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Autore	Jorg Stulke
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Sommario/riassunto	<p>Post-translational modifications (PTMs) are widely employed by all living organisms to control the enzymatic activity, localization or stability of proteins on a much shorter time scale than the transcriptional control. In eukarya, global analyses consistently reveal that proteins are very extensively phosphorylated, acetylated and ubiquitylated. Glycosylation and methylation are also very common, and myriad other PTMs, most with a proven regulatory potential, are being discovered continuously. The emergent picture is that PTM sites on a single protein are not independent; modification of one residue often affects (positively or negatively) modification of other sites on the same protein. The best example of this complex behavior is the histone "bar-code" with very extensive cross-talk between phosphorylation, acetylation and methylation sites. Traditionally it was believed that large networks of PTMs exist only in complex eukaryal cells, which exploit them for coordination and fine-tuning of various cellular functions. PTMs have also been detected in bacteria, but the early examples focused on a few important regulatory events, based mainly on protein phosphorylation. The global importance (and abundance) of PTMs in bacterial physiology was systematically underestimated. In recent years, global studies have reported large datasets of phosphorylated, acetylated and glycosylated proteins in bacteria. Other modifications of bacterial proteins have been recently described: pupylation, methylation, sirtuin acetylation, lipidation, carboxylation</p>

and bacillithiolation. As the landscape of PTMs in bacterial cells is rapidly expanding, primarily due to advances of detection methods in mass spectrometry, our research field is adapting to comprehend the potential impact of these modifications on the cellular physiology. The field of protein phosphorylation, especially of the Ser/Thr/Tyr type, has been profoundly transformed. We have become aware that bacterial kinases phosphorylate many protein substrates and thus constitute regulatory nodes with potential for signal integration. They also engage in cross-talk and eukaryal-like mutual activation cascades. The regulatory potential of protein acetylation and glycosylation in bacteria is also rapidly emerging, and the cross-talk between acetylation and phosphorylation has been documented. This topic deals with the complexity of the PTM landscape in bacteria, and focus in particular on the physiological roles that PTMs play and methods to study them. The topic is associated to the 1st International Conference on Post-Translational Modifications in Bacteria (September 9-10, 2014, Göttingen, Germany).
