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Induction of metabolic shifts in Streptomyces

The soil bacteria Streptomycetes are well known for their structurally highly diverse natural products, many of which turned out to serve man as invaluable drugs for example as antibiotics. In contrast to the intense pharmaceutical interest in such secondary metabolites their ecological relevance for the producing strain in its natural habitat is poorly understood. The sequencing of the complete genome sequences of model Actinomyces revealed a number gene clusters coding for potential secondary metabolites. Many products of these “sleeping genes” have not been identified so far. One possible reason for this discrepancy is that the organism has no need to produce the metabolites under standard fermentation conditions that are optimised usually for growth and high titre antibiotic production.

However, in nature Streptomyces have to face changing abiotic and biotic conditions that will require appropriate chemical responses and thus so called “sleeping genes” might be induced. How do Streptomyces coordinate their metabolism in interaction with their environment and for what purpose do their secondary products serve them?

To address these questions the impact of defined abiotic and biotic factors on the differentiation of Streptomyces is systematically investigated *S. coelicolor* and *S. avermitilis* were either grown under heavy metal ion stress or in coculture with other soil bacteria.

Studying microbial interactions of *S. avermitilis* with one *Pseudomonas* species the droplets of *S. avermitilis* that Streptomyces strains release onto their aerial mycelium were examined. Interestingly the droplets contain high amounts of sugars produced by the Streptomycete but no antibiotic activity. In coculture the sugar concentration decreases by factor 400 indicating the impact of present *Pseudomonas* strain on the physiology of *S. avermitilis*. Changes on the development of *Streptomyces coelicolor* under heavy metal stress have been monitored by metabolic and transcriptional profiling. Metal ion stress induces drastic changes in *Streptomyces coelicolor* cultures such as gene expression, growth, and secondary metabolite profile. These alterations resulted in differentiated subpopulations of *S. coelicolor* under heavy metal ion stress.

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