1-05. Functional pathogenomics of *Burkholderia glumae (oral)*

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The aim of this study was to characterize the interactions of rice and *Burkholderia glumae*, a causal agent of bacterial grain rot of rice, at molecular levels using whole genomic sequences and to identify genes important for pathogenicity and symptom development. To do these, we sequenced whole genome of the bacterium and constructed cosmid clone profiles. We generated pools of mutants using various transposons and determined mutation sites by sequencing rescued plasmids. We focused on studying toxoflavin biosynthetic genes, quorum sensing regulation, and Hrp type III protein secretion systems. We found that two possible operons consisting of five genes are involved in toxoflavin biosynthesis and their expression is regulated by quorum sensing and LysR-type regulator, ToxR. We have isolated the Hrp PAI of *B. glumae* and characterized by mutational analyses. The *hrp* cluster resembled most the putative Type III secretion systems of *B. pseudomallei*, which is the causative agent of melioidosis, a serious disease of man and animals. The Hrp PAI core region showed high similarity to that of *Ralstonia solanacearum* and *Xanthomonas campestris*, however some aspects were dissimilar.

1-06. Rice genes specifically expressed in a rice mutant gained resistance to rice blast.(oral)

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A gain-of-function mutant, SHM-11 obtained through gamma-ray mutagenesis, is resistant to rice blast caused by *Magnaporthe grisea* while wild type Sanghaehyanghyella is highly susceptible to the same disease. The resistance in the mutant was not race-specific when we tested with four races (KJ-201, KI-1113a, KI-313, KI-409) of *M. grisea*. To identify genes involved disease resistance in the gain-of-function mutant, genes specifically expressed in the mutant were selected by suppression subtractive hybridization using cDNAs of blast-inoculated mutant and wild type as a tester and a driver, respectively. Random 200 clones from the subtracted library were selected and analyzed by DNA sequencing. The sequenced genes represented three major groups related with disease resistance; genes encoding PR proteins, genes probably for phytoalexin biosynthesis, and genes involved in disease resistance signal transduction. A gene encoding a putative receptor-like protein kinase was identified as highly expressed only in the gain-of-function mutant after blast infection. The role of the putative receptor-like protein kinase gene during blast resistance will be further studied.