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Isolation and characterization of a novel gene which is involved in plant disease resistance

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Objectives

To understand the role of a novel gene, which contains LRR domains, we generated transgenic rice plants overexpressing the gene and analyzed them.

Materials and Methods

1. Materials

Plant - *Oryza sativa* cv Hwacheong

Agrobacterium strain - LBA4404

2. Methods

Callus were obtained from rice seeds. *Agrobacterium* carrying the overexpression construct were inoculated onto rice callus and selected on the media containing PPT.

Results and Discussion

Plants have evolved sophisticated defense mechanisms to resist against their pathogens. Inducible responses are dependent on successful recognition of the invading pathogen. Successful recognition events are mediated via the direct or indirect interaction between the product of a microbial avirulence gene and the corresponding plant disease resistance (R) gene product. Most R gene known in plant so far has tandem copies of leucine rich repeat region. In this study, we have isolated a novel gene encoding a leucine rich repeat (LRR) protein expressed highly upon pathogen attack from *Oryza sativa* by a differential screening. This gene encodes a 22.8kDa protein in size and consists of a signal peptide at its N terminal end and leucine zipper domain at the right next to the signal peptide and five tandem copies of LRR domain. This gene is highly induced upon the infection of *Magnaporthe grisea* and *Xanthomonas oryzae pv. oryzae*(Xoo). It is also induced in salicylic acid (SA), benzothiadiazole(BTH), wound and NaCl treated rice seedlings respectively. This gene is induced earlier upon the infection of incompatible race than compatible. Taken together it appears to be involved either directly or indirectly in the recognition event of the interaction between plant and pathogen. Characteristics of transgenic plants overexpressing this gene will be discussed in detail. This work is funded by NIAB and ARPC to Dr. Duk-Ju Hwang.

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