Genome mining reveals the evolutionary origin and biosynthetic potential of basidiomycete polyketide synthases.

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Abstract

Numerous polyketides are known from bacteria, plants, and fungi. However, only a few have been isolated from basidiomycetes. Large scale genome sequencing projects now help anticipate the capacity of basidiomycetes to synthesize polyketides. In this study, we identified and annotated 111 type I and three type III polyketide synthase (PKS) genes from 35 sequenced basidiomycete genomes. Phylogenetic analysis of PKS genes suggests that all main types of fungal iterative PKS had already evolved before the Ascomycota and Basidiomycota diverged. A comparison of genomic and metabolomic data shows that the number of polyketide genes exceeds the number of known polyketide structures by far. Exploiting these results to design degenerate PCR primers, we amplified and cloned the complete sequence of armB, a PKS gene from the melleolide producer Armillaria mellea. We expect this study will serve as a guide for future genomic mining projects to discover structurally diverse mushroom-derived polyketides.

Beteiligte Forschungseinheiten

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