

Tricholoma vaccinum host communication during ectomycorrhiza formation.

Wagner K, Linde J, Krause K, Gube M, Koestler T, Sammer D, Kniemeyer O, Kothe E (2015)
Tricholoma vaccinum host communication during ectomycorrhiza formation. *FEMS Microbiol Ecol* 91(11),

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Abstract

The genome sequence of *Tricholoma vaccinum* was obtained to predict its secretome in order to elucidate communication of *T. vaccinum* with its host tree spruce (*Picea abies*) in interkingdom signaling. The most prominent protein domains within the 206 predicted secreted proteins belong to energy and nutrition (52%), cell wall degradation (19%) and mycorrhiza establishment (9%). Additionally, we found small secreted proteins that show typical features of effectors potentially involved in host communication. From the secretome, 22 proteins could be identified, two of which showed higher protein abundances after spruce root exudate exposure, while five were downregulated in this treatment. The changes in *T. vaccinum* protein excretion with first recognition of the partner were used to identify small secreted proteins with the potential to act as effectors in the mutually beneficial symbiosis. Our observations support the hypothesis of a complex communication network including a cocktail of communication molecules induced long before physical contact of the partners.

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doi: 10.1093/femsec/fiv120

PMID: 26449385