Identification of Potential Targets of the Grr1p SCF Ubiquitin Ligase in Fungi

Elizabeth Mullins, Department of Biological and Physical Sciences, Montana State University Billings, Billings, MT 59101

Joy Goffena, Department of Biological and Physical Sciences, Montana State University Billings, Billings, MT 59101

Kurt A. Toenjes, Department of Biological and Physical Sciences, Montana State University Billings, Billings, MT 59101

David K. Butler, Department of Biological and Physical Sciences, Montana State University Billings, Billings, MT 59101

The opportunistic human pathogen *Candida albicans* causes both superficial and life-threatening systemic infections and is a leading cause of fungal disease in immunocompromised individuals. *C. albicans* can grow in different cell shapes, or morphologies, including yeast-like cells and a variety of filamentous forms, such as true hyphae and pseudohyphae. Yeast, hyphae and pseudohyphae have been observed at the sites of *Candida* infection and there is strong evidence that morphogenesis, the transition between yeast and filamentous growth forms, is essential for virulence. Several studies have implicated ubiquitin-dependent proteolysis in the regulation of morphogenesis, yet the mechanism by which this pathway does so is largely unknown. Previously, we have shown that deletion of the GRR1 gene results in the constitutive formation of filamentous growth forms. The Grr1 protein is a component of an SCF ubiquitin ligase system that selectively targets proteins for degradation. Thus, the loss of Grr1-mediated proteolysis presumably leads to the aberrant accumulation, and inappropriate activity, of a protein or proteins that induce filamentous growth. The spectrum of proteins targeted for degradation by Grr1 is not known. The goal of this project is to identify Grr1 targets in *Saccharomyces cerevisiae*, an experimentally tractable model system for pathogenic fungi. We are using a novel proteomics-based approach to isolate and characterize proteins that are ubiquitinated in a Grr1-dependent fashion. The successful identification of Grr1p targets will be important for developing a

working model of the pathways involved in the yeast to filamentous growth transition in pathogenic fungi.