Abstract

Streptomyces is the largest antibiotic-producing genus in the microbial world. Manumycin-type antibiotics are a small group of its metabolites. Their antibiotic activities are not very important but they show biological properties which can be potencially used e. g. to treat inflammation, cancer or Alzheimer´s disease. The structure of manumycin compounds is formed by a central unit with connected upper and lower polyketide chain. The lower chain is mostly terminated by so called C_5N unit. The substance U-62162 produced by the strain *Streptomyces verdensis* differs significantly from the other members of the manumycin-type metabolites in the structure of the lower chain which is fully saturated and lacking the C_5N unit. The U-62162 biosynthetic gene cluster was sequenced and functions of identified open reading frames were deduced. Heterologous expressions of the cluster showed some genes reguired for the biosynthesis of the upper chain to be encoded on a different part of the chromosome. The insertional inactivation of the *vrdER* gene confirmed the enoylreductase to be responsible for the saturation of the lower chain. DSBA oxidoreductase, which gene is located at the edge of the cluster, is probably not involved in the biosynthesis. The insertion of genes for the biosynthesis of the C_5N unit did not resulted in a formation of derivates with the unit attached to the lower chain, whether saturated nor unsaturates. The cause of the failed attachment is not yet understood.