

# **Identification of the novel penicillin biosynthesis gene *aatB* of *Aspergillus nidulans* and its putative evolutionary relationship to this fungal secondary metabolism gene cluster.**

Spröte P, Hynes MJ, Hortschansky P, Shelest E, Scharf DH, Wolke SM, Brakhage AA (2008) Identification of the novel penicillin biosynthesis gene *aatB* of *Aspergillus nidulans* and its putative evolutionary relationship to this fungal secondary metabolism gene cluster. *Mol Microbiol* 70(2), 445-461.

## Details



## **Abstract**

The final step of penicillin biosynthesis in the filamentous fungus *Aspergillus nidulans* is catalysed by isopenicillin N acyltransferase encoded by the *aatA* gene. Because there is no bacterial homologue, its evolutionary origin remained obscure. As shown here, disruption of *aatA* still enabled penicillin production. Genome mining led to the discovery of the *aatB* gene(AN6775.3) which has a similar structure and expression pattern as *aatA*. Disruption of *aatB* resulted in a reduced penicillin titre. Surface plasmon resonance analysis and Northern blot analysis indicated that the promoters of both *aatA* and *aatB* are bound and regulated by the same transcription factors AnCF and AnBH1f. In contrast to *aatA*, *aatB* does not encode a peroxisomal targeting signal (PTS1). Overexpression of a mutated *aatB*(PTS1) gene in an *aatA*-disruption strain(leading

to peroxisomal localization of AatB) increased the penicillin titre more than overexpression of the wild-type *aatB*. Homologues of *aatA* are exclusively part of the penicillin biosynthesis gene cluster, whereas *aatB* homologues also exist in non-producing fungi. Our findings suggest that *aatB* is a parologue of *aatA*. They extend the model of evolution of the penicillin biosynthesis gene cluster by recruitment of a biosynthesis gene and its cis-regulatory sites upon gene duplication.

## Involved units

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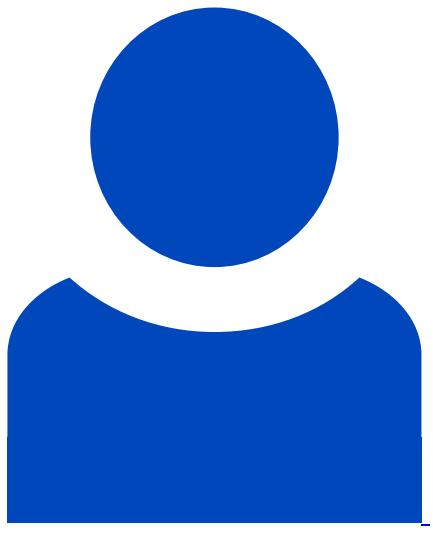
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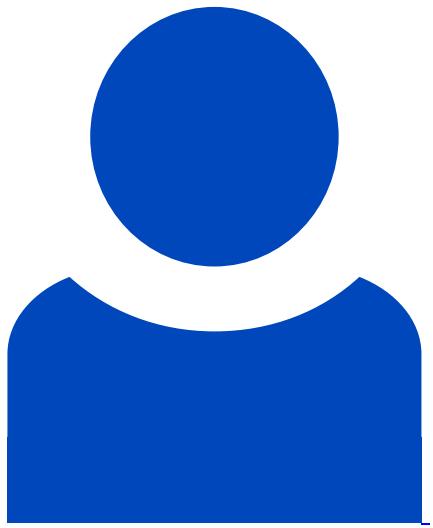
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### **Topics**

[Prediction of gene regulatory elements in fungi](#)

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