Rewiring of the Austinoid Biosynthetic Pathway in Filamentous Fungi.

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Abstract

Filamentous fungi produce numerous high-value natural products (NPs). The biosynthetic genes for NPs are normally clustered in the genome. A valuable NP class is represented by the insecticidal austinoids. We previously determined their biosynthesis in the fungus Aspergillus calidoustus. After further computational analysis looking into the austinoid gene clusters in two additional distantly related fungi, *Aspergillus nidulans* and *Penicillium brasilianum*, a rearrangement of the genes was observed that corresponded to the diverse austinoid derivatives produced by each strain. By advanced targeted combinatorial engineering using polycistronic expression of selected genes, we rewired the austinoid pathway in the fungus *A. nidulans*, which then produced certain compounds of interest under industrially favored conditions. This was possible by exploiting the presence of genes previously thought to be irrelevant. Our work shows that comparative analysis of genomes can be used to not only discover new gene clusters but unearth the hidden potential of known metabolic pathways.

Beteiligte Forschungseinheiten

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Stille Gencluster

Identifier

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