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## Genome-Wide Analysis of Hypoxia-Responsive Genes in the Rice Blast Fungus

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Rice blast fungus, *Magnaporthe oryzae*, is the most destructive pathogen of rice in the world. This fungus has a biotrophic phase early in infection and switches to a necrotrophic lifestyle after host cell death. During the biotrophic phase, the fungus competes with host for nutrients and oxygen. Continuous uptake of oxygen is essential for successful establishment of blast disease of this pathogen. Here, we report transcriptional responses of the fungus to oxygen limitation. Transcriptome analysis using RNA-Seq identified 1,047 up-regulated genes in response to hypoxia. Those genes were involved in mycelial development, sterol biosynthesis, and metal ion transport based on hierarchical GO terms and well-conserved among three different fungal species. In addition, null mutants of three hypoxia-responsive genes were generated and tested for their roles on fungal development and pathogenicity. The mutants for a sterol regulatory element-binding protein gene, *MoSRE1*, and C4 methyl sterol oxidase gene, *ERG25*, exhibited increased sensitivity to hypoxia-mimetic agent, increased conidiation, and delayed invasive growth within host cells, suggesting important roles in fungal development. However, such defects did not cause any significant decrease in disease severity. The other null mutant for alcohol dehydrogenase gene, *MoADH1*, showed no defect in the hypoxia-mimic condition and fungal development. Taken together, this comprehensive transcriptional profiling in response to a hypoxia condition with experimental validations would provide new insights on fungal development and pathogenicity in plant pathogenic fungi.