Improving resistance to CBB in Andean common bean using MAS

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Introduction

Common Bacterial Blight (CBB), caused by *Xhantomonas campestris* pv. *phaseoli* (Smith) (XCP), a seed-borne disease, is one of the major production constraint worldwide. There are >20 CBB resistance QTL with large or small effects distributed across all 11 chromosomes introduced into *P. vulgaris* breeding lines by intra or interspecific hybridization. Phenotypic selection following inoculation with the pathogen was used in the ITACyL bean breeding program to introduce resistance to CBB into Spanish commercial landraces. Several markers were developed for use in MAS for CBB resistance including SAP6, SU91 and BC420. The objective in this project was to test the effectiveness of these markers out of their mapped population as a tool to complement phenotypic selection by inoculation methods.

Material and Methods

Two double crosses and their reciprocal were used in this research:
Cross 1: Beluga/MCA-40-4//Tremaya/4D-50-1
Cross 2: Tremaya/4D-50-1// Beluga/MCA-40-4
Cross 3: Cueto/MCA-82-3//ZJ-1192/ITA-485-1-22
Cross 4: ZJ-1192/ITA-485-1-22// Cueto/MCA-82-3
The parents used and their characteristics appear in Table 1.Genetic resistance was provided by 4D-50-1, MCA-40-4, MCA-82-3 and ITA-485-1-22; these genotypes are advanced breeding lines that came from the gamete selection for introgression and pyramiding for resistant to bacterial blight diseases (Asensio- S.-Manzanera et al. 2005, 2006). All parents and the F_1 were inoculated in the trifoliolate leaf by the multiple-needle technique in the greenhouse with XCP isolate #659, at a concentration of 5 x 10^8 cfu. Disease evaluation was made from 14 to 21 days after inoculation, using a rating scale from 1 to 9. Plants with scores from 1 to 3 were considered resistant (R), 4 to 7 intermediate (I) and 7 to 9 susceptible (S). Young tissue from an unexpanded trifoliolate leaf was taken for DNA extraction and screened for the presence or absence of the three SCAR markers in a single multiplex PCR (Miklas et al. 2000). All plants were harvested individually for progeny test, and the next generation ($F_{1:2}$) evaluated for CBB reaction in the field with the same XCP isolate using the spray-inoculation. The disease severity index (DSI) and F_1/F_2 correlation were calculated.

Results and Discussion

Crosses #1 and #2 had higher proportion of CBB resistant plants than crosses #3 and #4 (Table 2). Similar results were found in the $F_{1:2}$. These results could be expected because of the CBB resistance genes present in the parents. Progeny tests were positive and highly significant demonstrating effectiveness of direct selection for resistance to CBB in F_1.
The results of molecular marker assays showed that SAP6 and SU91 were more frequent in these populations (Table 3). The marker group most frequent was SAP6 +SU91, and no individual had all three markers. The presence of markers was associated with lower DSI and it was more evident when SAP6+SU91 were present. These results showed the effectiveness of MAS, although 14,4% of F_1 plants and their 8,7% of $F_{1:2}$ without any markers were resistant. We concluded that, in our populations, as reported by Duncan et al. (2006), direct selection was more effective. It is necessary to develop additional molecular markers for QTL of CBB resistance in Andean populations.

Table1. Origin and CBB reaction of parents used in double-crosses.

Parents	Origin	CBB reaction	Genepool
Beluga	Michigan State University	Susceptible	Andean
MCA-40-4	ITACyL Advanced breeding line	Resistant	Recombinant
Tremaya	ITACyL Breeding cultivar	Intermediate	Recombinant
4D-50-1	ITACyL Advanced breeding line	Resistant	Recombinant
Cueto	ITACyL Landrace	Susceptible	Andean
MCA-82-3	ITACyL Advanced breeding line	Resistant	Recombinant
ZJ-1192	Comercial Cultivar	Susceptible	Andean
ITA-485-1-22	ITACyL Advanced breeding line	Resistant	Recombinant

Table 2. The number of plants and the mean disease severity index (DSI) of two double-crosses (and their reciprocals) for CBB.

Cross	F_1	R [1, 4)	I [4,7)	S[7,9]	Total	$F_{1:2}$	R [1, 4)	I [4,7)	S[7,9]	Total
1	N	64	12	36	113	N	40	36	41	117
	DSI	*1.75*	*5*	*8.53*	*4.27*	DSI	*1.27*	*5.14*	*7.39*	*3.27*
2	N	28	16	24	68	N	23	22	28	73
	DSI	*1.96*	*4.75*	*8.33*	*4.86*	DSI	*1.26*	*5.54*	*7.5*	*4.94*
3	N	9	9	31	49	N	2	21	32	55
	DSI	*2.11*	*5*	*8.48*	*6.67*	DSI	*1*	*5.33*	*7.28*	*6.30*
4	N	15	11	24	50	N	5	31	16	52
	DSI	*2.06*	*4.63*	*8.5*	*5.72*	DSI	*1.8*	*4.83*	*7.18*	*5.27*

Table 3. The number of plants and the mean disease severity index for the presence or absence of CBB resistance SCAR markers (SAP6, SU91 and BC420) according to classes determined by phenotypic evaluation.

Cross		SAP6+	SAP6 -	SU91+	SU91-	BC420+	BC420 -	SAP6 +SU91	SAP6 - SU91- BC420-
1	**R**	43	21	21	44	1	66	19	18
	I	8	4	2	9	0	7	2	4
	S	24	12	9	28	0	37	8	11
	Total/DSI	*75/4.32*	*37/4.19*	*42/3.90*	*81/4.43*	*1/2*	*110/4.25*	*29/3.83*	*33/4.24*
2	**R**	15	13	4	24	0	28	4	13
	I	8	8	3	13	1	13	2	7
	S	7	17	2	22	0	24	2	17
	Total/DSI	*30/ 3.97*	*389/5.58*	*9/3.77*	*59/5.05*	*1/4*	*65/5.20*	*8/3.63*	*37/5.59*
3	**R**	3	6	1	8	3	6	0	3
	I	2	7	0	9	1	8	0	6
	S	5	26	2	29	2	29	1	23
	Total/DSI	*10/5.7*	*39/6.92*	*3/5.67*	*46/6.74*	*6/4.16*	*43/7.02*	*1/3.83*	*32/7.38*
4	**R**	7	8	1	14	0	15	1	8
	I	4	7	0	11	1	10	0	6
	S	5	19	0	24	1	23	0	18
	Total/DSI	*16/4.56*	*34/6.26*	*1/3*	*49/5.77*	*2/6.5*	*48/5.68*	*1/3.63*	*32/6.26*

References

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