T2-2 Systematic Analysis of Protein Interactions Using Direct Nano Flow Tandem Mass Spectrometry

NATSUME Tohru

Biological Information Research Center (AIST), Japan Biological Information Research Center (JBIC)

Aomi 2-41-6, Koutou, Tokyo 135-0064
TEL:+81-3-3599-8140,FAX: +81-3-3599-8134 natsume@jbirc.aist.go.jp

B I O G R A P H Y

昭和36年 8 月23日生
昭和61年　東京大学農学系研究科修了
昭和61年　京都大学医用高分子研究センター 研究員
平成 5 年　京都大学医学博士
平成 8 年　科学技術庁科学技術振興事業団 創造科学推進事業
　　御子柴プロジェクト 研究員
平成12年　文部科学省庁ゲノム・フロンティア
　　次世代プロテオーム解析プロジェクト 研究統括補佐
平成13年　産業技術総合研究所主任研究員
　　生物情報解析研究センター機能ゲノムグループ・チームリーダー
　　（現在に至る）

専門分野：タンパク質化学、細胞生物学、バイオロジカルマス・スペクトロメトリー
研究テーマ：タンパク質相互作用解析、バイオインフォマティックス

Key words: porotein-protein interaction, proteomics, mass spectrometry

To determine functions of genes at the protein level, a process termed proteomics, which involves protein-protein interaction analysis, attempts are made to discover potential interacting partners or to establish novel members of the functional protein machinery complex. One of the most powerful means for identifying proteins from cellular compartments or macromolecular complexes is liquid chromatography (LC) based electrospray tandem mass spectrometry (MS/MS). To enhance sensitivity and resolution of MS/MS analysis, we have developed novel direct nano flow LC-MSMS system (DNLC-MS/MS). This system enables us to identify 100-150 proteins in a single run at low femotomole lebel without pre-separation of each component by 2D or 1D-electrophoresis. In this approach, protein components in even the largest macromolecular complex can be identified comprehensively in high-throughput and automated manner.

Systematic efforts to understand protein-protein interactions are under way in our research project using human full length cDNA. In the project, the cDNAs (bait) were fused to an epitope tag sequence and expressed in human cells. The expressed tagged proteins, together with their associating partners (prey), were purifed from cell lysate using anti-tag affinity beads. The isolated protein compexes were identified using the DNLC-MS/MS system. So far, approximately 800 analyses (250 human cDNAs) have been performed.

Supported by NEDO (New Energy and Industrial Technology Development Organization).