

TRANSCRIPTOME PROFILING OF TWONEAR-ISOGENIC RICE LINES INFECTED BY *Magnaporthe oryzae* USING RNA-SEQ

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Rice blast caused by the fungus *Magnaporthe oryzae* is a major constraint in production worldwide and causes losses of up to 100% of the yield depending on cultivar susceptibility, environmental conditions and management system. The molecular basis of the defense response to rice blast remains poorly characterized. A thorough understanding of the molecular response mechanisms against rice blast will aid in the design of novel strategies to engineer rice cultivars with durable resistance. The research described here focused on early signaling events involved in the expression of rice genes in plants infected with *M. oryzae* using RNA-Seq technique for differential gene expression we analyzed the rice transcriptome in infected leaves at 24 hours post-inoculation. Gene expression analysis was performed and the results demonstrated that there are many complex modifications at transcript level when leaves of two near-isogenic rice lines were infected with this fungus. The sensitivity and high dynamic range of RNA-Seq allowed the identification of genes critically involved in conferring resistance during the early steps of defense perception-signaling. Quantitative RT-PCR was performed to confirm these observations. The putative role of specific plant genes identified in this study is discussed.

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