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QTL Analysis for Seed Protein Concentration in Soybean with two RIL populations

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[Introduction]

Soybean seeds having unique seed composition consist of approximately 40% protein, 20% oil, 35% carbohydrate and 5% ash. Among them, seed protein and sugar concentrations are important traits that affect the quality of soyfoods. Therefore many studies and breeding programmes have been conducted to find QTL related to protein and sugar concentrations and develop cultivars with high protein and sugar content. The objective of this study was to identify QTL related to seed protein and sugar concentrations using two RIL populations and high-density SNP markers.

[Materials and Methods]

A total of 426 lines and three parents from two RIL populations derived from crossing between 'YS2035-B-91-1-B-1' and 'Saedanbaek' (YS), and 'Saedanbaek' and 'Ilmi' (SI) were used for SNP genotyping and QTL analysis. The protein concentration was determined by the Dumas method using Rapid N Cube. The parents and RILs were genotyped using a 180K SNP chip array. Linkage map construction and QTL analysis were conducted using QTL IciMapping software V4.1.

[Results and Discussion]

Out of the total 180,375 SNP markers, 27,896 and 27,724 were polymorphic between the parents. After removing the redundant markers, a total of 3,443 and 2,329 markers were finally utilized to construct the linkage map construction. The linkage maps snapped a total length of 6,234 and 6,053 cM with an average of 1.87 cM and 2.85 cM. QTL for seed protein concentration were detected on ten chromosome (2, 3, 5, 8, 11, 13, 15, 17, 18, and 20) YS population and six chromosome (8, 9, 13, 15, 19 and 20) in SI population. The LOD values of the QTL ranged from 3.2 to 43.1, and PVE by QTL ranged from 1.7 to 49.6%. Among them, major QTL (PVE > 10%) were detected on chromosome 13, 15 and 20. Our results could be useful to further understand the genetic research on soybean seed composition and applied in breeding programmes.

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