

Genomic mining for *Aspergillus* natural products.

Bok JW, Hoffmeister D, Maggio-Hall LA, Murillo R, Glasner JD, Keller NP (2006) Genomic mining for *Aspergillus* natural products. *Chem Biol* 13, 31-37.

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Abstract

The genus *Aspergillus* is renowned for its ability to produce a myriad of bioactive secondary metabolites. Although the propensity of biosynthetic genes to form contiguous clusters greatly facilitates assignment of putative secondary metabolite genes in the completed *Aspergillus* genomes, such analysis cannot predict gene expression and, ultimately, product formation. To circumvent this deficiency, we have examined *Aspergillus nidulans* microarrays for expressed secondary metabolite gene clusters by using the transcriptional regulator *LaeA*. Deletion or overexpression of *laeA* clearly identified numerous secondary metabolite clusters. A gene deletion in one of the clusters eliminated the production of the antitumor compound terrequinone A, a metabolite not described, from *A. nidulans*. In this paper, we highlight that *LaeA*-based genome mining helps decipher the secondary metabolome of *Aspergilli* and provides an unparalleled view to assess secondary metabolism gene regulation.

Beteiligte Forschungseinheiten

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Leibniz-HKI-Autor*innen



Dirk Hoffmeister

[Details](#)

Identifier

PMID: 16426969