

PB-17

Genome Wide Association Study for *Phytophthora sojae* Resistance with the Two Races Collected from Main Soybean Production Area in Korea with 210 Soybean Natural Population

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[Abstract]

Recently days, soybean production in paddy field is increasing, from 4,422 ha in 2016 to 10,658 ha in 2021 in Korea. It is easy for Phytophthora stem and root rot (PSR) occurring in paddy field condition, when it is poorly drained soils with a high clay content, and temporary flooding and ponding. Therefore PSR resistant soybean cultivar is required. The objective of this study is to identify QTL region and candidate genes relating to PSR resistance of the race in main soybean cultivation area in Korea. 210 soybean materials including cultivars and germplasm were used for inoculation and genome-wide association study (GWAS). Inoculation was conducted using stem-scar method with 2 replications in 2-year for the race 3053 from Kimje and 3617 from Andong. 210 materials were genotyped with Soya SNP 180K chip, and structure analysis and association mapping were conducted with QTLMAX V2. The results of inoculation showed that survival ratio ranged from 0% to 96.7% and mean 9.7% for 3053 and ranged from 0% to 100% and mean 7.6% for 3617. Structure analysis showed linkage disequilibrium (LD) was decayed below $r^2=0.5$ at 335kb of SNP distance. Significant SNPs (LOD>7.0) were identified in Chr 1, 2, 3, 4, 5, 11, 14, 15 for 3053 and Chr 1, 2, 3, 7, 10, 14 for 3617. Especially, LD blocks (AX-90455181;15,056,628bp~AX-90475572; 15,298,872bp) in Chr 2 for 3053 and 3067 were duplicated. 29 genes were identified on these genetic regions including *Glyma.02g147000* relating to ribosome recycling factor and defense response to fungus in Soybase.

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