

Transcriptional Activation of Diverse Defense-Related Genes Triggered by *Xanthomonas oryzae* pv. *oryzae* in Rice

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[Introduction]

Bacterial blight, caused by *Xanthomonas oryzae* pv. *oryzae*, is a serious disease problem of rice causing damage to rice quality and yield.

[Materials and Methods]

To understand the transcriptional gene network involved in resistance against *Xoo*, a whole-genome oligonucleotide microarray of two popular *japonica* rice Dongjin and Jinbaek were used to infer transcripts of inducible genes between compatible and incompatible interactions at 48 hour post inoculation. A large number of genes are more evident in the resistant cultivar, which is threefold higher than in susceptible plant. Up-regulation of genes with predicted functions in signaling and transcription signifies orchestration of defense signals and robust cellular reprogramming leading to incompatible interaction.

[Results]

To further identify genes crucial to immunity, 13 *Xoo*-DEGs of different protein class were cloned and overexpressed using CaMV 35S promoter into rice. Most of the overexpression plants displayed improved resistance when screened against *Xoo* Korean race K2. Elevated transcripts levels of several defense-related genes at the downstream of defense signal network also corroborate the phenotype reaction of the transgenic plants. ROS levels continuously magnified after inoculation which indicates robust cellular sensing necessary to initiate cell death. Moreover, expression assays revealed regulation of these genes by cross-communicating signal-transductions pathways mediated by salicylic acid. These collective findings revealed the complexity of key immune signaling conduits critical to mount full defense against *Xoo* in rice.

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