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Mass spectrometry-based approach coupled to computational tools for proteomics investigation of bacterial membrane

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The recent development of gel-free proteomics approach allows a significant improvement over gel-based analysis. At ITB-CNR (Institute of Biomedical Technologies of National Research Council) proteomics laboratory, the gel-free MudPIT (Multidimensional Protein Identification Technology) methodology is used for biomarker discovery for developing clinical methods and for identifying novel antibacterial targets. However, the investigation of complex biological samples such as human tissue or microbiological samples requires the development of computational tools for processing and handling the great amount of data produced by mass-spectrometry experiments. Our workflow involves user-friendly tools for characterization of biomarkers and proteotypic peptides useful for validation step. In addition, MAProMa, home-built software performs both rapid comparison of protein lists identified in samples and an estimation of differentially expressed proteins. It is based on a label-free quantitative approach and it allows the visualization of data in a format more comprehensible to biologists and clinicians (Biomarker Validation, Technological, Clinical and Commercial Aspects). Here, we present these technologies and tools applied to the study of bacterial cell envelope. In particular, the workflow based on MudPIT analysis of sample and computational interpretation of data allowed the discrimination between transmembrane and extra membrane domains of proteins providing information about their localization. The obtained results evidence the importance of computational tools for extracting available data and they may be useful for suggesting new therapeutic strategy to lead to novel anti-bacterial targets.

Biography

Sara Motta has obtained her degree in Biology (Physiopathology) in October 2011 at the University of Milano-Bicocca (Faculty of Mathematics, Physics and Natural Sciences). From January 2012, she has a research fellowship at the Institute of Biomedical Technologies of National Research Council (ITB-CNR), Proteomics and Metabolomics Laboratory. Her current research activities at the ITB-CNR concern the study of proteins isolated from bacteria in order to identify possible targets for the development of new therapeutic strategy against bacterial infections. She has 3 papers published in peer-reviewed journals and other in publishing phase.

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