
Keynote Lecture

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Physiological proteomics of Gram-positive model bacteria

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The genome sequence of an organism, the blueprint of life, does not explain life. Because proteins are the main workhorses of cell physiology, it is the proteome that largely translates the genome sequence into cell function. The knowledge on physiology and molecular genetics of model bacteria such as *Bacillus subtilis* and *Staphylococcus aureus* combined with the new perspective of functional genomics/proteomics should bring a new quality in understanding the life style of these model organisms.

Complex mechanisms of global gene expression control guarantee that each single protein is provided in sufficient amounts, at the right time window and at the right place to organize cellular life. For our model bacteria we identified almost 70 to 80% of the proteome, absolute quantitative data included, shown in the first part of the talk. The main challenge that follows is to understand how hundreds of different proteins leaving the ribosome tunnel organize the main processes of life. Proteomics is a great toolbox to follow the fate of the single proteins from birth at the ribosome via aggregate formation, modification, damage, repair and finally to death in the Clp machines.

In the second part the question will be addressed: How can we use proteomics to understand cell physiology and pathophysiology of both model organisms. This will be demonstrated for selected starvation and stress responses.

Key words: Physiological proteomics; *Bacillus subtilis*