) Takada R. et al. Developmental Cell, 11,791-801 (2006)

Proteomics for biomarker discovery

Peptides and proteins are directly correlate with various physiological phenomena and pathological conditions. The research is conducted to do the comprehensive analysis of them for searching biomarkers using body fluids such as urine. The workflow for the sample pretreatment followed by comparative analysis among multiple samples has been established. We have also developed the software for comparative analysis of multiple samples obtained by mass spectrometry.

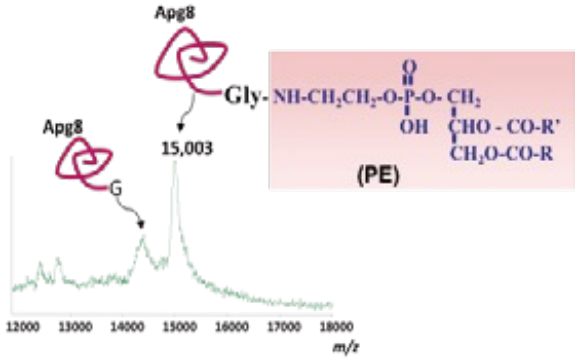

Figure 2. Novel protein-lipid modification by a ubiquitin-like modification mechanism Nature 488-492408, (2000).

Study on fragmentation of biomolecules in mass spectrometry

We are studying the characteristic fragmentations observed for peptides, glycans and lipids, and applied them for their structural analyses. We have found that MS or MS/MS of peptides containing methyllysine, trimethyllysine, acetyllysine, phosphorylated serine/threonine, and oxidized methionine showed modification-specific fragmentation. They are useful for the identification of these modified amino acids.

This lab will not accept students in 2024

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