

A major gene for grain cadmium accumulation in soybean (*Glycine max* [L.] Merr.)

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Introduction

Cadmium (Cd) is a pollutant heavy metal though naturally present in soils in low quantities. It is highly toxic to biological organism even at low concentrations. This trace metal can accumulate in the human body over the time as a result of ingesting food containing it [1]. Substantial variation in Cd uptake by the root and its posterior accumulation in the grain has been reported among soybean (*Glycine max* [L.] Merr.) cultivars [2].

Results and Comments

Analysis by QTL Cartographer 2.0 revealed one major locus associated with seed Cd accumulation. The main effect of the QTL was relatively large, as reflected by high LOD scores, 34.92 and 22.77 for F₇ and F₈ respectively. This QTL was closely linked to the novel microsatellite marker Gm09_AT_09 on molecular linkage group (MLG) K and explained approximately 70 % of the total phenotypic variation in the populations. Non-normality on the distribution of the measured trait and the large effect of QTL, suggested that seed Cd accumulation might be controlled by one major gene. The identified QTL could be useful in marker-assisted selection (MAS) of soybean for developing varieties with low seed Cd accumulation.

Table 1. Putative QTL a LOD score 9.46 detected in a soybean RILs F₇ and F₈ population.

QTL	MLG	Interval	POS (cM)		LOD		Add. ^a		Var. ^b (%)	
			F ₇	F ₈	F ₇	F ₈	F ₇	F ₈	F ₇	F ₈
Cd	K	Gm09_ATT_21	36.6	36.6	25.9	18.9	0.09	0.20	66.8	54.6
		Gm09_AT_09	40.9	40.9	34.9	22.8	0.10	0.21	71.8	59.1

^a Add. = Additive effect.

^b Var. = Variance explained.

Table 2. Association between seed Cd concentration and genotypes of SSR marker proximal to QTLs for Cd in soybean RILs F₇ and F₈.

Material	Segregating marker (proximal to QTL)	Genotype ^a	Number of lines	Cd ^b ± SD	
				F ₇	F ₈
RILs	Gm09_AT_09	HH	42	0.34 ± 0.07	0.79 ± 0.22
		HF	2	0.33 ± 0.05	0.75 ± 0.14
		FF	49	0.16 ± 0.03	0.39 ± 0.12
Harosoy				0.43 ± 0.18	0.60 ± 0.17
Fukuyutaka				0.17 ± 0.08	0.16 ± 0.06

^a HH = homogeneous for Harosoy genotype, HF = heterozygous, FF = homogeneous for Fukuyutaka genotype.

^b Cd = Seed Cd concentration.

References

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- [2] Arai T., Ae N., Sugiyama M., Takahashi M. 2003. Genotype differentiation in cadmium uptake and distribution in soybean. Plant Soil 251: 247-253.
- [3] Lander ES, Green P, Abrahamson J, Barlow A, Day MJ, Lincoln SE, Newberg L (1987) Mapmaker: an interactive computer package for constructing primary genetic linkage maps of experimental and natural population. Genomic 1:174-181.

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Methodology

The aim of this research was to identify quantitative trait loci (QTLs) for Cd concentration in soybean seed using 93 recombinant inbred lines (RILs) in the F₇ and F₈ generations of the cross between cv. Harosoy and cv. Fukuyutaka, which differ in grain Cd accumulation. Randomly picked seeds from each RIL were used for DNA isolations and Cd concentrations analyses in each generation. Simple sequence repeat (SSR) analyses were performed using genomic DNA extracted from the F₇ and F₈ generations and the soybean linkage map constructed by MAPMAKER/EXP. ver. 3.0 [3]. Twenty linkage groups comprising 189 SSR markers and covering 2422cM of genome length were constructed from the RILs F₇ and F₈ populations..

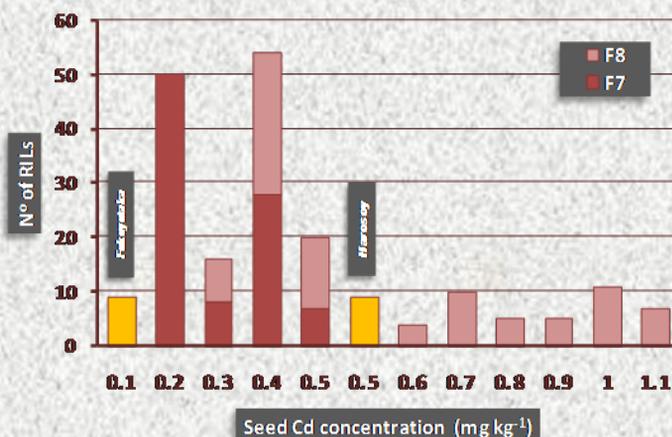


Figure 1. Frequency distribution of seed Cd concentration in soybean RILs F₇ and F₈ populations and the parents.

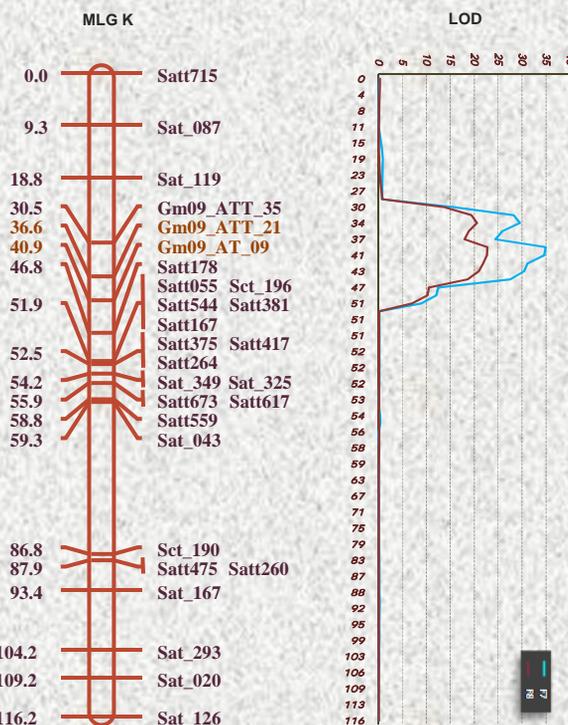


Figure 2. Position of QTL for seed Cd concentration in soybean RILs F₇ and F₈ populations. Figure in the left side of the MLG K indicate LOD peak at the QTL.