

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

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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).

Involved units

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