The Bean Anthracnose Resistance Gene *Co-5*, is Located in Linkage Group B7

Campa A.[1]; C. Rodríguez-Suarez[2], A. Pañeda[2], R. Giraldez[2], J.J. Ferreira[1]
[1] Área de Cultivos Hortofrutícolas, S.E.R.I.D.A., Villaviciosa, Asturias, Spain [2] Área de Genética, Dpto. Biología Funcional, University of Oviedo, Spain

Introduction

Anthracnose, caused by fungus *Colletotrichum lindemuthianum* (Sacc.&Magn.) Scrib., is one of the most important diseases of common bean (*Phaseolus vulgaris* L.), causing economic losses in many parts of the world. At least, nine independent genes involved in the genetic control of the resistance to this pathogen have been described in common bean (Kelly&Vallejos, 2004). However, only six anthracnose resistance genes have been mapped: *Co-1* in linkage group B1; *Co-2* in B11; *Co-3/Co-9* in B4; *Co-4* in B8; *Co-6* in B7. In addiction, the existence of other anthracnose resistance genes in the genetic map of common bean has been suggested: *Co-x* and *Co-w* in linkage group B1, *Co-u* in B2*, Co-y* and *Co-z* in B4 and *Co-v* in B7 (Kelly *et al*., 2003).

The *Co-5* resistance gene was originally described in the bean cultivar TU. This is one of the twelve differential cultivars used for the identification of pathogenic variants of the fungus, containing resistance to numerous races (Mahuku & Riascos, 2004). The results of various allelism tests using specific races showed that the resistance present in TU is independent of genes *Co-1*, *Co-2*, *Co-3/Co-9* and *Co-4* (Kelly & Vallejos, 2004). The objective of this study was to map the *Co-5* anthracnose resistance gene using molecular markers previously included in genetic maps of common bean.

Material and Methods

The analysis was developed on a F_2 population obtained from the cross between the differential cultivars TU and MDRK. The TU cultivar is resistant to race 38 while the MDRK cultivar is susceptible to this race. The evaluation for the reaction against race 38 was carried out on a total of 86 $F_{2:3}$ families. At least 16 F_3 seedlings derived from each F_2 plant were inoculated using race 38 according to standard methods (Pastor Corrales *et al*., 1994).

In order to position the *Co-5* gene, the segregation of different SCAR or RAPD markers linked to anthracnose resistance genes (including the SCAR SAB3, previously linked to *Co-5*; Vallejos & Kelly, 2001), and SSR markers previously included in the genetic map of common bean (Blair *et al*., 2003), were used. The different DNA markers were analyzed according to the instructions of the respective authors. On the other hand, the phaseolin segregation and other seed proteins were examined. The seed proteins analysis and the designation of the different bands were carried out according to Ferreira *et al*. (2000).

The genetic distance between the loci were determined with the aid of MAPMAKER using a LOD score minimum of 3.0 (Lander *et al*., 1987).

Results and Discussion

The $F_{2:3}$ population was evaluated for resistance to race 38, and the observed segregation showed a fit to a 1:2:1 ratio, agreeing with the hypothesis of one dominant resistance gene being involved in the resistance ($\chi^2_{1:2:1}$= 0.34; p>0.05). Table 1 shows the analysis of linkage between the resistance gene and several markers. The resistance locus was linked to marker SAB3 (*Co-5*), and showed an independent segregation of the molecular markers linked to other anthracnose resistance genes: $OF10^{500}$, linked to *Co-1* (Young & Kelly, 1997); SCAReoli, linked to *Co-2* (Geffroy *et al*., 1998); SW12, linked to *Co-3/Co-9* (Méndez-Vigo *et al*., 2005); $OI16^{850}$, linked to *Co-4* (Cardoso *et al*., 2000); $OAK20^{890}$ linked to Co-6 gene (Young & Kelly, 1997); and $OF10^{1000}$, linked to *Co-10* gene (Alzate-Marín *et al*., 2003). This indicates that the gene involved in this resistant reaction is *Co-5*.

On the other hand, the resistance was linked to the seed proteins, phaseolin (Phs) and Sp4/Sp5. Phaseolin is the main seed protein and it has been mapped on linkage group B7. In order to confirm the localization of *Co-5* in this linkage group, molecular markers BM183 and SAS8, mapping on B7 (Blair *et*

al., 2003; Larsen &Miklas, 2004), were also analyzed (Table 1). Phs, Sp4/Sp5, SAS8, BM183, SAB3 and the resistance gene were located in the same linkage group, and a genetic map was developed (Figure 1).

In linkage group B7, the presence of two anthracnose resistance genes (*Co-v* and *Co-6*), has been described (Kelly *et al*., 2003). The absence of linkage found between $OAK20_{890}$ and the resistance gene studied in this work confirms the independence between *Co-6* and *Co-5*. However, the proximity between *Co-v* and the phaseolin (Kelly *et al*., 2003), suggests a possible allelism or close linkage between *Co-v* and *Co-5*. A cluster including resistances to several diseases, closely linked to marker SAS8, in linkage group B7, has been also described (Larsen & Miklas, 2004). The results obtained here concerning the relative positions of SAS8 and *Co-5* with respect to the phaseolin (Figure 1), suggest that *Co-5* is not included in such cluster.

Table 1. Observed ratios, recombination frequencies (RF) and LOD obtained in the population derived from the cross TU x MDRK for the resistance to race 38 of *C. lindemuthianum* and different markers situated in the genetic map of common bean. +/- = presence/ absence of the corresponding marker; R/r = resistant/ susceptible.

				F_2 plants										
				RR			Rr			rr				
Markers	Linked gen or linkage group	TU (RR)	MDRK (rr)	+/+	+/-	-/-	+/+	+/-	-/-	+/+	+/-	-/-	RF	LOD
Phs	B7	S (-)	T (+)	1	3	18	5	25	4	13	2	1	0.13	12.49
Sp4/Sp5	B7	-	+	9		13	26		8	15		1	0.25	3.23
SAS8	B7	+	-	16		3	30		8	8		11	0.30	1.96
BM183	B7	+	-	16		6	27		9	11		8	0.43	0.20
SAB3	*Co-5*	+	-	22		0	32		6	3		15	0.12	8.61
SCAReoli	*Co-2*	+	-	13		9	21		17	12		7	0.50	0.00
SW12	*Co-3/Co-9*	+	-	14		7	29		8	11		8	0.46	0.06
$OF10^{1000}$	*Co-10*	+	-	12		8	29		8	8		11	0.42	0.29
$OF10^{500}$	*Co-1*	+	-	16		5	28		10	15		4	0.50	0.00
$IO16^{850}$	*Co-4*	+	-	13		3	24		6	11		4	0.44	0.00
$OAK20^{890}$	*Co-6*	-	+	13		4	23		8	14		2	0.44	0.11

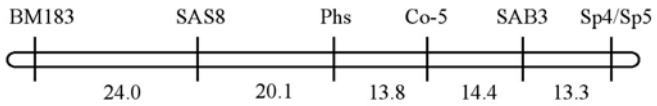

Figure 1. Relative positions of three molecular markers, two seed proteins and the *Co-5* gene, involved in the resistance against race 38.

References

Alzate-Marín A.L., M.R. Costa, K.M. Arruda, E.G. de Barros, M.A. Moreira. 2003. *Euphytica* 133:165-169
Blair M.W., F. Pedraza, H.F. Buendia, E. Gaitán-Solís, S.E. Beebe, P. Gepts, J. Thome. 2003. *Theor Appl Genet* 107:1362-1374
Cardoso de Arruda M., A.L. Alzate-Marín, J.M. Chagas, M. Alves, E .Gonzalves de Barros. 2000. *Phytopathology* 90:758-761.
Ferreira J.J., E. Álvarez, M.A. Fueyo, A. Roca, R. Giraldez. 2000. *Euphytica* 113:259-263
Geffroy V., F. Creusot, J. Falquet, M. Sévignac, A.F. Adam-Blondon, H. Bannerot, P. Gepts, M. Dron. 1998. *Theor Appl Genet* 96:494-502
Kelly J.D., P. Gepts, P.N. Miklas, D.P. Coyne. 2003. *Field Crops Research* 82: 135-154
Kelly J.D., V.A.Vallejo. 2004. *HortScience* 39(6): 1196-1207
Lander E.S., P. Green, J. Abrahamson, A. Barlo, M.J. Daly, S.E. Lincoln, L. Newburg. 1987. *Genomics* 1:174-181
Larsen R.C., P. Miklas. 2004. *Phytopathology* 94:320-325
Méndez-Vigo B., C. Rodríguez-Suárez, A. Pañeda, J.J. Ferreira, R. Giraldez. 2005. *Euphytica* (in press)
Muhuku G.S. J.J. Riascos. 2004. *European Journal of Plant Pathology* 110:253-263
Pastor-Corrales M.A.; O. A. Erazo, E. Estrada, S.P. Singh. 1994. *Plant Dis*. 78:959-962
Young R.A., J.D. Kelly. 1997. *Crop Sci*. 37: 940-946
Vallejo V., J D. Kelly. 2001. *Annu. Rep. Bean Improv. Coop*. 44: 121-122