## MOLECULAR MARKER ASSISTED DIFFERENTIATION OF NEW BEAN BREEDING LINES

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## Introduction

In recent years, various bean breeding lines with similar morphological traits were developed in the North of Spain by SERIDA (Servicio Regional de Investigacion y Desarrollo Alimentario). These lines carry different anthracnose resistance genes and exhibit different growth habits. Initially two new breeding lines were developed that carried the anthracnose resistance genes Co-2 and Co-9, originating from the parental donors S34 and A493 respectively. These new breeding lines were phenotypically identical to Andecha, the most important commercial bean in the North of Spain. This is an important advantage in our country were 90% of the cultivated bean have Type IV growth habit type and required a trellis for support or corn to climb. We also developed a new line with determinate growth habit, named Xana that is very similar to Andecha. The breeding programs were combined to develop two additional breeding lines with determinate growth habit that carry the anthracnose resistance genes Co-2 and Co-9.

The combined breeding program described has developed 5 new breeding lines that are phenotypically identical to Andecha, the most commercial bean in the North of Spain. All these materials with different genetic combinations cannot be easily differentiated, therefore molecular markers provide a useful tool for a quick differentiation instead of morphological differentiation. We have chosen molecular markers based in "Polymerase Chain Reaction" as RAPD, SCAR or CAP, because of their easy use (Ortiz et al, 2000). The molecular markers, linked to specific genes, have also the important advantage that most are already mapped. There are already reported quite many molecular markers linked to specific mapped genes that can be used with a wide spectrum of bean materials. The objective of this work was to examine the utility of some molecular markers linked to the known genes *Co-2*, *Co-9* and *Fin*, for the differentiation of 6 materials morphologically identical.

## Results

At the beginning of the work we collected and tested many molecular markers linked to the selected genes (Table 1). Some of the markers were previously developed by our group some years ago, and others come from literature. From a total number of 22 molecular markers analyzed, only 7 were monomorphic in our material. The other 15 displayed polymorphism, and the most useful markers that differentiated our lines are shown on Table 2. Two markers linked to Co-2 gene and one molecular marker linked to Co-9, that worked in our material were chosen.

Marker	Size (bp)	Туре	Gene	Phase	Reference		
OQ04	600	RAPD	Co-2	Repulsion	Méndez de Vigo, 2001		
OQ04	1440	RAPD	Co-2	Coupling	Young & Kelly, 1996		
B355	1000	RAPD	Co-2	Coupling	Young & Kelly, 1996		
SCAreoli	500	SCAR	Co-2	Coupling	Méndez de Vigo, 2001		
SCAreoli	1000	CAP	Co-2	Coupling	Geffroy et al, 1998		
SB12	350	SCAR	Со-9	Coupling	Méndez de Vigo et al 2002		
OI19	500	RAPD	Co-9	Coupling	Méndez de Vigo, 2001		
OZ10	800	RAPD	Fin	Coupling	Pañeda, 2001		
OA04	1100	RAPD	Fin	Repulsion	Pañeda, 2001		
OD08	1150	RAPD	Fin	Repulsion	Unpublished results		
OI19	375	RAPD	Fin	Repulsion	Pañeda, 2001		
OQ03	450	RAPD	Fin	Coupling	Park et al, 1999		
OF16	1400	RAPD	Fin	Coupling	Park et al, 1999		
OA17	600	RAPD	Fin	Coupling	Park et al, 1999		
OA17	950	RAPD	Fin	Coupling	Park et al, 1999		
OU12	450	RAPD	Fin	Coupling	Park et al, 1999		
OU19	350	RAPD	Fin	Coupling	Park et al, 1999		
OU19	450	RAPD	Fin	Coupling	Park et al, 1999		
ON12	800	RAPD	Fin	Coupling	Park et al, 1999		
OV10	250	RAPD	Fin	Coupling	Park et al, 1999		
OK19	450	RAPD	Fin	Coupling	Park et al, 1999		
OT14	800	RAPD	Fin	Coupling	Park et al, 1999		

 Table 1. Molecular markers analyzed for this study.

All the molecular markers linked to *Fin* gene (Park et al, 1999) were monomorphic in our material. This is a frequent problem in common bean, because of the big differences between the genetics pools, therefore we initiated a search for new molecular markers linked to this gene. The F2 population proceeded from a cross between Andecha (Fin) and BRB130 (fin), and we characterized all the F2:3 families to detect homozygous and heterozygous individuals. The screening was conducted using BSA method (Michelmore, 1991) with around six hundred random Operon primers and sixteen were found to be significantly associated with the *Fin* gene (Pañeda, 2001). For the present work we have select some RAPD markers that proved useful in our material (Table 2).

Marker	Gene	Andecha	Xana	<b>S34</b>	A493	A1183	A1220	X1358	X1319
OQ04 <sup>600</sup>	Co-2	+	+	-	+	-	+	-	+
$OQ04^{1400}$	Co-2	-	-	+	+	+	-	+	-
SCAeroli <sup>500</sup>	Co-2	+	+	-	-	-	+	-	+
SCAeroli <sup>1000</sup>	Co-2	-	-	+	-	+	-	+	-
OI19 <sup>500</sup>	<i>Co-9</i>	+	+	-	-	+	-	+	-
$SB12^{350}$	<i>Co-9</i>	-	-	-	+	-	+	-	+
OI19 <sup>375</sup>	Fin	-	+	-	-	-	-	+	+
OZ10 <sup>800</sup>	Fin	+	-	+	+	+	+	-	-
OA04 <sup>1100</sup>	Fin	-	+	-	-	-	-	+	-
$OD08^{1150}$	Fin	-	+	-	-	-	-	+	+

Table 2. Results for the molecular markers that were polymorphic in our materials

We are also working with another architectural trait because plant architecture is an important trait in breeding programs for common bean. There are some commercial lines (Cimera) in the North of Spain that are morphological similar to Andecha and we need to develop new molecular markers to differentiate between future breeding lines. The main feature that differentiates these two commercial lines is the pod distribution. Cimera is a line with Type IVa growth habit, with the pods uniformly distributed along the plant, whereas Andecha has Type IVb growth habit, with pods mainly in the upper part of the plant (Debouck and Hidalgo, 1985). We studied the genetic of this trait, and we found evidence for a new locus involved in the genetic control of the pod distribution in the indeterminate climbing habits (p=0,68 for the single dominant locus IVa).

The patterns for the polymorphic useful markers are show in Table 2, and from all of them we selected:  $OQ04^{600}$  and  $OQ04^{1400}$  linked to the anthracnose resistance gene *Co-2*,  $OI19^{500}$  linked *Co-9* gene, and  $OI19^{375}$ ,  $OD08^{1150}$  and  $OZ10^{800}$  linked to *Fin* gene for further study. The results for the selected markers, confirm the presence of *Co-2* gene in A1183 and X1358 lines and *Co-9* gene in A1220 and X1319 lines. We can conclude with the present results that molecular markers can be used to differentiate without mistake genetically similar breeding lines.

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