Burkholderia rhizoxinica sp. nov. and Burkholderia endofungorum sp. nov., bacterial endosymbionts of the plant-pathogenic fungus Rhizopus microsporus.

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Abstract

Several strains of the fungus Rhizopus microsporus harbour endosymbiotic bacteria for the production of the causal agent of rice seedling blight, rhizoxin, and the toxic cyclopeptide rhizonin. R. microsporus and isolated endobacteria were selected for freeze-fracture electron microscopy, which allowed visualization of bacterial cells within the fungal cytosol by their two parallel-running envelope membranes and by the fine structure of the lipopolysaccharide layer of the outer membrane. Two representatives of bacterial endosymbionts were chosen for phylogenetic analyses on the basis of full 16S rRNA gene sequences, which revealed that the novel fungal

endosymbionts formed a monophyletic group within the genus Burkholderia. Inter-sequence similarities ranged from 98.94 to 100%, and sequence similarities to members of the Burkholderia pseudomallei group, the closest neighbours, were 96.74-97.38%. In addition, the bacterial strains were distinguished from their phylogenetic neighbours by their fatty acid profiles and other biochemical characteristics. The phylogenetic studies based on 16S rRNA gene sequence data, together with conclusive DNA-DNA reassociation experiments, strongly support the proposal that these strains represent two novel species within the genus Burkholderia, for which the names Burkholderia rhizoxinica sp. nov. (type strain, HKI 454T=DSM 19002T=CIP 109453T) and Burkholderia endofungorum sp. nov. (type strain, HKI 456T=DSM 19003T=CIP 109454T) are proposed.

Beteiligte Forschungseinheiten

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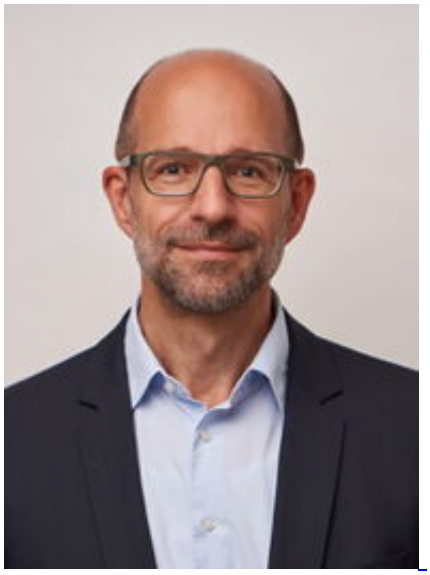

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