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Genome-wide Association Analyses for Resistance to *Phytophthora sojae* and *Pseudomonas amygdali* pv. *tabaci* in Soybean

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[Abstract]

Phytophthora root and stem rot (PRSR) and wildfire disease (WFD) of soybean are frequently observed in the field of South Korea. The most environmentally friendly way to control PRSR and WFD is to use soybean varieties with resistance to *Phytophthora sojae* (*P. sojae*) and *Pseudomonas amygdali* pv. *tabaci*. Plant germplasm is an important gene pool for soybean breeding and improvement. In this study, hundreds of soybean accessions were evaluated for the two pathogens, and genome-wide association analyses were conducted using 104,955 SNPs to identify resistance loci for the two pathogens. Of 193 accessions, 46 genotypes showed resistance reaction, while 143 did susceptibility for PRSP. Twenty SNPs were significantly associated with resistance to *P. sojae* on chromosomes (Chr.) 3 and 4. Significant SNPs on Chr.3 were located within the known *Rp*s gene region. A region on Chr. 4 is considered as a new candidate resistance loci. For evalation of resistance to WFD, 18, 31, 74, 36 and 34 genotypes were counted by a scale of 1-5, respectively. Five SNP markers on Chrs 9, 11, 12, 17 and 18 were significantly associated with resistance to *P. amygdali* pv. *tabaci.* The identified SNPs and genomic regions will provide a useful information for further researches and breeding for resistance to *P. sojae* and *P. amygdali* pv. *tabaci*.

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