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MASS SPECTROMETRY-BASED PROTEOMICS: CHALLENGES AND OPPORTUNITIES

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Mass spectrometry-based proteomics is extensively used for the identification of proteins from complex mixtures, their expression, quantification, post-translational modifications and study the interactions among proteins. Using proteomics, the biology of several complex diseases was studied. However, the problems associated with reproducibility, false discoveries, lack of proper standards, problems in *de novo* sequencing lead the researcher to look for validation methods. A thorough understanding of these techniques and their limitations is crucial in facilitating the development of new strategies to overcome the existing problems and advancement of the technology. The limitations associated with the sensitivity, comprehensiveness involved with mass spectrometry should be understood. Sample preparation, handling and data analysis plays a critical role on the results. The huge amounts of MS data generated is analyzed using different algorithms. These algorithms require the protein/genome data base for the identification of proteins. This approach cannot be used for the species whose genome sequence is not known. In this situation, *de novo* sequencing followed by homology search is the method of choice for the identification of proteins. The opportunities in developing different technologies and strategies in the proteomics work flows play a critical role in utilizing proteomics effectively.

BIOGRAPHY

Medicharla Venkata Jagannadham is working as a senior Principal Scientist and Project Leader at the Centre for Cellular and Molecular Biology. He has vast experience in protein chemistry and proteomics. He published more than 50 research papers, with some papers having more than 100 citations. 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 studies of outer membrane vesicles of Gram-negative bacteria.

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