

High Performance Proteomics as a Tool in Biomarker Discovery

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Since about 10 years the word PROTEOME catches the attention of more and more researchers in the life science field. At about the same time the term high throughput proteome analysis came up with the intention to analyse all proteins in a complex protein mixture in parallel. Thus, a huge amount of data is produced from a single sample and the following analysis and validation becomes the time limiting step.

However, the limited number of available biomarkers for diagnosis, status of the disease, therapy control and prediction of the course of the disease demands for new efforts in finding new ones. Especially, proteomics raises high expectations in finding new and reliable biomarker for human diseases.

By applying micro dissection combined with saturation DIGE technology and mass spectrometry we could succeed in finding new biomarker candidates for pancreatic carcinoma including samples of six tumour progression stages and liver cirrhosis. This technology allows us to analyze quantitatively the proteome of just 1000 cells from individual patient samples (4 to 9 samples) and to get reproducible proteomics data pointing to about 30 new biomarker candidate proteins for either disease. Validation of these candidate biomarkers is still in progress and quantitative PCR and immunohistochemistry are employed for this purpose. So far, most all of the candidate biomarker could be tested to be positive in these further validation steps.

Thus, **high performance proteomics** is the basic principle for reliable results which allows us to discover new biomarker candidates for pancreatic cancer and liver cirrhosis using minute amounts of patients' material. How to reach this goal will be presented in the lecture.