Chapter 1

Introduction

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Magnaporthe oryzae is a filamentous ascomycetous fungus responsible for rice blast disease. Rice blast disease causes losses of around 10%–30% of the total yield annually; however regional epidemics have been reported to cause losses of up to 80% of the total crop yield when predisposing conditions favor the disease development. Currently, disease management relies mainly on the breeding of resistant cultivars. However, due to the emergence of new races of the rice blast fungus, host resistance is transient. Development of novel methods to control rice blast needs detailed understanding of the disease as well as the biology of the pathogen. Availability of *M. oryzae* genome sequence, combined to recent developments in molecular genetics has made it feasible to identify major genes involved in various stages of host infection. Substantial progress in understanding of the disease has been made and many important genes required for early stages of infection have been identified. These include genes involved in development of appressoria, a bulbous structure involved in penetration of fungus into host tissue. Some highly conserved mitogen-activated protein kinase (MAPK) pathways have been identified to be essential for differentiation of appressoria and plant penetration. PMK1, MPS1, and OSM1 are three distinct MAPK genes to be identified for their role in pathogenesis-related development in *M. oryzae*.

PMK1 is the functional homolog of FUS3/KSS1 in budding yeast *Saccharomyces cerevisiae*. Δ*pmk1* mutants fail to develop appressoria and fail to form infection lesions in plants. However, *pmk1* mutants form appressorium in the presence of exogenous cAMP indicating that PMK1 operates downstream to the cAMP-mediated signal during appressorium morphogenesis. PMK1 homologs have been identified in a number of other phytopathogenic

fungi involved in diverse diseases. All of these MAPK genes have been reported to be essential for pathogenicity, suggesting that components of MAPK signaling pathway for pathogenesis related development are widely conserved. PMK1 MAPK pathway is functionally related to FUS3/KSS1pheromone signaling pathway; therefore other genes of this pathway have also been studied for their possible role in pathogenesis. *M. oryzae* MST7 and MST11 genes which are homologs of yeast Ste7 and Ste11 have also been demonstrated to be essential for appressoria development and host tissue colonization. Fus3 in yeast regulates the mating process by phosphorylating downstream proteins like Ste12 and Far1. Ste12 is a transcription factor involved in regulation of expression of genes related to mating process in *S. cerevisiae.* MST12 (a homolog for *S. cerevisiae* STE12) has been functionally characterized in *M. oryzae.* Gene deletion mutants of MST12 have been found to be non-pathogenic due to their inability to form penetration peg to breach the host tissue.

Most of the genes related to PMK1 MAPK pathway have been characterized and many of them have been found to be involved in pathogenesis related development of fungus. However, some of the genes like homolog of yeast STE2/STE3 receptors and FAR1 still remain unidentified. The primary reason that hinders their identification and characterization is their low sequence similarity with the proteins presents in *M. oryzae*. FAR1 (factor arrest resistant) is responsible for the cell cycle arrest at G1 phase due to inactivation of Cdc28-Cln2 complex in yeast during mating. The present study identifies a homolog of yeast FAR1 in rice blast fungus on the basis of bioinformatics and complementation studies. Functional analysis of this gene will help in understanding the mechanism and signal pathways involved in pathogenesis related development of rice blast fungus *M. oryzae*