Real-Time Tandem Mass Spectral Data Analysis for Protein Sequence Identification

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The Wisconsin Alumni Research Foundation (WARF) is seeking commercial partners interested in developing a technique for real-time identification and characterization of proteins by peptide sequencing of product ions analyzed with mass spectrometry (MS).

Overview

Protein characterization has become an integral part of modern biology, even inspiring a new discipline known as proteomics, or the classification of proteins based on the genome of an organism. MS is the most widely used technique to characterize proteins. To utilize mass spectrometry, the proteins undergo a process known as ion fragmentation. Tandem MS is the breaking apart of the proteins by ion fragmentation followed by the measuring of the mass/charge ratio via MS.

Two of the ion fragmentation techniques currently in use are collision-activated dissociation (CAD) and electron transfer dissociation (ETD). CAD involves the collisions of the peptide with an inert gas to create b-type and y-type fragments. ETD uses the electron transfer from radical anions to peptide cations to create c-type and z-type fragments. The two resultant sets of fragments, or product ions, can be analyzed using MS to determine the complete amino acid sequence of the peptide. However, in both techniques, other fragments are created as well that complicate the peptide identification process.

Since its development in 2004, ETD has become the preferred method for peptide fragmentation. Recent developments have led to drastically improved resolution for ETD, which has allowed for more advancement to occur in the field of proteomics.

The Invention

UW-Madison researchers have developed a technique that allows for real-time identification of unknown peptides using mass spectral analysis to identify and characterize proteins during a tandem mass spectral analysis.

With sufficient MS resolution, the z-type product ions of the ETD technique can be uniquely identified, in turn allowing for immediate identification of c-type product ions. Because of the labeling of both product ions, other spectra peaks due to noise can be eliminated and the overall spectra quality can be determined. The masses of the z- and c-type product ions are compared against a computer database to identify one or more "putative chemical compositions," which are the amino acid sequences of the peptide. The putative chemical compositions then are confirmed by comparison to peptide amino acid sequences in a database or via *de novo* analysis using a computational model without extrinsic comparison. The results from either of these methods can be used to identify and characterize the protein from which the peptide was derived. This process is incorporated into an algorithm that can make automated decisions to determine the best course of action for the mass spectral analysis.

Applications

- Protein sequence identification and characterization using tandem mass spectrometry analysis
- Real-time identification of peptide amino acid composition

Key Benefits

- Identifies peptides in real-time
- Can be applied to isolated proteins or complex mixtures thereof
- Algorithm makes automated decisions to determine best method for mass spectral data analysis
- Able to determine spectra quality
- Makes reliable protein sequences without the use of databases

Additional Information

For More Information About the Inventors

- Joshua Coon
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Tech Fields

- Analytical Instrumentation, Methods & Materials : Mass spectrometry
- Research Tools : Genomics & proteomics

For current licensing status, please contact Jennifer Gottwald at jennifer@warf.org or 608-960-9854