

A whole genome screen for linkage disequilibrium and association mapping of genes related to seed protein content in soybean

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Objective

The objective of this study was to map linkage disequilibrium of soybean seed protein related by differences in allele frequency between two subgroups, high and low protein content populations.

Materials and Methods

Forty-eight each from high and low soybean seed protein content genotypes were able to obtain from USDA Soybean Germplasm Collection (<http://www.ars-grin.gov/npgs/index.html>) (Table 1). They were classified into two subgroups with high and low protein content populations. Also, each subgroup was separated into three origin groups (Korea,, China and Japan). Data were collected from 131 SSR markers located within 5-10cM of QTLs associated with soybean seed protein content and 39 SSR markers selected randomly. After the primary linkage group was determined on the basis of public USDA map information, allele distributions were compared statistically with means of contingency table.

Results and Discussion

In soybean seed protein research, linkage analysis has been very successful for mapping quantitative trait loci (QTLs). However, this strategy is time-consuming because several generations are required before linkage analysis is performed. Also, recombination rarely occurs and gene regions identified by linkage is often large since linkage focuses on recent. In contrast to linkage studies, association studies use natural populations, reducing the time for analysis. Moreover, target regions are extremely small because association studies are drawn from historic recombination. A set of 170 SSR markers were surveyed across a total of 96 germplasms that were classified high and low protein population. In result, it was shown that tightly linked markers to QTLs for soybean seed protein content detected by linkage analysis revealed significant *P* values. Some markers exceptionally showed significant *P* values, having some distance away from soybean seed protein QTLs detected by linkage analysis. Association analysis might be a powerful tool to identify QTL in soybean. Newly identified QTLs associated with soybean seed protein content are expected.

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Table 1. Characteristics of the plant materials used in the study.

	Population subdivision	
	High Protein population	Low protein population
No. of germplasms	48	48
Maturity group (No.)	IV - VI : 38 VII - VIII : 10	I - II : 28 V - VI : 20
Protein content (%)	50.8 - 57.4	31.7 - 38.7
Origin	Korea : 14 China : 24 Japan : 10	Korea : 12 China : 24 Japan : 12

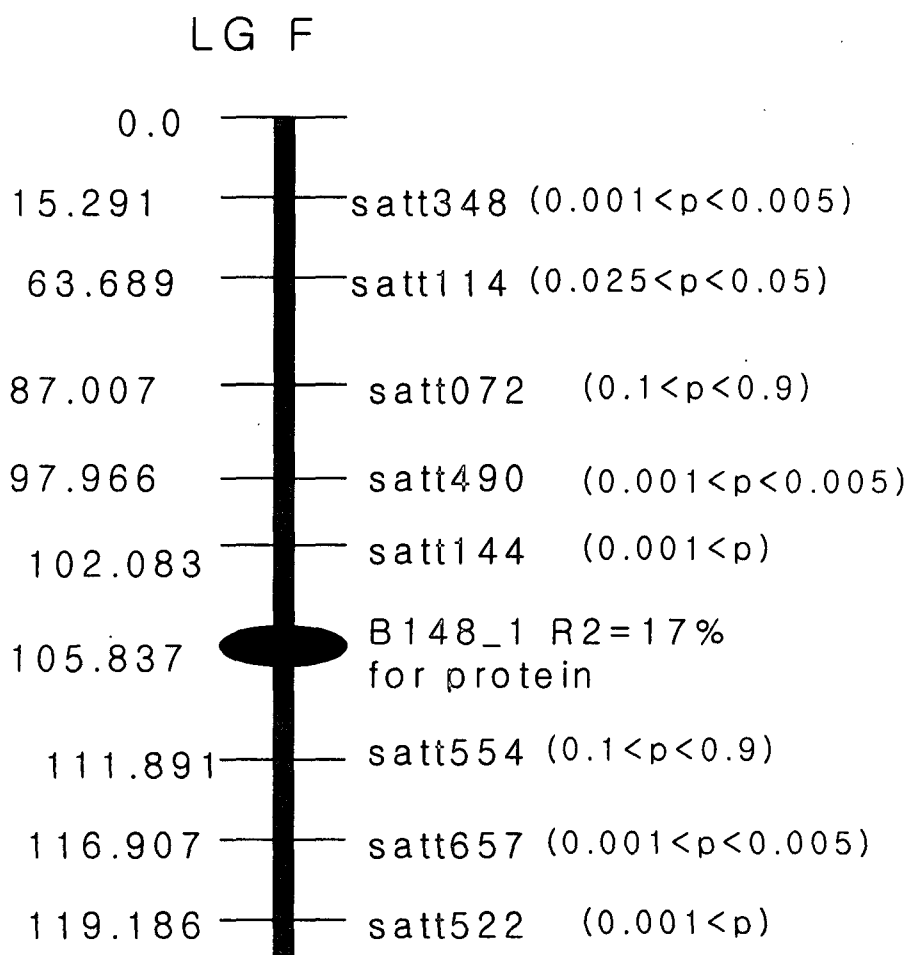


Figure 1. Soybean linkage disequilibrium map on LG F with SSR markers. Left shows relative position on chromosome and right shows p-value of each marker. An oval figure indicates QTL associated with soybean seed protein content.