

Division-3-04

Genome Wide Association Study for Agronomic Traits in Wild Soybean (*Glycine soja*)

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[Introduction]

Soybeans (*Glycine max*) are one of the most important crops in the world because they are not only high in protein and oil content, but also contain all of the essential amino acids. Wild soybean (*Glycine soja*) is the wild ancestor of cultivated soybean and preserve valuable gene pool for improving agronomic traits in soybean. Advances in high-throughput genotyping techniques have facilitated approach to SNP genotyping. Genome wide association study (GWAS) is being used as a powerful tool to discover and validate QTLs and candidate genes associated with variety of agricultural traits.

[Materials and Methods]

The 203 wild soybean accessions were planted in the experimental field of Chonnam National University, 2015 and 2016. The agronomic traits including days to flowering (DtF), days to maturity (DtM), number of pods (NoP) and one-hundred seed weight (100SW) were investigated. Also, the protein, oil and amino acid contents were analyzed using Kjeldahl, Soxhlet method and amino acid auto-analyzer (S433-H, SYKAM), respectively. All accessions were genotyped using 180K Axiom® Soya SNP array. GWAS was performed with linear mixed model using restricted maximum likelihood algorithm in QTLmaxV2.

[Results and Discussion]

The 203 wild soybean accessions were divided into 4 clusters by ADMIXTURE, principal component analysis and neighbor-joined cluster. GWAS identified 18 SNPs linked to DtF, 32 SNPs to DtM, and 41 SNPs to 100SW. Through the detected SNP marker few genes governing specific traits were selected as candidate genes. Among them, Glyma.06g119400 and Glyma.11g251500 were related to DtF, Glyma.12g210900 was commonly related to DtF and DtM, and Glyma.14g205200 was related to 100SW. In addition, we identified two genes, Glyma.11g015500 and Glyma.20g050300, responsible for protein and oil content respectively. In amino acids, we identified that Glyma.01g053200 and Glyma.03g241600 genes were related to 9 amino acids (Ala, Asp, Glu, Gly, Leu, Lys, Pro, Ser, Thr). The identification of SNP markers associated with agronomic traits are expected to be helpful for the development of molecular markers that can be used for soybean breeding.

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