

Genome mining reveals the presence of a conserved gene cluster for the biosynthesis of ergot alkaloid precursors in the fungal family Arthrodermataceae.

Wallwey C, Heddergott C, Xie X, Brakhage AA, Li SM (2012) Genome mining reveals the presence of a conserved gene cluster for the biosynthesis of ergot alkaloid precursors in the fungal family Arthrodermataceae. *Microbiology* 158(Pt 6), 1634-1644. [PubMed](#)

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Projects

Secretome analysis/pathogenicity mechanisms of *Arthroderma benhamiae*

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Abstract

Genome sequence analysis of different fungi of the family Arthrodermataceae revealed the presence of a gene cluster consisting of five genes with high sequence similarity to those involved in the early common steps of ergot alkaloid biosynthesis in *Aspergillus fumigatus* and *Claviceps purpurea*. To provide evidence that this cluster is involved in ergot alkaloid biosynthesis, the gene ARB_04646 of the fungus *Arthroderma benhamiae* was cloned into pQE60 and expressed in *Escherichia coli*. Enzyme assays with the soluble tetrameric His(6)-tagged protein proved unequivocally that the deduced gene product, here termed ChaDH, catalysed the oxidation of chanoclavine-I in the presence of NAD(+), resulting in the formation of chanoclavine-I aldehyde. The enzyme product was unequivocally proven by NMR and MS analyses. Therefore, ChaDH functions as a chanoclavine-I dehydrogenase. $K(m)$ values for chanoclavine-I and NAD(+) were 0.09 and 0.36 mM, respectively. Turnover number was 0.76 s⁻¹.

Identifier

doi: 10.1099/mic.0.056796-0 PMID: 22403186