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Haplotype-based Association Analysis of the Genes related to Biosynthesis of Isoflavone and Soyasaponin in Korean Soybean Core Collection

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[Introduction]

Soybean is important food resource because they contain a variety of secondary metabolites in addition to vegetable protein sources. The secondary metabolites are primarily composed of isoflavone and soyasaponin in soybean. The biosynthesis pathway of isoflavone and soyasaponin are well known, but the genetic factors for their biosynthesis regulation still needs to be further studied. We performed haplotype analysis, using re-sequencing data to detect mutation in Korean soybean core collection. The natural mutations identified their relationship with the content of secondary metabolites. The genotype grouping by haplotype analysis is expected to explain the change of the secondary metabolite content.

[Materials and Methods]

We performed haplotype analysis using re-sequencing data of Korean soybean core collection (424 samples). Twenty-six genes related to biosynthesis of the isoflavones (twenty genes) and soyasaponins (six genes) were selected for the haplotype analysis. The isoflavones and soyasaponins contents were analyzed using a UHPLC (Dionex Ultimate 3000, Thermo Scientific) instrument equipped with an AcclaimTM RSLC Polar Advantage II (2.2 μ m, 2.1 mm \times 150 mm) column.

[Results and Discussion]

Natural SNPs of the twenty-six genes were identified in Korean soybean core collection. Some SNPs showed high correlation between the genotype and phenotypes (isoflavones and soyasaponins) by the haplotype based association analysis. In the case of soyasaponin, it was confirmed that the change in total soyasaponin content was significant according to the haplotype of the *CYP93E1* gene. The soyasaponin content of group1 (Val³⁶¹) and group2 (Leu³⁶¹) were 118.33 mg kg⁻¹ and 129.21 mg kg⁻¹, respectively, and the *p*-value was <0.05. The five genes were selected according to a significance test between isoflavones content and related gene haplotype. Non-synonymous mutations and indels in *GmCHS2*, *GmCHS9*, *GmCHR1*, *GmCHS2* and *GmCHR5* were closely related to total isoflavone content. The significant changes in the content of soyasaponin and isoflavone were confirmed according to the genotypes classified by haplotype analysis. The haplotype-based association analysis is expected to be used for the development of molecular markers and genes related to various secondary metabolites in soybean.

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