Posttranslational modifications and structural alterations of protein synthesis elongation factor Tu in *Actinomyces* in relation to their life cycle

Protein synthesis elongation factor Tu represents a multifunctional protein with potential role in signaling and regulation of cell metabolism. The complex life cycle of Streptomycetes requires monitoring of changes in their environment and signaling pathways to control it. Here we present the results of analysis of membrane phosphoproteomes from individual morphological stages of *Streptomyces coelicolor* with the aim to follow developmentally dependent heterogeneity and phosphorylation of intrinsic and externally added *Strepomyces aureofaciens* EF-Tu in membrane proteomes. We used *Mycobacterium smegmatis*, fast growing non-pathogenic *Mycobacterium*, as a non-differentiating actinomycete comparative model. Phosphorylation of intrinsic *M. smegmatis* and externally added *Streptomyces* EF-Tu was followed in membrane proteomes from exponential and stationary phase of *M. smegmatis* liquid culture. We have found that Streptomycetes membrane fraction contains protein kinase(s) catalyzing phosphorylation of both, its own, and an externally added EF-Tu, whereas *Mycobacterium* membrane fraction contains protein kinase phosphorylating only its own EF-Tu. *In vitro* phosphorylation of EF-Tu was shown in cell-free extract from dormant spores of *Streptomyces coelicolor* by a protein kinase present in spores. EF-Tu phosphorylation was observed on both intrinsic *S. coelicolor* factor and externally added purified EF-Tu from *S. aureofaciens*, on two isoforms. Putative serine and threonine residues as potential phosphorylation targets were determined in primary sequence and demonstrated on 3D structure model of EF-Tu.