

Transcriptome Dynamics of Cysteine Protease-Mediated Response Against *Xoo* Race K3a in Rice

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[Introduction]

Pathogen infection modulates defense reactions in the host cells. Numerous findings proved that papain-like cysteine proteases (PLCPs) function as a central hub in plant defense. While diverse roles of PLCPs in different pathosystems have become more evident, information on which gene networks and signaling pathways are activated to orchestrate downstream responses remains limited.

[Materials and Methods]

To understand the biological significance of cysteine protease against *Xanthomonas oryzae* pv. *oryzae*, RNAi-mediated knockout and overexpression of xylem cysteine protease gene were constructed in rice. Pathogenicity test showed that transgenic rice attenuated the virulence of *X. oryzae* pv. *oryzae* race K3a which could be attributed to a high accumulation of hydrogen peroxide and free salicylic acid. To provide useful insights into genome-wide transcriptome profile during early interaction with the pathogen, next-generation sequencing of RNA from transgenic and wild type plants infected for 30 minutes was carried out.

[Results]

A total of 2,086 combined differentially expressed genes were identified, 471 of which were exclusively regulated in the transgenic library. The resistance observed in transgenic rice is ascribed to an extensive participation of genes with predicted functions in intracellular signal transduction, transcription activity, secondary metabolic process including phenylpropanoid and lignin biosynthesis, and defense response. Moreover, protein-protein interaction network revealed the indispensable network of defense layer in transgenic rice.

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