

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

Erdmann S, Freihorst D, Raudaskoski M, Schmidt-Heck W, Jung EM, Senftleben D, Kothe E (2012) Transcriptome and functional analysis of mating in the basidiomycete *Schizophyllum commune*. *Eukaryot Cell* 11(5), 571-589. [PubMed](#)

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### Projects

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

[Details](#)

A surface hydrophobin in ectomycorrhiza interaction

[Details](#)

### 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.

**Identifier**

doi: 10.1128/EC.05214-11 PMID: 22210832