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Discovery of Novel SNPs for *Sg-1* Gene Involved in Soyasaponin Biosynthesis from Soybean Core Collection

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[Introduction]

Soyasaponin is a type of glycoside like steroids, steroid alkaloids, or triterpene. It is known as a component that enhances the human body's immunity. Soybean contains a lot of functional small molecules with various physiological activities such as isoflavone and soyasaponin. Soyasaponin composition in soybean seeds varies with seed tissue and differs among varieties. So far, individual genes involved in the biosynthesis mechanism of soyasaponin have been reported in various populations, but genome-wide association studies for seed accumulation of soyasaponin have not yet been reported. Hence, SoyaSNP array and whole genome resequencing data were used to identify the genetic factors involved in the biosynthesis of group A soybean saponins.

[Materials and Methods]

Soybean core collection (430 samples) representing the genetic diversity of whole resources were constructed based on 170,223 SNP information of 180K Axiom® 180k SoyaSNP array for 2,872 soybean genetic resources. The 430 accessions of soybean core collections were planted at an interval of 70*15cm in experiment field of National Institute of Crop Science in 2017 and 2018. Soyasaponin content analysis was analyzed for 328 overlapping resources by year among 430 resources.

[Results and Discussion]

The annual heritability (H^2) of Aa and Ab derivatives belonging to group A soyasaponins were 98.31% and 97.83% in 2017 and 2018, respectively. The 16 markers with $-\log_{10}(p) > 5$ associated with Aa and Ab derivatives were mapped on chromosome 7. In the 34.16kb LD block, 8 markers with $R^2 \leq 1$ were identified, and 3 candidate genes including Glyma.07g254600 (*Sg-1*) were detected. Functional haplotype for three candidate genes showed that soyasaponin derivative Aa and Ab content was mainly determined by alleles of *Sg-1*. In addition, the 14 novel genotypic variants closely associated with group A soyasaponin contents were discovered for *Sg-1* from whole genome resequencing data. Therefore, this study is meaningful in that it effectively discovered markers and useful genes associated with soyasaponin based on various genomic information, and these results can contribute to the improvement of soybean varieties by validating the novel *Sg-1* markers in the future.

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