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Pathogenicity assay of *Xanthomonas oryzae* pathovar *oryzae* *hrp* disrupted mutants

Cho, Hee Jung, Jeong Gu Kim, Young Jin Park, Eun-Sung Song, Tae-Whan Noh¹,
Dong-Hee Lee² and Byoung-Moo Lee*

National Institute of Agricultural Biotechnology, RDA, Suwon, 441-707, Korea

¹Honam Agricultural Research Institute, RDA, Iksan, 570-080, Korea

²Department of Life Science, Ewha Womans University, Seoul, 120-420, Korea

Objectives

We study about hypersensitive reaction and pathogenicity (*hrp*) genes in PAIs (pathogenicity islands) of *Xanthomonas oryzae* pathovar *oryzae* to understand the bacterial type III secretion system (TTSS) and plant-microbe interaction.

Materials and Methods

1. Material

Xanthomonas oryzae pathovar *oryzae* KACC10859, EZ::TNTM<KAN-2>, Milyang-23, Nutrient broth

2. Methods

We carried out gene disruption by homologous recombination. In this study, we disrupted 26 *hrp*-genes by Tn insertional mutagenesis and marker exchange. PCR amplification and Southern blot was carried out to confirm the genes disruption.

Results and Discussion

Xanthomonas oryzae pv. *oryzae*(Xoo) causes bacterial blight (BB) in rice and one of the most damaging disease internationally. In severely cases, the disease can cause yield losses as high as 50%. In phytopathogenic bacteria, the type III protein secretion system (TTSS) encoded by *hrp* genes plays a central role in eliciting defense responses, such as the rapid cell death response called the hypersensitive reaction (HR), on non-host or resistant host plants and pathogenesis on susceptible hosts pathogenesis. A *hrp* gene cluster was identified in the Xoo KACC10331 genome that included 26 genes inclusive of *hpa2* and *hrpF*. The *hrp*-related genes were disrupted by marker exchange and the mutants were inoculated on riceto assay their pathogenicity. Functional genomics studies on *hrp*-related genes using DNA microarray and yeast-two hybrid are also in progress. All of these researches will be helpful to understand the bacterial type III secretion system (TTSS) and plant-microbe interaction.