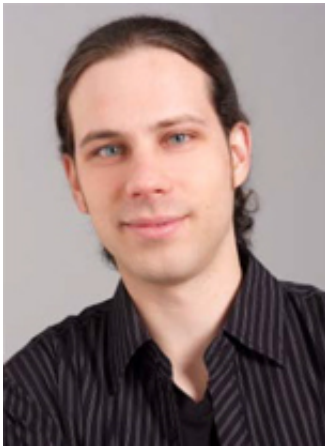




Gerald Lackner

The genome of the endofungal bacterium *Burkholderia rhizoxinica*

Symbiosis – the close association of two biological species – is a common survival strategy found in nature. The bacterium *Burkholderia rhizoxinica* is an endosymbiont of the phytopathogenic fungus *Rhizopus microsporus*, living within the hyphae of its host. It serves its host as intracellular toxin factory providing the fungus with the antimitotic compound rhizoxin. Rhizoxin is a pathogenicity factor against plants and causes symptoms of a severe plant disease called ‘rice seedling blight’. Furthermore, rhizoxin was in clinical trials as an antitumor agent. Consequently, the *Burkholderia-Rhizopus* alliance has numerous implications for natural product research and drug development. In addition, since *B. rhizoxinica* is the first symbiont of fungi that could be grown in pure culture, it has become a model system for bacterial-fungal interaction. I conducted experiments aiming at the elucidation of molecular mechanisms underlying fungal-bacterial interaction like infection and vertical transmission of symbionts. First, the whole genome of *B. rhizoxinica* was sequenced by shotgun technology and closed by finishing reactions. After automated annotation of the genome, I identified candidate genes that might be essential for endofungal lifestyle. The establishment of a gene inactivation strategy and a new bioassay allowed the generation and testing of mutant endosymbionts for defects in fungal-bacterial symbiosis. We expect that a better understanding of microbial communication might open new ways for efficient control of microorganisms with applications in biotechnology or agriculture.

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