

Novel traits of Trichoderma predicted through the analysis of its secretome.

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Abstract

Mycotrophic species of *Trichoderma* are among the most common fungi isolated from free soil, dead wood and as parasites on sporocarps of other fungi (mycoparasites). In addition, they undergo various other biotrophic associations ranging from rhizosphere colonization and endophytism up to facultative pathogenesis on such animals as roundworms and humans. Together with occurrence on a variety of less common substrata (marine invertebrates, artificial materials, indoor habitats), these lifestyles illustrate a wealthy opportunistic potential of the fungus. One tropical species, *Trichoderma reesei*, has become a prominent producer of cellulases and hemicellulases, whereas several other species are applied in agriculture for the biological control of phytopathogenic fungi. The sequencing of the complete genomes of the three species (*T. reesei*, *T. virens*, and *T. atroviride*) has led to a deepened understanding of *Trichoderma* lifestyle and its molecular physiology. In this review, we present the *in silico* predicted secretome of *Trichoderma*, and - in addition to the unique features of carbohydrate active enzymes - demonstrate the importance of such protein families as proteases, oxidative enzymes, and small cysteine-rich proteins, all of that received little attention in *Trichoderma* genetics so far. We also

discuss the link between Trichoderma secretome and biology of the fungus.

Beteiligte Forschungseinheiten

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