Linkage Relationship Between a Common Bean Seed Protein and *Fin/fin*, a Gene Involved in the Genetic Control of Growth Habit

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Introduction

Plant growth habit is an important trait in common bean related to aspects such as yield or severity of different diseases. For this trait, four main phenotypes have been described in this specie (Singh, 1982; Debouck & Hidalgo, 1985), and different loci have been described as being involved in its genetic control (Bassett 1996; Tar´an *et al*., 2002). The first described locus was the *Fin/fin* gene (Norton, 1915) whose recessive genotypes (*finfin*) show determinate growth habit. This gene was located in B1 linkage group (Gepts *et al*., 1993; Koinange *et al*., 1996; Johnson & Gepts, 2002), close to *Ppd/ppd*, a gene involved in the genetic control of photoperiod sensitivity (Coyne & Schuster, 1974; Gu *et al.,* 1998). At present, not many efficient molecular markers linked to *Fin/fin* have been reported.

In this work a linkage relationship between a seed protein and the *Fin/fin* gene is described.

Materials and Methods

In order to investigate the inheritance of seed proteins and growth habit (determinate/indeterminate), two segregations were analysed. The first population was constituted by 104 $F_{2:7}$ recombinant inbred lines (RILs) derived from a cross between Xana (*finfin*) and Cornell 49 242 (*FinFin*). The second progeny included 226 F_2 seeds obtained from a cross between Sanilac (*finfin*) and G12587 (*FinFin*). The G12587 parent is an indeterminate landrace with photoperiod sensitivity. In addition, 193 accessions preserved in the S.E.R.I.D.A. collection, showing different growth habit phenotype, were analyzed for seed proteins.

The seed protein analysis and the designation of the different polypeptide bands were carried out according to Ferreira *et al*. (2000). Figure 1 presents a SDS polyacrylamide gel in which the *Sp9* (42 Kd) and *Sp10* (38Kd) polypeptides are indicated. The co-dominant nature of these two polypeptides have been previously described (Ferreira *et al*., 2000). The genetic distance between the loci were determined with the aid of MAPMAKER (Lander *et a*l., 1987), using a LOD score minimum of 3.0.

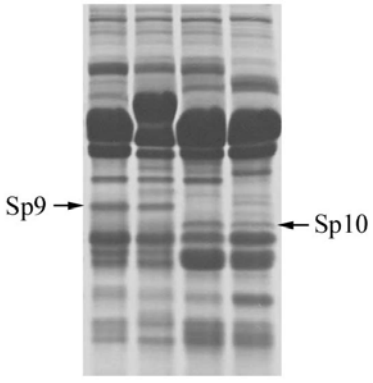

Figure 1.- SDS polyacrylamide gel (17% w/v) showing the allelic seed proteins *Sp9/Sp10* in four $F_{2:7}$ RILs derived from the cross between Xana (*Sp9Sp9*) and Cornell 49 242 (*Sp10Sp10*).

Results and Discussion

In the RILs Xana/Cornell 49 242 population, the observed phenotypic ratio for growth habit was 40 determinate and 59 indeterminate ($\chi^2_{1:1}$=3.65; p>0.05), indicating that this trait is determined by a single gene (*Fin/fin*). On the other hand, a segregation of 43 *Sp9* : 57 *Sp10* ($\chi^2_{1:1}$=1.96; p>0.05) was obtained. The *Sp9/Sp10* seed protein loci was linked to *Fin/fin* at a recombination fraction of 0.039 (LOD= 18.28), corresponding to 4.0 cM.

The efficiency of this molecular marker in the selection of determinate habit was successfully tested in the F2 progeny derived from a cross between Sanilac (*Sp10*, photoperiod insensitive) and

G12587 (*Sp9*, photoperiod sensitive). A total of 246 seeds were analyzed, and a segregation of 52 *Sp9 :* 120 *Sp9/Sp10* : 48 *Sp10* ($\chi^2_{1:2:1}$ =2.92; p>0.05) was obtained. The 48 seeds with the *Sp10* phenotype were selected and grown in the greenhouse, and 39 of them survived. Among these plants, 6 had determinate growth habit and were photoperiod sensitive, 32 were determinate and photoperiod insensitive, and only one exhibited indeterminate growth habit and photoperiod insensitivity. These results support the close linkage between the *Sp9/Sp10* locus, the *Fin/fin* gene and the *Ppd/ppd* gene, and their location in the B1 linkage group.

Finally, the polymorphism for the *Sp9/Sp10* seed protein was investigated in 193 accessions conserved in the S.E.R.I.D.A. collection (Table 1). The *Sp9* polypeptide was the most common in determinate accessions while the *Sp10* polypeptide was the most common in indeterminate materials. This association can be attributed to the linkage between the molecular marker and the phenotypic trait previously described.

Table 1. Identification of *Sp9/Sp10* proteins in 193 accessions conserved in the S.E.R.I.D.A. collection

Material	Determinate Sp9	Determinate Sp10	Indeterminate Sp9	Indeterminate Sp10
Accessions	21	3	64	105

Several RAPD markers linked to the *Fin/fin* gene have been previously identified (Park *et al.*, 1999; Pañeda *et al.*, 2004**),** although only four of them ($OF16_{1400}$, $OQ3_{450}$, $OA17_{950}$, $OA17_{600}$) were closer than 5 cM. These molecular markers are dominant and mostly showed coupling linkage with the dominant allele of *Fin/fin*. In this work, evidence of a new maker tightly linked to the *Fin/fin* gene is presented. Due to its co-dominant inheritance and to its probable linkage to the *Ppd/ppd* gene, the *Sp9/Sp10* protein can be very efficient in marker assisted selection for growth habit and photoperiod insensitivity.

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