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Perspecive

Overview of Immnunoproteomics and its Applications

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DESCRIPTION

The study of huge collections of proteins (proteomics) involved in the immune response is known as immunoproteomics. Immunoproteomics has the potential to be a useful method in the field of infectious disease biomarker discovery, especially when the pathogen is difficult to culture *in vitro*. SELDI technology has only recently been used to identify biomarkers to distinguish Helicobacter pylori strains associated with different phases of the disease. In this method, serum antibody "signatures" can be discovered. Antigenic protein discovery and characterisation are required for the creation of vaccines, which have a high interest as a therapeutic alternative to treatment. Immunoproteomics can be used to make broad diagnostic recommendations or to choose biomarkers.

Immunoproteomics is a concept that combines protein separation (2-DE, gel-free separation), immunological detection (Western blotting), and MS or immunocapture and MS to identify disease associated antigens that stimulate immune responses. The 2-DE method was used to extract proteins from cells or tissues. Patients' serum, which may contain disease-specific antibodies, is used to detect antigenic proteins, which are then detected using enzyme-labeled secondary antibodies. The relevant areas from the gel are excised and in-gel digested to identify immunogenic proteins. MS or tandem MS is used to examine the digest, then peptide fingerprinting or sequence tag methods are used.

Antigen profiling using immunocapture MS, on the other hand, starts with the immobilisation of antibodies taken from the patient's serum. Protein A or G, a bacterial-derived protein with a particular affinity for the Fc domain of antibodies, captures almost all antibodies. The antigens specific to antibodies found in patient serum were then captured using a protein mixture applied to a column or beads on which antibodies are bound. Finally, using MALDI-TOF-MS or surface-enhanced laser desorption/ionization MS, antigens eluted from antibodies are used to identify proteins. Antigen profiles in colon cancer patients were discovered using this immunocapture MS method. Antigen profiling using immunocapture MS, on the other hand, starts with the immobilisation of antibodies taken from the patient's serum. Protein A or G, a bacterial-derived protein with a particular affinity for the Fc domain of antibodies, captures almost all antibodies. The antigens specific to antibodies found in patient serum were then captured using a protein mixture applied to a column or beads on which antibodies are bound. Finally, using MALDI-TOF-MS or surface-enhanced laser desorption/ionization MS, antigens eluted from antibodies are used to identify proteins. Antigen profiles in colon cancer patients were discovered using this immunocapture MS method.

The Peptide Mass Fingerprinting (PMF) approach can be used to compare a peptide's mass spectrum to a database of previously described protein digests. If the mass spectrum of the protein of interest and the database protein has a lot of homology, the protein of interest is almost certainly present in the sample. For many years, two-dimensional gel electrophoresis (2-D gel) techniques in combination with western blotting have been employed to determine the magnitude of immunological responses. For qualitative analysis, this can be achieved by comparing individual samples to molecular-weight size markers, and for quantitative analysis, against known levels of protein standards. Antibody or other affinity reagents are used in affinity proteomics, which is a high-throughput approach of examining the proteome. In contrast to a solid substrate like a microarray, large numbers of immune-related cytokines and associated indicators can be tested simultaneously in solution.

CONCLUSION

Immunoproteomics is and has been used to improve scientific understanding of the pathogenesis and course of autoimmune diseases. Gene and, ultimately, protein expression can be evaluated with high accuracy using biochemical techniques. The molecular mechanisms producing pathology in diseases like multiple sclerosis and Crohn's disease could be understood with this information. Because of the relatively high stability of serum antibodies, serum antibody identification has shown to be particularly effective as a diagnostic tool for a variety of disorders in modern medicine. Antibody isolation is also accomplished using immunoproteomic methods. Scientists are able to identify possible protein targets of antibodies by identifying and sequencing antibodies. It is feasible to determine the antigen(s) responsible for a specific immunological response this way.

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Antibodies involved in the pathophysiology of autoimmune diseases may be identified and engineered, potentially opening up new avenues for disease treatment.

It is feasible to find viable targets for innovative medications by identifying the antigens responsible for a specific immune response. Furthermore, specific antigens can be categorised based on immunoreactivity in order to identify future vaccine formulations. Immunoproteomic techniques such as western blotting can be used to measure the efficacy of a vaccination in addition to identifying vaccine candidates.