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Mass Spectrometry & Purification Techniques

Opinion Article

Protein Identification and Quantification through the Application of Proteomics Technologies

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DESCRIPTION

Proteomics technologies provide several prospects for expanding the understanding of biology and finding new biomarkers. Tandem Mass Spectrometry (MS) is the primary platform for proteomics, but in order to conduct useful research, a variety of other tools, resources, and knowledge are unavoidably needed. They include genetics and bioinformatics, as well as protein separation science and protein biochemistry in general. Before tandem MS and subsequent bioinformatics analysis to identify proteins, a variety of procedures are available for protein (or peptide) separation. The three main techniques are Liquid Chromatography-Mass Spectroscopy (LC-MS), Gel LC-MS, and 2D electrophoresis (2DE) and subsequent MS.

There are several tried-and-true approaches for protein measurement in addition to protein identification. One possibility is difference gel electrophoresis (DIGE) after 2DE, however MS-based techniques are currently favoured (most frequently iTRAQ-Isobaric Tagging for Relative and Absolute Quantification or SILAC - Stable Isotope Labeling by Amino Acids). The preparation of the samples is essential for successful research, and subcellular fractionation can offer more information on protein localization than entire cell lysates. Another viable alternative is differential detergent solubilization. By using immunodepletion with biological fluids, it is feasible to eliminate the most prevalent proteins. Moreover, sample enrichment is frequently utilised in several studies, most notably phosphoproteomics after the first purification of phosphopeptides.

Proteomics generates huge datasets, and tools that make it easier to do the required extensive analysis of this data are always getting better. In addition to the advantages that proteomics

Identification and quantification of low abundance proteins is a serious problem since proteomes are extremely complicated. Moreover, weakly soluble proteins including membrane proteins and multiprotein complexes are challenging to analyse. Without a question, though, proteomics has already offered important insights into how biological processes work, and this will continue as technology advances.

Blood and biopsied specimen-based proteomic approaches offer reproducible and quantitative tools that can complement clinical assessments and help clinicians in the diagnosis and treatment of inflammatory bowel disease. Proteomics offers significant opportunities for either improving the biological understanding or discovering biomarkers (IBD). Finding relevant biomarkers can sometimes lead to the differential diagnosis of Crohn's disease (CD) and Ulcerative Colitis (UC) as well as the prediction of therapy response.

For protein (or peptide) separation before MS/MS as well as bioinformatics analysis to identify proteins, a variety of workflows are available. These include two-dimensional electrophoresis (2-DE) and subsequent Mass Spectrometry (MS), liquid chromatography-MS, difference gel electrophoresis after 2-DE, isobaric tags for relative and absolute quantification (iTRAQ), stable isotope labelling by amino acids, and label-free quantification. With examples of emerging biomarkers focusing on the diagnosis, treatment response, prognosis, and even colitis-associated carcinogenesis in both animal models and human patients, this study introduces the present state and outlook of these sophisticated proteomic technologies.

Protein biomarkers for early and precise diagnosis might aid doctors in enhancing patient care. Also, the biomarkers could help doctors anticipate disease.

Individuals with a low risk of illness flare-ups may choose not to take drugs that come with a risk of side effects. Moreover, identifying illness- and course-specific biomarker profiles can be utilised to pinpoint the biological processes that contribute to the onset and management of the disease. The future development of preventative and therapeutic methods can be enhanced with a better understanding of illness processes in general. Hence, the clinical use of a panel of biomarkers is a diagnostic and prognostic tool that may be very valuable. The current technical advancements in proteomic research which determine and quantify the total protein content have made it possible to find new biomarkers. There are several IBD-associated protein biomarkers that have been identified, however none of them have been effectively used in clinical practise to identify CD from UC patients.

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The obvious area to look for new biomarkers is in the intestinal tissue, which may subsequently be checked in blood, urine, or faeces. Given the complexity of the proteins found in intestinal biopsy samples and recent advancements in mass spectrometry-driven quantitative proteomics, it is now possible to conduct a more extensive and accurate biomarker discovery effort than ever before.