



# Proteomic analysis of mycelial proteins from *Magnaporthe oryzae* under nitrogen starvation

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**ABSTRACT.** *Magnaporthe oryzae* is an important model system in studies of plant pathogenic fungi, and nitrogen is a key nutrient source affecting microbial growth and development. In order to understand how nitrogen stress causes changes in mycelial proteins, we analyzed differentially expressed mycelial proteins from the *M. oryzae* virulent strain CH-63 using two-dimensional electrophoresis and mass spectrometry in complete medium or under nitrogen starvation conditions. A total of  $975 \pm 70$  and  $1169 \pm 90$  protein spots were detected in complete medium and under nitrogen starvation conditions, respectively. Forty-nine protein spots exhibited at least 2-fold up-regulation or down-regulation at the protein level according to PDQuest7.4. Moreover, 43 protein spots were successfully identified by matrix-assisted laser desorption/ionization-time-of-flight/time-of-flight mass spectrometry. Among these spots, 6 proteins were functionally unknown and 37 proteins were categorized into 5 groups according to

their functions, including development, metabolism, biosynthesis, and biological process. These 37 proteins were further analyzed for their enriched metabolic pathways by KOBAS2.0, and 14 proteins were found to be involved in glycolysis, tricarboxylic acid cycle, and nitrogen metabolism. Taken together, the regulation of *M. oryzae* growth under the nitrogen starvation conditions appears to be complex because of the various proteins and enzymes involved.

**Key words:** Mass spectrometry; Mycelium; Nitrogen stress; Proteome; Rice blast fungus