

Transcriptome and functional analysis of mating in the basidiomycete *Schizophyllum commune*.

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Abstract

In this study, we undertook a functional characterization and transcriptome analysis that enabled a comprehensive study of the mating type loci of the mushroom *Schizophyllum commune*. Induced expression of both the *bar2* receptor and the *bap2(2)* pheromone gene within 6 to 12 h after mates' contact was demonstrated by quantitative real-time PCR. Similar temporal expression patterns were confirmed for the allelic *bbr1* receptor and *bbp1* pheromone-encoding genes by Northern hybridization. Interestingly, the fusion of clamp connections to the subterminal cell was delayed in mating interactions in which one of the compatible partners expressed the *bar2* receptor with a truncated C terminus. This developmental delay allowed the visualization of a green fluorescent protein (Gfp)-labeled truncated receptor at the cell periphery, consistent with a localization in the plasma membrane of unfused pseudoclamps. This finding does not support hypotheses envisioning a receptor localization to the nuclear membrane facilitating recognition between the two different nuclei present in each dikaryotic cell. Rather, Gfp fluorescence observed in such pseudoclamps indicated a role of receptor-pheromone interaction in clamp fusion. Transcriptome

changes associated with mating interactions were analyzed in order to identify a role for pheromone-receptor interactions. We detected a total of 89 genes that were transcriptionally regulated in a mating type locus A-dependent manner, employing a cutoff of 5-fold changes in transcript abundance. Upregulation in cell cycle-related genes and downregulation of genes involved in metabolism were seen with this set of experiments. In contrast, mating type locus B-dependent transcriptome changes were observed in 208 genes, with a specific impact on genes related to cell wall and membrane metabolism, stress response, and the redox status of the cell.

Beteiligte Forschungseinheiten

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