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Elucidation of hyphal growth process in the filamentous yeast Sch. japonicus.

The model organism *Sch. japonicus* is a non-pathogenic filamentous yeast, which can differentiate to form elaborately branched hyphae which invade deep into solid medium. Its ability to form mycelium makes this organism an attractive non-pathogenic model for studies of the yeast-hyphal interconversion process that is critical for pathogenicity in many pathogenic fungi, including *C. albicans*, *C. neoformans*, and *A. fumigatus*. The genes controlling yeast-hyphal interconversion have been the focus of recent investigations, as they have great potential as targets for novel antifungal drugs. The project consists to identify genes that are repressed in the presence of hyphal growth inhibitors. Messenger RNA will be isolated from yeast cells grown in the absence and presence of these inhibitors, and then subjected to microarray analyses. Genes that are repressed, inhibiting hyphal growth will be identified. Subsequently, their corresponding protein products will be identified based upon algorithm analysis from the *Sch. japonicus* sequencing genome project. Gene products that are involved in the transition from the unicellular yeast form to the invasive hyphal form will be characterized at the molecular level to identify their importance and roles into the mycelial phase. Molecular biology approaches will be used to characterize the morphology transition genes.