Genome sequence of the model mushroom *Schizophyllum commune.*

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Projects

 Expression and localization of G-protein coupled pheromone receptor Bar2 in the basidiomycete *Schizophyllum commune*
Details

Abstract

Much remains to be learned about the biology of mushroom-forming fungi, which are an important source of food, secondary metabolites and industrial enzymes. The wood-degrading fungus *Schizophyllum commune* is both a genetically tractable model for studying mushroom development and a likely source of enzymes capable of efficient degradation of lignocellulosic biomass. Comparative analyses of its 38.5-megabase genome, which encodes 13,210 predicted genes, reveal the species's unique wood-degrading machinery. One-third of the 471 genes predicted to encode transcription factors are differentially expressed during sexual development of S. commune. Whereas inactivation of one of these, fst4, prevented mushroom formation, inactivation of another, fst3, resulted in more, albeit smaller, mushrooms than in the wild-type fungus. Antisense transcripts may also have a role in the formation of fruiting bodies. Better insight into the mechanisms underlying mushroom formation should affect commercial production of mushrooms and their industrial use for producing enzymes and pharmaceuticals.

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