

QTL mapping of basal root whorl number in common bean (*Phaseolus vulgaris* L).

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INTRODUCTION

Plant root characteristics are of primary importance in determining the ability of a plant to acquire nutrients and water. Basal root whorl number (BRWN) has been associated with nutrient (especially phosphorus) uptake efficiency in common bean. Whorls are defined as distinct tiers of basal roots that emerge along the base of hypocotyls, ranging from 1 to 4 (rarely 5) whorls among bean cultivars. Each whorl bears typically 3-4 roots.

OBJECTIVE

Perform quantitative trait loci analysis of BRWN and basal root number in two populations of recombinant inbred lines of common bean derived from parents contrasting for BRWN.

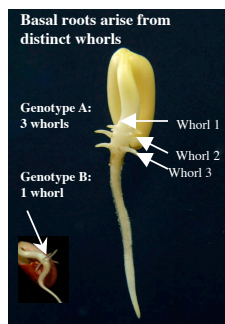


Figure 1. Genotypes with 1 whorl and 3 whorls.

MATERIAL AND METHODS

Phenotypic data on BRWN was obtained from the seedlings of the RILs 3 days after imbibition. QTL analysis was conducted using QTL Cartographer version 2.0 for Windows. QTL for BRWN, basal root number, and their combined effects were identified with Composite Interval Mapping (CIM).



Figure 2. Root phenotyping of bean seedlings 3 days after imbibition with 0.5 mM of calcium sulfate at 28 °C.

RESULTS

Preliminary results showed few QTL associated with these traits. We found that almost 25% of the variation for BRWN in DOR364 x G19833 and over 58% of the variation for BRWN in G2333 x G19839 RIL populations were controlled by a single locus.

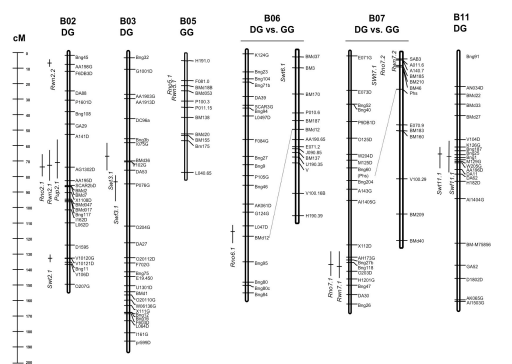


Figure 3. Preliminary results of QTL mapping of basal root whorl number of DOR364 x G19833 and G2333 x G19839 RIL populations of common bean.

Population	Trait (unit)	QTL name	LG ¹	Nearest marker	LOD ²	R ²	TR ²	Additive effect	Positive allele
DOR364 x G19833	BRWN	Rwo2.1	B2	AA198G	2.71	0.1994	0.3708	-0.115	G19833
		Rwo2.2	B2	AG1302D	3.69	0.1557	0.5265	-0.147	G19833
	Average no. Roots	Rwo7.1	B7	O203D	5.29	0.2473	0.4042	-0.173	G19833
		Rwo2.1	B2	AG1302D	3.31	0.1103	0.4887	-0.379	G19833
	Average Seed weight (PSI)	Rwo6.1	B6	BM412	3.07	0.1192	0.5293	0.355	DOR364
		Rwo7.1	B7	O203D	4.10	0.1425	0.4887	-0.387	G19833
	Seed weight (g/100S) (CIAT - Darien - HP)	Swo2.1	B2	V10120G	3.43	0.1013	0.5482	-0.017	G19833
		Swo3.1	B3	BM436	4.40	0.1689	0.5995	0.022	DOR364
	Seed weight (g/100S) (CIAT - Darien - HP)	Swo11.1	B11	Bag25	3.92	0.1257	0.5729	-0.019	G19833
		Swo5.1	B3	PN70G	3.94	0.1023	0.5768		DOR364
Seed weight (g/100S) (CIAT - Darien - HP)	Swo8.1	B4	G122G	3.08	0.0878	0.6598		G19833	
	Swo11.1	B11	Bag1	7.50	0.2163	0.5814		G19833	
G2333 x G19839	BRWN	Rwo5.1	B5	BM4018D	3.37	0.2263	0.4185	-0.168	G19839
		Rwo7.1	B7	SAB3	13.41	0.5872	0.9247	-0.392	G19839
	No. Basal roots	Rwo5.1	B5	BM118b	3.43	0.1529	0.5025	-0.511	G19839
		Rwo7.1	B7	SAB3	10.31	0.6140	0.8388	-1.216	G19839
	Seed weight (PSI)	Swo6.1	B6	BM170	6.29	0.3175	0.7445	-0.036	G19839
		Swo7.1	B7	BM210	8.54	0.3877	0.7179	-0.042	G19839
Seed weight (g/100S) (CIAT - Darien - HP)	Hwo6.1	B6	BM3	5.38	0.1788	0.6428	-3.475	G19839	
	Hwo11.1	B11	Bag1	10.25	0.3233	0.6074	-4.451	G19839	

¹LG = linkage group as defined by Freyre et al (1998). ²LOD threshold of 2.5 used for QTL detection, empirical LOD thresholds based on 1000 permutations as recommended by Churchill and Doerge (1994). R² = proportion of variance explained by QTL at a site. TR² = proportion of variance explained for the QTL and the background markers.

Table 1. QTL for BRWN and basal root number in the DOR364 x G19833 and G2333 x G19839 RIL populations. Circled values highlight a highly significant QTL for BRWN found in both populations.

CONCLUSION

- The results indicate that few QTL are associated with basal root whorl number in common bean.
- The high proportion of variance explained by a single locus suggests that this trait can be used as a criterion for selection of genotypes with better performance in low phosphorus environments.

AKNOWLEDGEMENTS

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