

Consistency of QTLs for Soybean Seed Size across Generations

Jongil Chung[†] and James E. Specht*

Department of Agronomy, Gyeongsang Natl. Univ. Chinju city, 660-701, Korea

**Department of Agronomy, University of Nebraska-Lincoln, Lincoln, NE68583-0915, USA*

Abstract

Soybean [*Glycine max* (L.) Merr.] seed size is a important yield component and is a primary consideration in the development of cultivars for specialty markets. Our objective was to examine the consistency of QTLs for seed size across generations. A 68-plant F_2 segregation population derived from a mating between Mercury (small seed) and PI 467.468 (large seed) was evaluated with RAPD markers. In the F_2 plant generation (i.e., F_3 seed), three markers, OPLO9a, OPMO7a, and OPAC12 were significantly ($P<0.01$) associated with seed size QTLs. In the $F_2 \times F_3$ generation (i.e., F_4 seed), four markers, OPAO9a, OPG19, OPLO9b, and OPP11 were significantly ($P<0.01$) associated with seed size QTLs. Just two markers, OPLO9a and OPLO9b were significantly ($P<0.05$) associated with seed size QTLs in both generations. The consistency of QTLs across generations indicates that marker-assisted selection for seed size is possible in a soybean breeding program.

Key words : RAPD, Seed size, QTL, Generation

Introduction

Seed size is quantitatively inherited in soybean. A change in seed size will have a significant effect on seed yield, if all other yield components are held constant. Molecular markers based upon DNA polymorphism have greatly simplified the genetic analysis of quantitative traits, providing a reliable and extensive framework of qualitative markers to which quantitative trait loci (QTL) can be linked (Stuber¹). Several reports have been published on soybean QTLs for seed size (Mansur et al.², Mian et al.³, and Maughan et al.⁴). We identified several RAPD markers linked to seed size QTLs in F_2 population (Chung and Specht⁵). In this study,

QTL reproducibility and consistency for seed size was examined across generations.

Materials and Methods

The study was conducted with a F_2 and $F_2 \times F_3$ generations derived from a mating between the cultivar Mercury (small seed) and the plant introduction PI 417.468 (large seed). A random sample of F_2 seeds were planted on 17 May 1995 in the University of Nebraska- Lincoln, Nebraska, USA East campus field nursery in a bordered block of six 25-seed plots that were 0.75 m x 0.90 m. At maturity, individual F_2 plants were individually harvested. A random sample of 25 F_3 seeds

[†] Corresponding author

derived from each of the 107 F_2 plants planted on 17 May 1996 in the UNL East Campus field nursery in plots 0.90 m long spaced 0.75 m apart. The experimental design for this field test was a randomized complete block, with four replications of the 107 entries (i.e., $F_{2:3}$ lines). When the F_3 plants in each plot reached maturity, they were threshed in bulk. The harvested seed was air-dried to a constant moisture. Seed size (g/100 seed) for the F_2 plant generation were measured by weighing the F_3 seed produced by each F_2 plant and dividing by the number of seeds. In the $F_{2:3}$ families, two samples of 100-seed were weighed from each of the four replicates grown in the field. The eight estimates were averaged to obtain a mean seed size for each family. DNA extraction, RAPD marker analysis, construction of linkage map, and QTL analysis procedures were reported in previous paper (Chung and Specht⁵).

Results and Discussion

A genetic map was constructed from the 156 segre-

gating RAPD markers. Of the 156 markers, 113 were found to be genetically linked and formed 29 linkage groups, with 43 markers unlinked. The linkage map spanned 1043 cM across all 29 linkage groups, with markers separated by an average distance of 9.2 cM (Chung and Specht⁵). The results of single factor analysis for F_2 and $F_{2:3}$ generation are presented in Table 1. Three markers, OPM07a and OPAC12 on linkage group 19, and OPL09a on linkage group 16 had highly significant effects on seed size ($P<0.01$) in F_2 generation. Four markers OPA09a on linkage group 2, OPG19 and OPP11 on linkage group 10, OPL09b on linkage group 17 were significantly ($P<0.01$) associated with QTL for seed size in $F_{2:3}$ generation. Just two markers, LO9a and LO9b were significantly ($P<0.05$) associated with seed size QTLs in both generations.

Inconsistency of QTLs associated with agronomic traits across populations and environments in soybean has been previously reported by Lee et al.⁶ and Mian et al.³. Replicate F_2 (or F_n) populations from the same mating tested together in multiple environments is the

Table 1. RAPD loci putatively associated with seed size (g/100 seed) QTLs in F_2 plants and $F_{2:3}$ lines, as detected by single-factor analysis of variance.

Markers	Linkage group	Generation	F-test probability	Marker means and standard deviations	
				Mecury	PI417.468
OPA09a	2	F_2	0.123	15.07±0.64	16.23±0.37
		$F_{2:3}$	0.004	14.79±0.53	16.57±0.30
OPM07a	19	F_2	0.005	13.89±0.77	16.31±0.33
		$F_{2:3}$	0.282	15.42±0.70	16.25±0.30
OPAC12	19	F_2	0.005	13.89±0.77	16.32±0.33
		$F_{2:3}$	0.282	15.42±0.70	16.25±0.30
OPG19	10	F_2	0.069	14.96±0.62	16.29±0.37
		$F_{2:3}$	0.002	14.73±0.50	16.63±0.30
OPL09a	16	F_2	0.006	15.48±0.35	17.59±0.65
		$F_{2:3}$	0.019	15.78±0.30	17.35±0.57
OPP11	10	F_2	0.066	14.95±0.61	16.30±0.37
		$F_{2:3}$	0.004	14.84±0.51	16.59±0.30
OPL09b	17	F_2	0.012	14.74±0.55	16.48±0.37
		$F_{2:3}$	0.008	15.05±0.47	16.62±0.32

best means of assessing QTL reproducibility. In our study, two markers, OPL09a and OPL09b were associated with seed size QTLs in across generations. The results indicate that these two markers linked to QTLs for seed size is true. However, experimental error associated with measurement of seed size in our F₂ generation may have resulted in a lack of detection of this QTL. Some of our F₂ plants produced less than 100 seed, so 100-seed weight for these was extrapolated from the weight of the actual number of seed. The consistency of QTLs across generations indicates that marker-assisted selection is possible in a soybean breeding program.

Conclusion

A 68-plant F₂ segregation population derived from a mating between Mercury (small seed) and PI 467.468 (large seed) was evaluated with RAPD markers. In the F₂ plant generation (i.e., F₃ seed), three markers, OPL09a, OPM07a, and OPAC12 were significantly (P<0.01) associated with seed size QTLs. In the F_{2:3} generation (i.e., F₄ seed), four markers, OPA09a, OPG19, OPL09b, and OPP11 were significantly (P<0.01) associated with seed weight QTLs. Just two markers, OPL09a and OPL09b were significantly (P<0.05) associated with

seed weight QTLs in both generations.

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초록 : 대두 종자크기에 대한 QTL의 consistency

정종일[†] · James E. Specht*
(경상대학교 농학과, *네브라스카 주립대학교 농학과)

대두 종자크기에 대한 QTL의 consistency을 알아보기 위하여 F₂, F₃ 세대에서의 분석결과를 요약하면 다음과 같다.

세 개의 마크, OPL09a, OPM07a, OPAC12 가 F₂ 세대에서 종자 크기에 대한 QTL과 높은 유의성을 나타내었고, F₃ 세대에서는 네 개의 마크, OPA09a, OPG19, OPL09b, OPP11 가 유의성을 나타내었다. 두개의 마크 OPL09a, OPL09b 가 두 세대에서 유의성을 나타내어 종자 크기에 대한 QTL의 consistency가 인정되었다.