MASS SPECTROMETRY IN PROTEOMICS: STUDIES OF PROTEIN INTERACTION

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Sequencing of entire genomes culminating with the human genome and those of several plants has changed the perspectives of modern biological science. Now in the post genome era functional genomics is becoming a buzz-word. This rather vague term involves studies of the expression and function of gene products on all levels. Proteomics is one of the key analytical tools in functional genomics and mass spectrometry the key instrumentation. Proteomics is performed on three levels: - Expression proteomics, i.e., which genes are expressed when and where? - Modification specific proteomics, i.e., which modified variants are present of each protein? - Cell map proteomics or interactomics, i.e., who interacts with who, when and how? We are in our research group performing proteomics studies on all three levels. Since we have the hypothesis that protein modifications are used in the living organism to regulate interactions and their kinetics, we want to investigate the interdependence between protein modification and protein interaction. In order to perform such studies we have developed a number of mass spectrometry based methods to study protein interaction. These include: - Pull-down of interacting proteins followed by identification of interacting partners using a proteomics approach. - Studies of interaction kinetics by combining surface plasmon resonance (BIA-technology) with mass spectrometry - Identification of the boundaries of the interaction interface by surface labelling and cross-linking followed by analysis by MS. -Studies of the interaction interface by deuterium exchange mass spectrometry. The present state of art of these different techniques will be illustrated using examples from our ongoing projects.