Functional and phylogenetic divergence of fungal adenylate-forming reductases.

Kalb D, Lackner G, Hoffmeister D (2014) Functional and phylogenetic divergence of fungal adenylate-forming reductases. *Appl Environ Microbiol* 80, 6175-6183.

Details

PubMed

Abstract

A key step in fungal l-lysine biosynthesis is catalyzed by adenylate-forming l-α-aminoadipic acid reductases, organized in domains for adenylation, thiolation, and the reduction step. However, the genomes of numerous asco- and basidiomycetes, contain an unexpectedly large number of additional genes encoding similar, but functionally distinct enzymes. Here, we describe the functional in vitro characterization of four reductases which were heterologously produced in Escherichia coli. The Ceriporiopsis subvermispora serine reductase Nps1 features a terminal ferredoxin:NADP(+)-reductase (FNR) domain and thus belongs to a hitherto undescribed class of fungal multi-domain enzymes. The second major class is characterized by the canonical terminal short chain dehydrogenase/reductase domain and represented by Ceriporiopsis subvermispora Nps3 as first biochemically characterized l-α-aminoadipic acid reductase of basidiomycete origin. Aspergillus flavus l-tyrosine reductases LnaA and LnbA are members of a distinct phylogenetic clade. Phylogenetic analysis supports the view that fungal adenylate-forming reductases are more diverse than previously recognized and belong to four distinct classes.

Beteiligte Forschungseinheiten

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Identifier

doi: AEM.01767-14

PMID: 25085485