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Identification of the Genomic Region Underlying Seed Weight in Soybean (*Glycine max*) via Genome-Wide Association Study

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[Introduction]

One of a yield component, Seed weight (SW) is a complex and agronomically important trait in soybean [*Glycine max* (L.) Merr.]. Previous many studies have identified quantitative trait loci (QTL) associated with seed weight in soybean recombinant inbred lines (RILs) and these QTL are documented in Soybase (Grant et al. 2010). Since linkage analysis is based on progeny isolated from two parents, linkage analysis of the bi-parental population can't find a fixed QTL in two parents (Yan et al. 2017). To solve this problem, GWAS using a population of various resources can be a powerful tool. In this study, we performed to identify major and minor candidate QTLs through GWAS on seed weight in 430 accessions with genetic diversity.

[Materials and Methods]

A total of 430 soybean accessions, including landraces and improved lines, were applied to evaluate the variation of 100-seeds weight. All accessions were bulk-harvested individually after full maturity in field of the National Institute of Crop Science, Rural Development Administration (Jeonju, Korea) in 2016, 2017 and 2018. A sample of 100 cleaned seeds from each accession was randomly taken and weighed. The data of 100-seeds weight were presented as grams per 100-seeds and used to evaluate GWAS.

[Results and Discussion]

100-seed weight of 430 accessions was distributed 7.3 ~ 59.4 g in 2016, 9.1 ~ 48 g in 2017 and 8.7 ~ 45.6 g in 2018. We performed a selection probability (SP) GWAS analysis using an average of 100 seed weights in 2016, 2017, and 2018, and identified SNPs that were significant with 100 seed weights using the Lasso method. As a result of SP GWAS, the top 10 SNPs were identified. The highest SP value was found in SNP of chromosome 6, followed by SNP of chromosome 16. These two SNPs were SNPs with 100 seed weights and high significance in both 2016, 2017 and 2018. As a result, we identified a number of candidate genes associated with 100 seed weight. The results of the present study could provide fundamental and practical information for both genetic research and breeding programs in soybean.

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