PHYSIOLOGICAL PROTEOMICS OF GRAM-POSITIVE BACTERIA

J. Bernhardt[1] , M. Hecker [1]

[1] Universität Greifswald, Institut für Mikrobiologie, F.-L.-Jahn-Straße 15, D-17487 Greifswald, Germany

Proteomics is an excellent tool to "bring the genome sequence to cell physiology". Because of their low complexity bacteria are useful model systems to transfer the "virtual life of the genes to the real life of the proteins" shown for our model bacteria *Bacillus subtilis* and *Staphylococcus aureus*.

A combination of gel-based and gel-free proteomics has been used to visualize the entire proteome of bacteria. In the presentation it will be shown that gel-based proteomics is still a valuable tool to cover the cytosolic and extracellular proteins and to visualize proteins newly synthesized in the cell. Low abundance proteins, however, can only be identified by gel-free proteomics. For the membrane and cell surface-associated proteomes, however, gel-free approaches are necessary to identify the proteins. Using a reasonable combination of gel-based and gel-free approaches almost 70 to 80 % of the proteins expressed under specific circumstances can be detected and quantified.

In the second part of the talk it will be shown that a combination of gel-based and gel-free proteomics is a powerful tool to address physiological issues. The panorama view of proteomics will help to come to a better understanding of pathogenicity and virulence of *Staphylococcus aureus*.