Widespread inter- and intra-Ddmain horizontal gene transfer of d-amino acid metabolism enzymes in eukaryotes.

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Details



Abstract

Analysis of the growing number of available fully-sequenced genomes has shown that Horizontal Gene Transfer (HGT) in eukaryotes is more common than previously thought. It has been proposed that genes with certain functions may be more prone to HGT than others, but we still have a very poor understanding of the selective forces driving eukaryotic HGT. Recent work uncovered that d-amino acid racemases have been commonly transferred from bacteria to fungi, but their role in the receiving organisms is currently unknown. Here, we set out to assess whether d-amino acid racemases are commonly transferred to and between eukaryotic groups. For this we performed a global survey that used a novel automated phylogeny-based HGT-detection algorithm (Abaccus). Our results revealed that at least 7.0% of the total eukaryotic racemase repertoire is the result of inter- or intra-domain HGT. These transfers are significantly enriched in plant-

associated fungi. For these, we hypothesize a possible role for the acquired racemases allowing to exploit minoritary nitrogen sources in plant biomass, a nitrogen-poor environment. Finally, we performed experiments on a transferred aspartate-glutamate racemase in the fungal human pathogen Candida glabrata, which however revealed no obvious biological role.

Involved units

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Leibniz-HKI-Authors



Matthias Brock

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Sascha Brunke

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Bernhard Hube

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Topics

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