

Evaluation of two novel root traits for soil resource acquisition in common bean

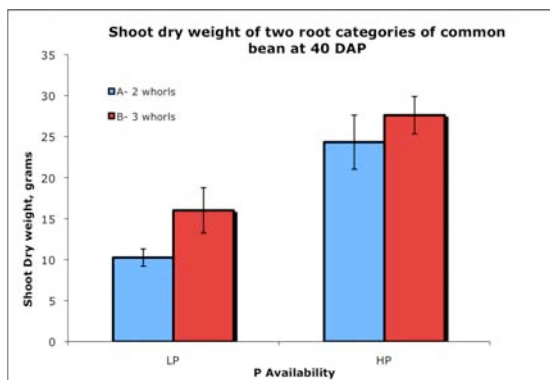
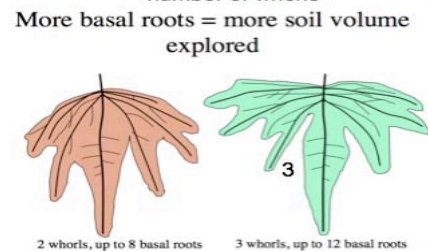
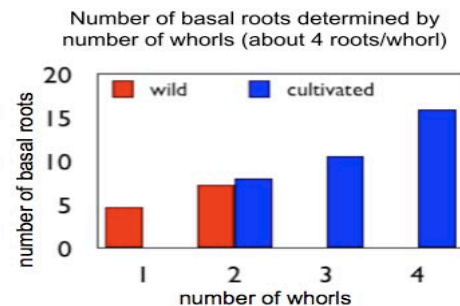
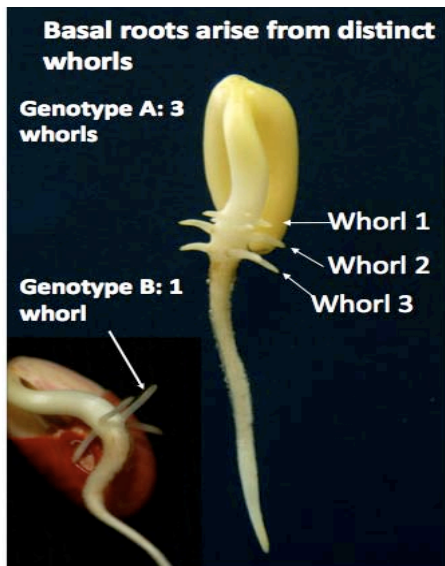
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Project overview

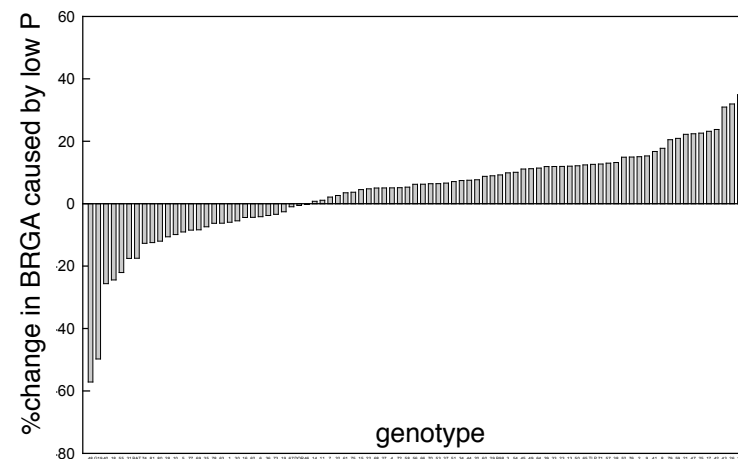
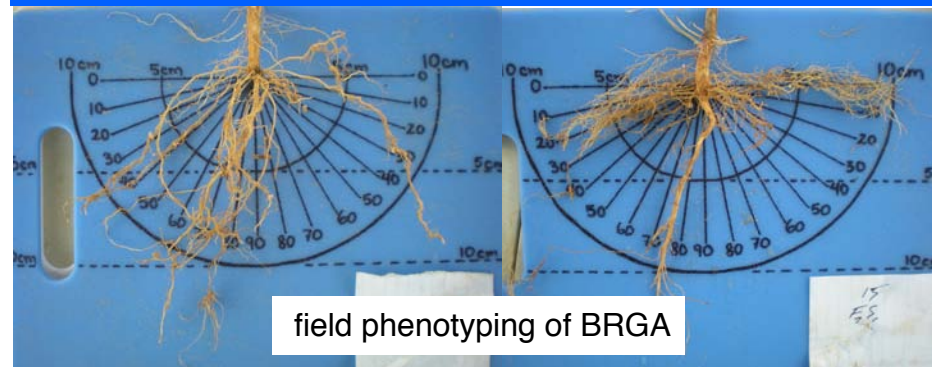
We have identified two root architectural traits that may be important for water and nutrient acquisition in common bean: *Basal Root Whorl Number* (BRWN) and the plasticity of *Basal Root Growth Angle* (BRGA). The overall goals of this project are to confirm the utility of these traits and to characterize their genetic control.

High BRWN increases P uptake



Bean genotypes with 3 whorls had greater biomass under low P conditions in the field than related genotypes (RILs) having 2 whorls. Bars are means \pm SE of 4 replicates, 3 RILs each category.

substantial genetic variation for BRGA plasticity - useful for water and P uptake?



Field evaluation of lines contrasting for BRGA plasticity in the field in Mozambique- trials also underway in Honduras and USA

BRWN is controlled by several strong QTL

Table. Quantitative trait loci (QTL) for root whorl and root number in composite interval mapping analysis of the DOR364 x G19833 and G2333 x G19839 RIL populations. Values represent significance (LOD) and determination coefficients explained by each QTL (R² and TR²). Linkage group location and nearest marker to the peak LOD value are given for each QTL.

Population	Trait (unit)	QTL name	LG ¹	Nearest marker	LOD ²	R ²	TR ²	Additive effect	Positive allele
DOR364 x G19833	Root Whorl No.	Rwn 2.1	B2	AA198G	2.71	0.1094	0.3708	-0.115	G19833
		Rwn 2.2	B2	AG1302D	3.69	0.1557	0.5265	-0.147	G19833
		Rwn 7.1	B7	O203D	5.29	0.2475	0.4042	-0.173	G19833
	Average no. Roots	Rno 2.1	B2	AG1302D	3.31	0.1103	0.4887	-0.379	G19833
		Rno 6.1	B6	BM412	3.07	0.1192	0.5293	0.355	DOR364
		Rno 7.1	B7	O203D	4.10	0.1425	0.4887	-0.387	G19833
	Average Seed weight (PSU)	Swr 2.1	B2	V10120G	3.43	0.1013	0.5482	-0.017	G19833
		Swr 3.1	B3	BM436	4.40	0.1689	0.5995	0.022	DOR364
		Swr 1.1.1	B11	Bug25	3.92	0.1257	0.5729	-0.019	G19833
	Seed weight (g/100S) (CIAT-Darien-HP)	Swr 3.1	B3	P076G	3.94	0.1023	0.5768		DOR364
		Swr 4.1	B4	G122G	3.08	0.0878	0.6598		G19833
Swr 1.1.1		B11	Bug1	7.50	0.2163	0.5814		G19833	
G2333 x G19839	No. Basal whorls	Rwn 5.1	B5	BM4018B	3.37	0.1753	0.4185	-0.168	G19839
		Rwn 7.1	B7	SAB3	13.41	0.5872	0.9247	-0.392	G19839
	No. Basal roots	Rno 5.1	B5	BM418b	3.43	0.1529	0.5025	-0.511	G19839
		Rno 7.1	B7	SAB3	10.31	0.6140	0.8888	-1.216	G19839
	Seed weight (PSU)	Swr 6.1	B6	BM170	6.29	0.3175	0.7445	-0.036	G19839
		Swr 7.1	B7	BM210	8.54	0.3877	0.7179	-0.042	G19839
	Seed weight (g/100S) (CIAT-Darien-HP)	Hw 6.1	B6	BM3	5.38	0.1788	0.6428	-3.475	G19839
		Hw 1.1.1	B11	Bug1	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); ³R² = proportion of variance explained by QTL at test site; ⁴TR²: proportion of variance explained for the QTL and the background markers.

