MAPPING OF QTL INVOLVED IN THE GENETIC CONTROL OF SEED TRAITS IN COMMON BEAN

E. Pérez-Vega[1], A. Campa[1], R. Giraldez[2] and J.J. Ferreira[1]

[1]Área de Cultivos Hortofrutícolas, SERIDA, Villaviciosa, Asturias, Spain; and [2]Área de Genética, Dpto. Biología Funcional, University of Oviedo, Spain

INTRODUCTION

Several genetic maps based on molecular markers have been reported in common bean (*Phaseolus vulgaris* L.) although a limited number of quantitative trait loci (QTL) have been incorporated in these genetic maps, being necessary a continuous effort in that respect. The QTL mapping has been mainly focused on genetic resistances rather than morphological or agronomic traits. Seed traits such as seed dimensions or seed weight are important traits in common bean. In this work, several QTL involved in the genetic control of four seed traits are incorporated in a genetic map developed from a recombinant inbred line population.

MATERIAL AND METHODS

A mapping population formed by 104 $F_{2:7}$ recombinant inbreed lines (RILs) derived from the cross Xana x Cornell 49242 was developed using the single seed descent method. 'Xana' is a determinate line, obtained in the SERIDA, having very large white seeds (100 g/100 seeds). 'Cornell 49242' is an indeterminate line having very small black seeds (23 g/100 seeds).
The population was grown and evaluated in Villaviciosa, Asturias (Spain) for three consecutive years (2004, 2005, and 2006). Two repetitions per line were analyzed in each evaluation. A total of four morphological quantitative traits were evaluated according to standard descriptors (IBPGR, 1982): seed length (mm), seed width (mm), seed height (mm), and seed weight (g). Each trait was estimated as the average of 10 measurements per year and per plot.

A genetic map was previously developed by Pañeda (2005) in this RIL population using the software JoinMap V3 (van Ooijen and Voorrips, 2001). This map included 177 AFLP markers, 26 SSR markers, 33 ISSR markers, 28 SCAR markers, 13 seed protein loci and 3 morphological loci (*Fin, P* and *asp*) grouped in 11 linkage groups. The linkage groups were identified based on the positions of microsatellites used in a map previously published by Blair *et al.* (2003). Quantitative trait loci were located using QTL Cartographer V2.5 (Wang *et al.*, 2005). Significant QTL were found through composite interval mapping analysis (CIM) with restrictive conditions. The CIM was carried out using 2 cM for walk speed and 300 permutations with a 5% significance level. The criterion in the QTL identification were LOD > 3 and a proportion of variance explained, R^2 > 10 %.

RESULTS AND DISCUSSION

The four traits showed continuous distributions in the RIL population and they were normally distributed (Figure 1). A total of 16 QTL were identified, distributed among 7 linkage groups: B2, B3, B6, B7, B8, B9 and B10 (Table 1). Five QTL explaining73 % of variation were identified for seed length. One of them (SL_1) was associated to the marker SW13, a SCAR linked to gene *I/i*. Four QTL explaining 67 % of variation were identified for seed width and one of them (SWi_1) was associated to the marker ROC11, a SCAR linked to gene *Bc-3/bc-3*. Loci *I/i* and *Bc-3/bc-3* are implicated in the genetic resistance to potyvirus. Two QTL explaining a 26 % of variation were

identified for seed height, one of them (SH_2) being associated to locus *P/p*, involved in the genetic control of seed color. Finally, five QTL explaining 80 % of variation were identified for seed weight. The molecular markers or loci closely linked to the QTLs found in the present work could be used as an indirect selection tool in breeding programs involving seed dimensions.

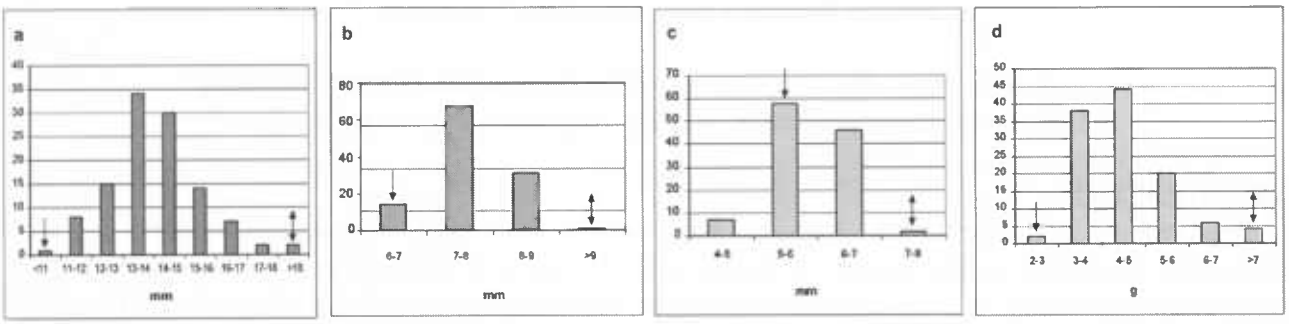

Figure 1. Frecuency distributions for seed traits: **a**: seed length, **b**: seed width, **c**: seed height, and **d**: seed weight of recombinant inbred lines derived from the cross Xana x Cornell 49242. *Arrows* indicate phenotyphic value of parents: ↓ Cornell 49242, ↕ Xana.

Table 1. Quantitative trait loci for four seed traits identified in a RIL population derived from the cross Xana/Cornell 49242. The proportion of variance explained (R^2) by each QTL and the LOD values for the associated marker are indicated. In addition, the phenotype (means) in the two possible genotypes in the RIL population is shown for the four traits. LG= linkage group. SE= standard error. P_1= Xana, P_2= Cornell 49 242.

							Phenotype population			
							Genotype P_1		Genotype P_2	
Trait	QTL	LG	Marker*	Marker type	LOD	R^2 (%)	Mean	SE	Mean	SE
Seed length	SL_1	B2	Sw13	SCAR	3,2	12	14,7	± 0,2	13,7	± 0,2
	SL_2	B3	$MCATETC^{220,95}$	AFLP	5,2	12	14,9	± 0,3	13,7	± 0,2
	SL_3	B6	ROC11	SCAR	4,8	15	14,8	± 0,2	13,5	± 0,2
	SL_4	B8	$MCTGEAT^{191,78}$	AFLP	3,4	20	13,9	± 0,2	14,6	± 0,3
	SL_5	B10	$MCATETC^{72,69}$	AFLP	3,3	14	14,7	± 0,2	13,8	± 0,2
Seed width	SWi_1	B6	ROC11	SCAR	7,8	22	7,9	± 0,1	7,4	± 0,1
	SWi_2	B8	$(ACTG)_4^{850}$	ISSR	4,1	25	7,5	± 0,1	7,8	± 0,1
	SWi_3	B9	$(AC)_8YG^{694}$	ISSR	3,6	10	7,6	± 0,1	7,7	± 0,1
	SWi_4	B10	$MCATETC^{240}$	AFLP	3,8	10	7,8	± 0,1	7,6	± 0,1
Seed height	SH_1	B3	$MCATEAG^{166}$	AFLP	4,5	14	6,2	± 0,1	5,6	± 0,1
	SH_2	B7	*P*	Morphological	3,5	12	6,0	± 0,1	5,7	± 0,1
Seed weight	SW_1	B6	$MCTGEAC^{115,62}$	AFLP	6,4	18	5,2	± 0,2	4,1	± 0,1
	SW_2	B7	$MCTGEAC^{276,38}$	AFLP	5,6	15	4,9	± 0,2	4,2	± 0,1
	SW_3	B7	$(AC)_8YT^{1029}$	ISSR	3,1	10	4,9	± 0,2	4,4	± 0,1
	SW_4	B8	$MCTGEAT^{191,78}$	AFLP	5,0	22	4,3	± 0,1	4,9	± 0,2
	SW_5	B8	$MCTGEAG^{167,36}$	AFLP	3,9	15	4,8	± 0,2	4,4	± 0,2

* Associated marker with the QTL

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