Differential expression of silent polyketide biosynthesis gene clusters in chemostat cultures of *Aspergillus nidulans*.

Sarkar A, Funk AN, Scherlach K, Horn F, Schroeckh V, Chankhamjon P, Westermann M, Roth M, Brakhage AA, Hertweck C, Horn U (2012) Differential expression of silent polyketide biosynthesis gene clusters in chemostat cultures of *Aspergillus nidulans*. *J Biotechnol* 160(1-2), 64-71.

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Abstract

The genome of the fungal model organism Aspergillus nidulans harbors nearly 30 polyketide synthase genes, yet the majority of these genes remain silent in the absence of particular stimuli. In this study, environmental conditions such as low specific microbial growth rate as well as nitrate, orthophosphate and glucose limitations were simulated under a continuous cultivation regime to induce the expression of silent polyketide synthase genes. In addition to offline and online bioprocess parameters, the physiological equilibrium was defined at the transcript level in terms of indicator gene expression. The different cultivation parameters resulted in a differential expression of two polyketide synthase genes coding for the biosynthesis of a variety of phenolic compounds, such as orsellinic acid, lecanoric acid, emodins, chrysophanol, shamixanthone, and sanghaspirodin. Further investigation of the metabolome revealed the formation of a novel prenylated benzophenone derivative designated as pre-shamixanthone. Our data indicate that

employing chemostat fermentations in combination with genome mining, transcriptome analysis and metabolic profiling represents a valuable approach for triggering cryptic biosynthetic pathways.

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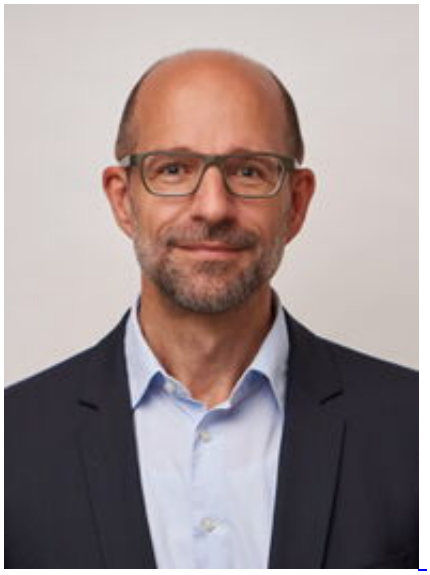
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Topics

Activation of silent gene clusters

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