

## ABSTRACT

### FUNCTIONAL CHARACTERIZATION OF PATHOGENICITY RELATED GENE(S) IN *MAGNAPORTHE ORYZAE*

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*Magnaporthe oryzae*, the causal agent of rice blast disease, serves as a model system in elucidating the infection pathways of plant pathogenic fungi. With the sequencing of the *M. oryzae* genome, there is a wealth of genetic information that needs to be linked to biological function and there is an increased interest to fully understand the various pathways leading to the development of the infection process. Sumoylation, a reversible posttranslational modification of proteins drive a wide variety of cellular processes and pathogenicity in *M. oryzae*. *M. oryzae* mutants lacking the SUMO (Small Ubiquitin-like MOdifier) was viable and they show dramatically reduced vegetative growth and conidiation. Additionally,  $\Delta Mosumo$  failed to form appressorium, which is critical for pathogenicity. Aberrant nuclear segregation, chitin distribution and septation also displayed by  $\Delta Mosumo$  mutant, indicating its role in cell cycle progression. The tagging of the MoSUMO peptide with GFP and live cell imaging has revealed that MoSUMO was

localized at nuclear and septal region in hyphae, whereas the expression is throughout the conidia and appressoria during development and infection in host tissue. Proteomic analysis of wild-type and  $\Delta Mosumo$  revealed absence of 72 protein, 36 protein spots were significantly up regulated and 56 spots were down regulated in  $\Delta Mosumo$ . The results from proteomic, molecular, and cellular approaches suggests that MoSUMO and/or sumoylated proteins play an important role in growth, development and pathogenicity of rice blast fungus.