

Biomarker Discovery Focusing on Application of Molecular Imaging to New Drug Development

Osamu Nishimura

Life Science Laboratory, Shimadzu Corporation

Institute for Protein Research, Osaka University

The sequence of human genome has been decoded and a new era of post-genome such as proteome, glycome and metabolome is now beginning. Among them, proteome is one of the major concerns. Though genomic information is useful, significant and indispensable in driving forward to new drug development, there are numerous hard barriers to get over in pursuing it for genomic information alone. What kind of approach can be a breakthrough of this bottleneck? One of the answers is a research on proteome, which promises a bright future in new drug development.

It is no doubt that a key instrument for this research is obviously mass spectrometer (MS), which plays an essential role to accelerate proteome analysis. The contribution of MS to this research field was recently recognized by the award of the Nobel Prize in Chemistry 2002 for 'The Discovery of Soft Laser Desorption Ionization' to Mr. Koichi Tanaka. However, the present proteome analysis technology has not reached to the sufficient scientific level yet. Further improvements of both its hardware and software are necessary.

Bearing this in mind, we have searched for a better method and recently established a novel proteome analysis system. Using this system, we found some new promising biomarker candidates from cancerous tissues in collaboration with Prof. Monden (Osaka University, Medical School).

In this presentation, we will discuss applications of these candidate proteins to new drug development including molecular imaging.