

Non-colinear polyketide biosynthesis in the aureothin and neoaureothin pathways: an evolutionary perspective.

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Abstract

Aureothin and neoaureothin (spectinabilin) represent rare nitroaryl-substituted polyketide metabolites from *Streptomyces thioluteus* and *Streptomyces orinoci*, respectively, which only differ in the lengths of the polyene backbones. Cloning and sequencing of the 39 kb neoaureothin (nor) biosynthesis gene cluster and its comparison with the aureothin (aur) pathway genes revealed that both polyketide synthase (PKS) assembly lines are remarkably similar. In both cases the module architecture breaks with the principle of colinearity, as individual PKS modules are used in an iterative fashion. Parsimony and neighbour-joining phylogenetic studies provided insights into the evolutionary process that led to the programming of these unusual type I PKS systems and to prediction of which modules act iteratively. The iterative function of the first module in the neoaureothin pathway, NorA, was confirmed by a successful cross-complementation.

Beteiligte Forschungseinheiten

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