

Structural and Functional Genomics of *Burkholderia glumae*, the Causative Agent of Rice Grain Rot

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Burkholderia glumae causes rice seedling and grain rot. We study the interactions of rice and the bacterium at genomics and molecular levels. Crop Functional Genomics Center funded to sequence the *B. glumae* BGR1 genome. Genomic sequencing by the sequencing consortium (Macrogen, GreenGene BioTech, Bioneer, and Eugentech) achieved 10.2× coverage and is now in closure phase. Total genome size of the bacterium is 7.1 Mb in size. There are two chromosomes, chromosome I (3.84 Mb) and chromosome II (2.77 Mb), and one plasmid (0.5 Mb). We predict there are more than 6,000 genes. Approximately 80% of the genes were assigned by COG. Overall genome was very closely related with *B. pseudomallei*, which is responsible for melioidosis of man and animals. For functional studies, we have generated various transposon mutant pools and constructed cosmid clone genomic profiles. Based on genome information and mutant analyses, we want to identify a set of genes that are under the HrpB regulon, novel genes responsible for pathogenicity and symptom development, and effector proteins that are predicted to be delivered to plant cells. We are also interested in secreted proteins that are independent of the Hrp type III secretion systems. We focus on the biosynthesis of toxoflavin, which is a major virulence factor, and its regulation by quorum sensing. We analyze candidates of effector proteins obtained by bioinformatic approaches and 2-D gel analysis followed by mass spectroscopic analysis. A genome-wide analysis of the bacterium will provide insights into novel interaction mechanisms between rice and bacterial plant pathogens.