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***Xanthomonas oryzae* pv. *oryzae* triggers complex transcriptomic defense network in rice**

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Abstract

High throughput transcriptome investigations of immunity in plants highlight the complexity of gene networks leading to incompatible interaction. To identify genes crucial to resistance against *Xanthomonas oryzae* pv *oryzae*, functional genetic analysis of selected differentially expressed genes from our microarray data set was carried out. A total of 13 overexpression vector constructs were made using 35S CaMV promoter which drive constitutive expression in rice. Most of the genes are developmentally expressed especially during maximum tillering stage and are commonly highly expressed in the leaves. When screened against *Xoo* strain K2, the transgenic plants displayed shorter lesion length compared with wild type Dongjin which indicates partial resistance. The levels of ROS continuously magnified after inoculation which indicates robust cellular sensing necessary to initiate cell death. Elevated transcripts levels of several defense-related genes at the downstream of defense signal network also corroborate the phenotype reaction of the transgenic plants. Moreover, expression assays revealed regulation of these genes by cross-communicating signal-transductions pathways mediated by salicylic and jasmonic acid. These collective findings revealed the key immune signaling conduits critical to mount full defense against *Xoo*.

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