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Short Communication

Role of Top-Down Proteomics for Mass Measurement using Ion Trapping Mass Spectrometer

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ABSTRACT

Top-down proteomics is a method of protein identification that uses an ion trapping mass spectrometer to store an isolated protein ion for mass measurement and tandem mass spectrometry analysis, or other protein purification methods such two-dimensional gel electrophoresis with MS/MS. Through the study of intact proteins, top-down proteomics may detect and quantify distinct proteoforms. The name comes from the fact that DNA sequencing is done in a similar way. Intact proteins are electrospray ionized and trapped in a Fourier transform ion cyclotron resonance (Penning trap), quadrupole ion trap (Paul trap), or Orbit rap mass spectrometer during mass spectrometry. Electron-capture dissociation or electron-transfer dissociation are used to fragment samples for tandem mass spectrometry. Prior to mass spectrometry-based proteomics, effective fractionation is necessary for sample handling.

Keywords: Protein identification; Mass measurement; Mass spectrometry; Top-down proteomics

DESCRIPTION

In the field of mass spectrometry-based proteomics, the rise of the "Top Down" technique has ushered in a new era of difficulty for protein characterization and identification. Injecting entire proteins into the mass spectrometer enables for more accurate analysis of post-translational changes while also avoiding several of the severe "inference" issues that plague peptide-based proteomics [1]. However, applying a Top Down technique to endogenous or other physiologically relevant samples frequently necessitates the use of one or more forms of separation prior to mass spectrometric analysis, which has just recently matured for whole protein analysis.

Recent developments in instrumentation, combined with new ion fragmentation techniques using photons and electrons, have enabled better protein characterization in cases that were before unsolvable [2]. Finally, the use of native electrospray mass spectrometry for the identification and characterization of whole protein complexes in the 100 kDa to 1 MDa range has shown great promise, with the prospect of complete compositional analysis for endogenous protein assemblies becoming a realistic goal in the coming years. The development of genome sequencing has accelerated our understanding of life, but it is insufficient for a complete description of a biological system [3]. Proteomics, which focuses on proteins, has emerged as another large-scale platform for bettering biology understanding. Annotation and correction of genomic sequences, quantification of protein abundance, and detection of post-translational modifications and discovery of protein-protein interactions are all possible with proteomic investigations [4]. Proteomics can be a valuable addition to genomes and transcriptomics in many ways. Transcript levels are less important than protein abundance in some systems, such as extracellular fluids or intracellular organelles. Furthermore, post-translational changes may precisely affect protein activity, which is likely the most significant component in comprehending biological pathways. While a range of technologies, such as cell imaging and protein arrays are capable of large-scale protein analysis, mass spectrometry-based approaches are exceptionally well adapted to handle proteome-wide research in terms of throughput and sensitivity.

CONCLUSION

Top Down proteomics is a promising alternative to digestion-based methods, promising comprehensive protein characterization on a proteome-wide scale. While measuring intact proteins poses numerous technological hurdles, the

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discipline has experienced significant advancements in separations tools, mass spectrometry instruments, and data processing. Miniaturization of separations and growing use of on-line and multidimensional separations are both on the rise. Mass spectrometers have become more capable of conducting on-line analysis as scanning speeds have increased, and data acquisition has shifted to an emphasis on protein identification rather than detection.

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