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Genome-wide association mapping of resistance genes to Phytophthora root rot in soybean

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Phytophthora root rot (PRR), which caused by the soil-borne oomycete *Phytophthora sojae* (*P. sojae*), is one of the most devastating diseases in the soybean production countries such as USA, Brazil, Argentina, India and China. Utilization of resistant varieties is the most economical and friendly-environmental method for controlling this disease. Hence, to screen resistance germplasms and discover new resistance genes is the foundation of soybean resistance breeding. In the present study, we identify the resistance of soybean mini core collection germplasm to fourteen *P. sojae* isolates using hypocotyls inoculation method. And association mapping of soybean mini core collection using single nucleotide polymorphism (SNP) markers to excavate loci associate with resistance to *P. sojae* isolates was carried out.

1. Characterization of Phytophthora resistance in soybean mini core collection. Many germplasms had a range resistance spectrum to *P. sojae* isolates. More than fifty percent of accessions have resistant reactions to at least four isolates, among them eighteen accessions show resistance to 8-11 *P. sojae* isolates. We investigated the distributions of resistance germplasms and found Sichuan, Jiangsu and Hubei provinces had the most number of resistant accessions. Germplasms from Hubei, Jiangsu, Fujian, Sichuan and Shandong provinces possessed broad spectrum resistance with resistance to more than 5 *P. sojae* isolates. Gene postulating shows 34 germplasms may not have any resistance gene, and 22 gremplasms may contain *Rps7* gene, and accession ZDD03733 may contain *Rps1a* + *Rps3b* or *Rps1c* + *Rps3b* gene combination.

2. Genome-wide association mapping of resistance to Phytophthora root rot in soybean mini core collection Genome-wide association analysis on soybean mini core collection genotyped with SNPs was associated with resistance to PRR. With population structure and kinship as covariates, adopting naive model, general linear model (GLM) and mixed linear model (MLM), 28 SNP markers are identified significantly Phytophthora resistance associations, including 15 loci localized in previous linkage mapped gene or QTL intervals. These results will serve as a basis for breeding of *P. sojae*-resistant soybean cultivars through marker-assisted selection.