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Chemical modification of peptides followed by mass spectrometry: Implications in proteomics

Medicharla V Jagannadham
CSIR-Centre for Cellular and Molecular Biology, India

Determination of the sequence of the peptides, obtained from the proteolysis digestion of a protein, using mass spectrometry, is a crucial requirement in proteomics. Sequence of the tryptic peptides is usually obtained by database search or by *de novo* sequencing. The poor spectral quality and signal to noise ratio interferes in the analysis. Different types of algorithms (MASCOT, SEQUEST and others) are used for interpretation of the mass spectral data. When the database is not available, *de novo* sequencing is the only way to determine the sequence. The *de novo* sequence can be obtained by employing different methods of fragmentation (CID, HCD, ETD and ECD), getting information on their sequence and combining this information. Even with MS instruments with high mass accuracy and speed of analysis, the reproducibility of the mass spectrometry-based proteomics is being questioned from time to time. Acetylation of peptides improved the spectral quality, exhibited by an increase in b ion intensities in the MS/MS spectra, improves the efficiency of *de novo* sequence and helped in validating the database search results. It is a simple reaction, which can be carried out on complex protein digests as is required in proteomics. The identification of proteins from an Antarctic bacterium *Pseudomonas syringae* Lz4W and other species using this strategy will be discussed.

Biography

Medicharla V Jagannadham is working as a senior principal scientist and project leader at the Centre for Cellular and Molecular Biology. He published 45 research papers in internationally reputed scientific journals. He trained several students, conducted meetings and workshops in proteomics. He received "Bharat Jyothi" award from India International Friendship Society, New Delhi in 2014 and "Eminent Mass Spectrometrist" award from the Indian Society for Mass spectrometry (ISMAS) in 2015. His current research Interests are proteomics, particularly in improving the *de novo* sequencing efficiency of peptides using MS techniques, structural and functional studied of outer membrane vesicles of Gram-negative bacteria.

jagan@ccmb.res.in

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