

Ras Module Function is Involved in Regulation of Sexual Development *Schizophyllum commune*

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The white rot fungus *Schizophyllum commune* is used as a model to investigate sexual development in hymenomycetes. We isolated the gene *gap1* encoding a GTPase-activating protein for Ras. Disruption of *gap1* should therefore lead to strains accumulating Ras in its activated, GTP-bound state and to constitutive Ras signaling. Mating behavior was not altered in $\Delta gap1$ monokaryons whereas growth rate in $\Delta gap1$ monokaryons was reduced about 25%. Dikaryotic $\Delta gap1/\Delta gap1$ strains displayed 50% growth reduction. Hyphal growth was disturbed showing a wavy growth pattern. In dikaryons, clamp formation was severely disturbed as hook cells failed to fuse with the penultimate cell at the site that in wildtype cells is marked by a peg formed from the mother cell. Instead, the dikaryotic character of the hyphae was rescued by fusion of the hooks with nearby developing branches. The mating type genes of the *B* factors encoding a pheromone receptor system are known to be required for clamp cell fusion. A role for Ras in the same process is discussed. Fruitbody formation was observed in homozygous $\Delta gap1/\Delta gap1$ dikaryons which, however, formed increased numbers of fruit body primordia, whereas the amount of fruit bodies was not raised. Mature fruit bodies formed no or abnormal gills. No production of spores could be observed. Similar phenotypes in fruitbody development had been previously described for elevated intracellular cAMP levels. Thus, the signalling of Ras is discussed with respect to cAMP signalling.