Establishment of antibody proteomics for identification of disease-related proteins and high-throughput isolation of monoclonal antibodies

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In recent drug discovery research, one of the most promising approaches is disease proteomics which systemically analyze and identify over-expressed or under-expressed proteins in diseased condition (disease-related proteins) compared with normal one**.** In the case of disease proteomics, hundreds of candidate disease-related proteins can be identified at a time by two-dimensional differential gel electrophoresis analysis (2D DIGE). Therefore, how to pick the really valuable proteins up from a number of candidate drug targets is a most important issue to be solved in world-wide. Here, we introduce our approach “antibody proteomics” toward above issues, which makes it possible to identify a variety of disease-related proteins by 2D-DIGE and prepare monoclonal antibodies to these proteins simultaneously by using phage antibody library. Because antibody proteomics has a potential isolating monoclonal antibodies to hundreds of disease-related proteins in a few weeks, this could be a fundamental technology for functional analysis of candidate disease markers identified by disease proteomics or for validation of them by combination of tissue microarray technology. Our methodology could also be useful and powerful tool for diagnostic or therapeutic antibodies. In this symposium, we will talk about the development and application of antibody proteomics and our view of future.