Identification and activation of novel biosynthetic gene clusters by genome mining in the kirromycin producer Streptomyces collinus Tü 365

Streptomycetes are prolific sources of novel biologically active secondary metabolites with pharmaceutical potential. S. collinus Tü 365 is a Streptomyces strain, isolated 1972 from Kouroussa (Guinea). It is best known as producer of the antibiotic kirromycin, an inhibitor of the protein biosynthesis interacting with elongation factor EF-Tu. Genome Mining revealed 32 gene clusters encoding the biosynthesis of diverse secondary metabolites in the genome of Streptomyces collinus Tü 365, indicating an enormous biosynthetic potential of this strain. The structural diversity of secondary metabolisms predicted for S. collinus Tü 365 includes PKS, NRPS, PKS-NRPS hybrids, a lanthipeptide, terpenes and siderophores. While some of these gene clusters were found to contain genes related to known secondary metabolites, which also could be detected in HPLC–MS analyses, most of the uncharacterized gene clusters are not expressed under standard laboratory conditions. With this study we aimed to characterize the genome information of S. collinus Tü 365 to make use of gene clusters, which previously have not been described for this strain. We were able to connect the gene clusters of a lanthipeptide, a carotenoid, five terpenoid compounds, an ectoine, a siderophore and a spore pigment-associated gene cluster to their respective biosynthesis products.