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A small protein is involved in tryptophan biosynthesis and morpho-physiological differentiation in Streptomyces coelicolor

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Streptomycetes, bacteria belonging to the phylum of Actinobacteria, are characterized by a complex life cycle (which includes the formation of a vegetative mycelium, an aerial mycelium and spores) and the production of many secondary metabolites, including antibiotics. At the cellular level, regulatory factors comprise regulatory proteins, small RNAs and small ORFs. It is known that small ORFs (smorfs) can regulate the translation of downstream elements and can even encode functional peptides involved in the regulation of specific pathways. In the model streptomycete S. coelicolor, smorfs (100-300 nucleotides) were identified in biosynthetic amino acid gene clusters, such as trpM in tryptophan's one. Previous phenotypic and proteomic analysis of a trpM-knockout mutant strain, revealed that TrpM, a small protein of 63 amino acids, is involved in tryptophan metabolism and in morpho-physiological differentiation. In this work we describe the construction and the characterization of a trpM knock-in mutant strain. This strain shows an earlier production of the aerial mycelium and an increased production of CDA (calciumdependent antibiotic) and actinorhodin antibiotics in comparison to the wild type strain. Moreover, it produces a larger amount of spores, as revealed by SEM analysis and spore quantification. All these results confirm the key role of TrpM in S. coelicolor tryptophan metabolism and morphophysiological differentiation. Moreover, the over-expression of trpM could be regarded as a novel strategy to increase antibiotic production in Streptomyces strains of industrial interest