Biosynthesis of antifungal and antibacterial polyketides by Burkholderia gladioli in coculture with Rhizopus microsporus.

Ross C, Opel V, Scherlach K, Hertweck C (2014) Biosynthesis of antifungal and antibacterial polyketides by Burkholderia gladioli in coculture with Rhizopus microsporus. *Mycoses* 57, 48-55.

Abstract

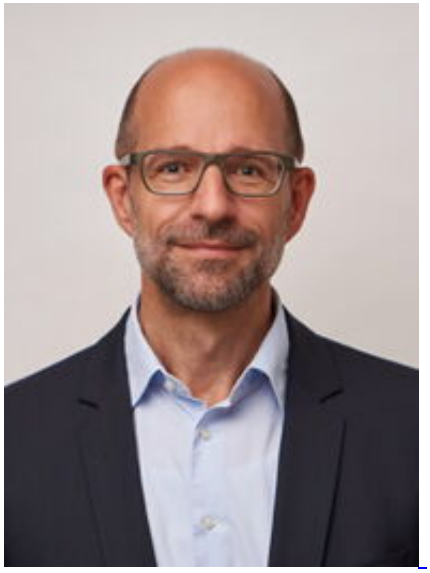
Fungi-bacteria interactions can impact the course of fungal infection and biotechnological use. The mucoralean fungus Rhizopus microsporus, traditionally used in food fermentations (tempe and sufu), is frequently accompanied by Burkholderia gladioli pv. cocovenenans. When producing tempe bongkrek, the bacterial contamination can lead to lethal food-related intoxications caused by the respiratory toxin bongkrekic acid. To unveil the metabolic potential of the fungus-associated bacterium, we sequenced its genome, assigned secondary metabolite biosynthesis gene clusters and monitored the metabolic profile under various growth conditions. In addition to the bongkrekic acid biosynthesis gene cluster we found gene clusters coding for the biosynthesis of toxoflavin and a complex polyketide. The orphan polyketide synthase gene cluster was activated under conditions that emulate tempe production, which enabled isolation and structure elucidation of four members of the enacyloxin family of antibiotics, out of which one is new. Moreover, we found that the fungus positively influences the growth of the bacteria and dramatically increases bongkrekic acid production in stationary culture, which inhibits the growth of the fungus. These results

showcase the context-dependent formation of antifungal and antibacterial agents at the fungal-bacterial interface, which may also serve as a model for scenarios observed in mixed infections.

Beteiligte Forschungseinheiten

Biomolekulare Chemie Christian Hertweck Mehr erfahren

Leibniz-HKI-Autor*innen



Christian Hertweck

Details

Claudia Roß

Details

Kirstin Scherlach

Details

Identifier

doi: 10.1111/myc.12246

PMID: 25250879