
Plant Pathology Seminar Series

“Genome-wide Association Analysis Tracks Bacterial Leaf Blight Resistance Loci in Rice Diverse Germplasm”

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Bacterial blight disease, caused by *Xanthomonas oryzae* pv. *oryzae* (Xoo), is one of the most economically important diseases of rice. Continuous rice cultivation in Asia has resulted in highly virulent Xoo races, causing yield reductions of up to 50% in certain environments (Mew et al. 1993). A range of resistance genes effective against Xoo have been discovered and characterized (Verdier et al., 2011). Despite this, several of the resistance genes widely deployed in modern rice varieties have already become ineffective due to rapid evolution of Xoo (Mew et al., 1992). The continuous “arms race” between Xoo and rice makes it imperative to discover and deploy new resistance loci to provide durable resistance in modern breeding lines. The worldwide collection of rice germplasm encompasses a wide range of diversity (Virk et al. 2000; Zhao et al., 2010), and can be exploited as a reservoir of useful genetic variation for bacterial leaf blight (BLB) resistance. The use of high-density molecular markers in combination with genetically diverse panels, identification of novel disease resistance through genome-wide association analysis (GWA) and allele mining is possible. GWA enables the discovery of novel alleles and allele combinations that are useful in crop improvement (Zhu et al., 2008; Tung et al., 2010). To identify genetic donors and BLB resistance loci, a global panel of 285 rice accessions was screened against nine representative Xoo strains. Using single nucleotide polymorphisms (SNPs) generated from genotyping-by-sequencing, loci associated with differential resistance to nine Xoo strains were identified. Strong associations of SNPs linked to seven known bacterial blight resistance genes were identified, and markers were designed for tracking and selection of these genes in breeding programs. In addition, significant SNPs on chromosomes 5, 6, 11, and 12 did not overlap with any known resistance loci, and could represent novel resistance loci. Further analysis revealed haplotypes correlated with resistance, and analysis of resistance alleles has enabled identification of new genetic donors. The results of the GWA have validated known genes underlying resistance in the diverse panel, and identified novel loci that may provide new sources of resistance. The SNP markers and genetic donors identified in this study will help plant breeders in improving and diversifying resistance to bacterial leaf blight in rice.

4:10 pm | Monday, September 10 | Johnson Hall 343
Plant Pathology 515, Fall 2018



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& Natural Resource Sciences

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