Insights on the Evolution of Mycoparasitism from the Genome of *Clonostachys rosea*.

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Abstract

Clonostachys rosea is a mycoparasitic fungus that can control several important plant diseases. Here we report on the genome sequencing of C. rosea and a comparative genome analysis, in order to resolve the phylogenetic placement of C. rosea and to study the evolution of mycoparasitism as a fungal lifestyle. The genome of C. rosea is estimated to 58.3 Mbp, and contains 14268 predicted genes. A phylogenomic analysis shows that C. rosea clusters as sister taxon to plant pathogenic Fusarium species, with mycoparasitic/saprotrophic Trichoderma species in an ancestral position. A comparative analysis of gene family evolution reveals several distinct differences between the included mycoparasites. C. rosea contains significantly more ATP-binding cassette (ABC) transporters, polyketide synthases, cytochrome P450 monooxygenases, pectin lyases, glucose-methanol-choline oxidoreductases and lytic polysaccharide monooxygenases compared with other fungi in the Hypocreales. Interestingly, the increase of ABC transporter gene

number in C. rosea is associated with phylogenetic subgroups B (multidrug resistance proteins) and G (pleiotropic drug resistance transporters), while an increase in subgroup C (multidrug resistance-associated proteins) is evident in T. virens. In contrast with mycoparasitic Trichoderma species, C. rosea contains very few chitinases. Expression of six group B and group G ABC transporter genes were induced in C. rosea during exposure to the Fusarium mycotoxin zearalenone, the fungicide Boscalid or metabolites from the biocontrol bacterium Pseudomonas chlororaphis. The data suggests that tolerance towards secondary metabolites is a prominent feature in the biology of C. rosea.

Beteiligte Forschungseinheiten

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