## **Disruption of MoNUC1 Gene Mediates Conidiation in Magnaporthe oryzae**

Authors : Irshad Ali Khan, Jian-Ping Lu, Xiao-Hong Liu, Fu-Cheng Lin

Abstract : This study reports the functional analysis of a gene MoNUC1 in M. oryzae, which is homologous to the Saccharomyces cerevisiae NUC1 encoding a mitochondrial nuclease protein. The MoNUC1 having a gene locus MGG 05324 is 1002-bp in length and encodes an identical protein of 333 amino acids. We disrupted the gene through gene disruption strategy and isolated two mutants confirmed by southern blotting. The deleted mutants were then used for phenotypic studies and their phenotypes were compared to those of the Guy-11 strain. The mutants were first grown on CM medium to find the effect of MoNUC1 gene disruption on colony growth and the mutants were found to show normal culture colony growth similar to that of the Guy-11 strain. Conidial germination and appressorial formation were also similar in both the mutants and Guy-11 strains showing that this gene plays no significant role in these phenotypes. For pathogenicity, the mutants and Guy-11 mycelium blocks were inoculated on blast susceptible barley seedlings and it was found that both the strains exhibited full pathogenicity showing coalesced and necrotic blast lesions suggesting that this gene is not involved in pathogenicity. Mating of the mutants with 2539 strain formed numerous perithecia showing that MoNUC1 is not essential for sexual reproduction in M. oryzae. However, the mutants were found to form reduced conidia (1.06±8.03B and 1.08±9.80B) than those of the Guy-11 strain  $(1.46 \pm 10.61A)$  and we conclude that this protein is not required for the blast fungus to cause pathogenicity but plays significant role in conidiation. Proteins of signal transduction pathways that could be disrupted/ intervened genetically or chemically could lead to antifungal products of important fungal cereal diseases and reduce rice yield losses. Tipping the balance toward understanding the whole of pathogenesis, rather than simply conidiation will take some time, but clearly presents the most exciting challenge of all.

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