

## Validation of molecular markers linked to alleles controlling growth habit in common bean (*Phaseolus vulgaris* L.)

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### Abstract

This work had objectives to determine the inheritance growth habit of the Andean cultivar Jalo-UEM using the F<sub>2</sub> populations from the Jalo-UEM × Cornell 49-242 and Jalo-UEM × Michelite crosses; and, to investigate the utility of Bmd45-AIA molecular marker for identifying plants having *FinFin* and/or *finfin* alleles in these segregating populations. Phenotypic and molecular analyses were conducted in two segregating populations derived from crosses between a line displaying a determinate growth (Jalo-UEM) and two cultivars with an indeterminate growth (Cornell 49-242 and Michelite) habit. A total of 21 molecular markers were tested with different amplification patterns in parents and populations. The marker that showed polymorphism was genotyped in F<sub>2</sub> populations of crosses. In the F<sub>2</sub> populations of the Jalo-UEM × Cornell 49-242 and Jalo-UEM × Michelite crosses, the phenotypic ratio of the two growth habits was 3*Fin*: 1*fin*, with  $p = 0.34$  and  $p = 0.62$ , respectively, for both crosses. This result demonstrates that the inheritance of the indeterminate growth habit was conferred by a single dominant gene, *Fin*. Molecular analysis using the microsatellite marker Bmd45-AIA revealed co-dominant segregation for both study populations, with fragment sizes of 207 and 245bp linked to the *Fin* (indeterminate) and *fin* (determinate) alleles, respectively. The segregation ratio of this marker was 1*Fin/Fin*: 2*Fin/fin*: 1*fin/fin* in the F<sub>2</sub> populations from the Jalo-UEM × Cornell 49-242 ( $p = 0.56$ ) and Jalo-UEM × Michelite ( $p = 0.42$ ) crosses. This study further establishes the relevance of the Bmd45-AIA marker for marker-assisted selection of common bean plants architecture and should allow common bean breeders to identify plants with different growth habit.

**Keywords:** Plant architecture; co-dominant segregation; inheritance of growth habit; microsatellite markers.

**Abbreviations:** BSA\_Bulked segregant analysis; D\_determinate; DH\_determinate homozygous; IE\_indeterminate heterozygous; IH\_indeterminate homozygous; I\_indeterminate; RAPD\_random amplified polymorphic DNA; SCAR\_sequence-characterized amplified regions; SSR\_simple sequence repeat.

### Introduction

The common bean (*Phaseolus vulgaris* L.) is one of the most important constituents of the human diet; in addition to being a great protein source, the common bean also has high carbohydrate content and provides vitamins, minerals and phenolic compounds with antioxidant properties that help prevent diseases (Machado et al., 2008). Because of these nutritional properties, beans are the main plant source of protein and dietary fiber for more than 500 million people in Latin America and Africa (Broughton, 2003). The common bean is a predominantly autogamous species and has wide phenotypic variability, especially for traits such as seed type (size, color, and other characteristics), phenology, plant growth habit and photoperiod sensitivity (Wallace, 1985).

Growth habit is one of the most important characteristics used for describing and selecting cultivars that are suitable for planting (Repinski et al., 2012). This feature may be classified as determinate (Type I) or indeterminate (Types II, III and IV). The evaluation of growth habit is determined by the growth of the stem, grade ability and twining ability, number of nodes, internode length and flower production (Singh, 1982; Debouck and Hidalgo, 1985). During the process of domestication, beans were adapted agroecologically and hence are insensitive to the photoperiod. For example, beans allowed adapting to higher latitudes with

longer days exhibit a different growth habit (Gepts and Debouck, 1991; Kwak et al., 2008; Repinski et al., 2012). The determinate growth habit is characterized by a limited number of nodes, with flowering beginning at the apex and moving to the base of the plant. Plants with determinate growth have a terminal meristem in the stem that develops from a vegetative to reproductive state, resulting in terminal inflorescence (Repinski et al., 2012). Plants with an indeterminate growth habit have a main stem with continuous growth originating from a succession of nodes and internodes, with flowering beginning from the base and moving to the apex of the plant. The indeterminate growth habit is characterized by stems with a terminal meristem that remain in the vegetative stage, regulating the growth and producing axillary inflorescences (Repinski et al., 2012). The goal of several breeding programs has been to select plants that exhibit determinate growth in combination with photoperiod insensitivity, to obtain varieties with a shorter flowering period, rapid and uniform ripening, earlier maturation and consequently, a low incidence of disease and ease of mechanized harvest (Coyne, 1980; Kelly et al., 1987; Myers, 1992; Singh, 1994; Singh and Munoz, 1999; Repinski et al., 2012). The growth habit of beans is determined by the presence of the gene *fin*. The presence of the dominant (*Fin*)

or recessive (*fin*) allele determines whether the growth habit is indeterminate or determinate, respectively (Park et al., 1999; Pañeda et al., 2008). The *Fin/fin* locus was first identified by Norton (1915) and mapped to linkage group Pv01 (Koinange et al., 1996; Johnson and Gepts, 2002). Gepts et al. (1993) identified an RFLP marker (D1051) linked to the gene *fin*. This locus appears to be responsible for the identification of the growth habits of most cultivars of Andean origin (Singh et al., 1991; Kwak et al., 2012). Tar'an et al. (2002) suggested the existence of a second growth habit gene (*GH*) for the common bean, located on a different linkage group from *fin*. These authors mapped the *GH* gene to the end of linkage group Pv11. This locus was significantly associated with quantitative trait loci (QTLs) for days to flowering, days to maturity and angle. Another, as yet unnamed locus, was mapped to linkage group Pv07 (Kolkman and Kelly, 2003) and may be responsible for determinacy observed in some Michigan navy bean cultivars, which arose from an artificial mutagenesis programme in the 1950s. Kwak et al. (2008) identified and mapped *PvTFL1y*, a candidate gene validated by Repinski et al. (2012) that co-segregated with the phenotypic locus for growth habit in linkage group Pv01. The gene *PvTFL1y* is a functional homolog of the gene *TFL1*, which controls growth habit in *Arabidopsis thaliana*. These results were obtained from populations of recombinant inbred lines (RILs) derived from a cross between a wild type plant (indeterminate growth habit) and a domesticated cultivar (determinate growth habit). Thus, due to the complexity and diversity of genetic information related to the inheritance of growth habit and the environmental effects that can limit phenotypic estimates, genetic improvement programs use molecular markers to select cultivars with good agronomic traits, such as growth habit, maturity and resistance to biotic and abiotic stresses (McClellan et al., 2002 and Tar'an et al., 2002). However, the need to grow plants until the end of the flowering period to identify their indeterminate or determinate growth habits represents an added difficulty in analyzing this characteristic during the breeding process. The use of indirect screening methods based on molecular markers linked to the *fin* gene would be of special interest in plant breeding (Pañeda et al., 2008). Previous studies have revealed that the molecular marker microsatellite Bmd45-AIA was linked to the *fin* gene (RF = 0.11; LOD = 10.73). This marker has been used to characterize different lines/cultivars of common bean as the growth habit (Pañeda et al., 2008). The use of Bmd45-AIA microsatellite marker is an important tool in the selection of superior genotypes for program improvement due to their co-dominant trait, multi-allelic and widely distributed across the genome. Previously, several dominant markers (RAPDs and proteins) had been described linked to the *Fin/fin* locus (Park et al., 1999; Pañeda et al., 2001; Campa et al., 2005). Because it is that markers have low reproducibility and does not distinguish heterozygous locus, the RAPD markers has been replaced by more repeatable markers as microsatellites and SCAR (Yu et al, 2000; Gaitán-Solis et al., 2002; Pañeda et al., 2008). Considering the importance to evaluate two new populations segregating for *Fin/fin* alleles, and subsequently use of superior segregant in common bean breeding programs, the present work had the objectives: 1- to determine the inheritance growth habit of the Andean cultivar Jalo-UEM using the F<sub>2</sub> populations from the Jalo-UEM × Cornell 49-242 and Jalo-UEM × Michelite crosses; 2 - to investigate the utility of Bmd45-AIA molecular marker for identifying plants having *FinFin* and/or *finfin* alleles in these segregating populations.

## Results and Discussion

### *Phenotypic analysis of the characteristic growth habit*

Phenotypic analysis of the 144 and 138 F<sub>2</sub> individuals from the Jalo-UEM × Cornell 49-242 and Jalo-UEM × Michelite crosses, when characterized by indeterminate and determinate growth habit revealed segregation pattern of 113 indeterminate plants and 31 determinate plants ( $\chi^2 = 0.92$ ;  $p = 0.34$ ) and of 106 indeterminate and 32 determinate plants ( $\chi^2 = 0.24$ ;  $p = 0.62$ ), respectively. Phenotypic evaluation of growth habit in the F<sub>2</sub> populations indicated a segregation ratio of 3 *Fin*: 1 *fin* for both crosses (Table 1). These results support the hypothesis that growth habit is conditioned by a single dominant gene. The dominant (*Fin*) allele conditions the indeterminate growth, while the recessive (*fin*) determined. Several authors, including Lamprecht (1935), Coyne and Schuster (1974), Valladares-Sanchez et al. (1979) and Gepts et al. (1993), have suggested a monogenic mode of inheritance for growth habit. Similar results were obtained by Park et al. (1999) when analyzing a cross between the cultivars PC-50 (determinate growth habit of Andean origin, with rust resistance) and Chicara 83-109 (indeterminate growth habit of Mesoamerican origin, susceptible to rust). The 3:1 ratio for growth habit (75 *Fin*: 19 *fin*;  $\chi^2 = 0.91$  and  $p = 0.34$ ) suggests that this trait is controlled by a single dominant gene (*Fin*). This hypothesis was confirmed in the F<sub>3</sub> generation, in which a 1:2:1 (number of families without a segregating indeterminate growth habit: segregating indeterminate growth habit and determinate: not segregating for growth habit determinate) ratio was observed. The same 3:1 ratio was also observed by Pañeda et al. (2008) in the F<sub>2</sub> generation of a cross of common bean cultivars Andecha (*Fin*) × BRB130 (*fin*), resulting in 63 individuals with an indeterminate growth habit and 14 determinate individuals ( $\chi^2 = 1.91$ ,  $p = 0.17$ ). These findings further support the hypothesis of a single gene controlling growth habit. The study of the growth habit is an important tool for breeding programs because it allows for the identification and selection of superior plants with rapid and uniform ripening, short flowering periods and ease of mechanical harvesting. These characteristics are present in common bean cultivars with a determinate growth habit, which can be identified by the presence of the *fin* allele. Pañeda et al. (2008) report that the introgression of recessive (*fin*) genes through conventional breeding is laborious and time consuming due to the need for progeny testing to identify desired genotypes. In addition, plant growth needs to be followed through the end of the flowering period to identify the growth habit. In addition to the factors described by Pañeda et al. (2008), environmental conditions (e.g., light and day length) may hamper the accurate phenotyping of cultivars by modifying the expression of morphological markers, thus leading to an erroneous analysis of growth habit (Kretschmer et al., 1979; Bered et al., 1997; Singh, 1982).

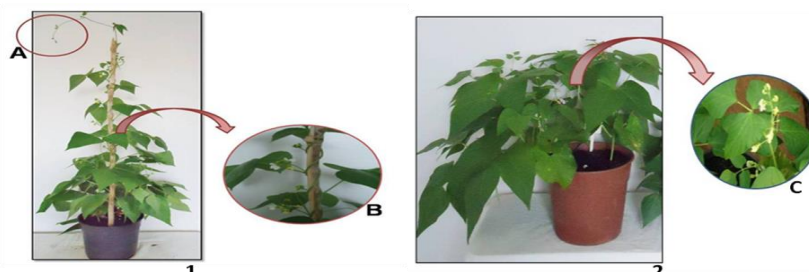
### *Molecular analysis of the characteristic growth habit*

The use of unconventional investigation methods, such as the use of molecular markers linked to the *Fin/fin* locus, may be of particular interest in plant breeding for the identification and selection of plants with a desired growth habit. In this study, of the 21 molecular markers (random amplified polymorphic DNAs (RAPDs), sequence-characterized amplified regions (SCARs), and simple sequence repeats (SSRs)) analyzed, the molecular marker Bmd45-AIA showed polymorphism in the parental and segregating populations. O

**Table 1.** Segregation for growth habit in F<sub>2</sub> populations derived from the Jalo-UEM × Cornell 49-242 and Jalo-UEM × Michelite crosses.

Crosses	Locus	Observed Ratio		Expected Ratio	$\chi^2$	P Value
		I	D	ID		
Jalo-UEM × Cornell 49-242	<i>Fin/fin</i>	113	31	3:1	0.9259	0.34
Jalo-UEM × Michelite	<i>Fin/fin</i>	106	32	3:1	0.2415	0.62

I = indeterminate; D = determinate.

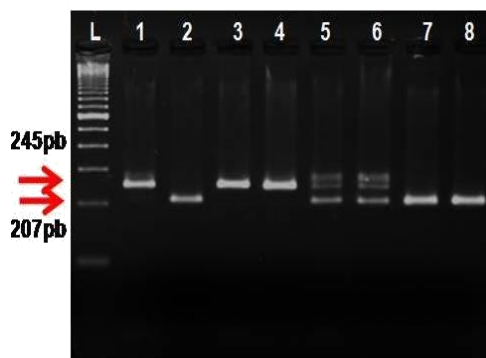


**Fig 1.** Growth habit in common bean plants (*Phaseolus vulgaris* L.). 1, Plant with indeterminate growth habit; A, Vegetative terminal meristem; B, Axillary inflorescence. 2, Plant with determinate growth habit; C, Reproductive terminal meristem/terminal inflorescence.

**Table 2.** Number of plants homozygous indeterminate growth, heterozygous indeterminate growth and homozygous determinate growth tested with molecular markers.

Crosses	Marker SSR	Locus	IH	IE	DH	Expected Ratio	$\chi^2$	P Value
Jalo-UEM × Cornell 49-242	Bmd45-AIA	<i>Fin/Fin</i>	41	71	32	1:2:1	1.15	0.56
		<i>Fin/fin</i>						
		<i>fin/fin</i>						
Jalo-UEM × Michelite	Bmd45-AIA	<i>Fin/Fin</i>	40	69	29	1:2:1	1.75	0.42
		<i>Fin/fin</i>						
		<i>fin/fin</i>						

IH = indeterminate homozygous; IE = indeterminate heterozygous; DH = determinate homozygous.



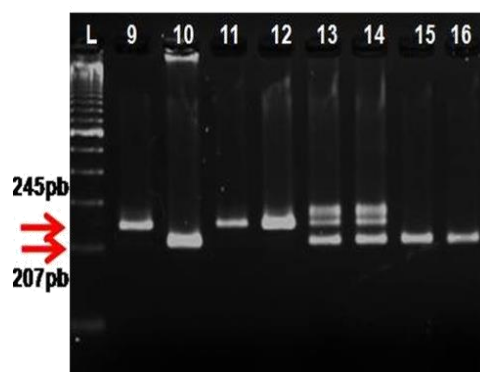
**Fig 2.** Electrophoretic analysis of the amplification products using the Bmd45-AIA molecular marker. L, 100 bp DNA ladder; 1, Jalo-UEM; 2, Cornell 49-242; 3, 4, homozygous F<sub>2</sub> plants with determinate growth; 5, 6, heterozygous F<sub>2</sub> plants with indeterminate growth; 7 and 8 homozygous F<sub>2</sub> plants with indeterminate growth. The arrows indicate the DNA bands of 245 bp and 207 bp linked to *fin* and *Fin*, respectively.

*Fin/fin* locus and the Bmd45-AIA marker revealed a segregation in the F<sub>2</sub> populations from Jalo-UEM × Cornell 49-242 and Jalo-UEM × Michelite at a ratio of 41 *Fin/Fin*:71 *Fin/fin*:32 *fin/fin* and 40 *Fin/Fin*:69 *Fin/fin*:29 *fin/fin*, respectively, indicating a good fit to the expected 1:2:1 ratio ( $p = 0.56$ ;  $p = 0.42$ , respectively) (Table 2). Molecular evaluation using a co-dominant microsatellite marker for both populations confirmed the hypothesis that a single dominant gene confers the indeterminate growth habit (Table 3). The use of genotype data from two populations allowed for the observation of both alleles in a heterozygous state (Faleiro, 2007), with the assumption that the segregation ratio would follow one indicative of dominant gene segregation (i.e., 1:2:1).

As illustrated in Figs 2 and 3, molecular analyses showed that the Bmd45-AIA marker amplified a heteromorphic band for indeterminate growth habit (207 bp) and another for determinate growth (245 bp). Recombinants were observed in the F<sub>2</sub> individuals from the Jalo-UEM × Cornell 49-242 and Jalo-UEM × Michelite crosses (three and two recombinants, respectively). Therefore, the recombination frequency for each cross was determined as 2.08 and 1.45%, respectively. The efficiency of the microsatellite marker Bmd45-AIA was calculated using the method of Beraldo et al. (2009) based on the molecular analysis of the two crosses. The efficiencies of the marker for the Jalo-UEM × Cornell 49-242 and Jalo-UEM × Michelite crosses were estimated at 81 and 82%, respectively. Thus, this marker should be efficient for use in

**Table 3.** Analysis of amplification of the corresponding SSR fragments in the F<sub>2</sub> populations Jalo-UEM × Cornell 49-242 and Jalo-UEM × Michelite.

Populations	Parental genotypes		F <sub>2</sub> plants		
	Marker Bmd45-AIA		Marker Bmd45-AIA		
	<i>FinFin</i> 207bp	<i>finfin</i> 245bp	<i>FinFin</i> 207bp	<i>Finfin</i> 207/245bp	<i>finfin</i> 245bp
Jalo-UEM × Cornell 49-242	Cornell 49-242	Jalo-UEM	41	71	32
Jalo-UEM × Michelite	Michelite	Jalo-UEM	40	69	29



**Fig 3.** Electrophoretic analysis of the amplification products using the Bmd45-AIA molecular marker. L, 100 bp DNA ladder; 9, Jalo-UEM; 10, Michelite; 11, 12, homozygous F<sub>2</sub> plants with determinate growth; 13, 14, heterozygous F<sub>2</sub> plants with indeterminate growth; 15 and 16, homozygous F<sub>2</sub> plants with indeterminate growth. Arrows indicate 245 bp and 207 bp bands, which are linked to *fin* and *Fin*, respectively.

marker-assisted selection for plant architecture in the common bean, resulting in high productivity for breeding programs.

Researches carried out by Pañeda et al. (2008) have revealed that the Bmd45-AIA marker showed a co-dominant segregation in a F<sub>2</sub> population derived from the cross Andecha (*Fin*) × BRB130 (*fin*) and being linked to the *fin* gene in the linkage group Pv01 (RF = 0.11; LOD = 10.73). Moreover, this marker was also used to determine the association of the gene pool (Mesoamerican and Andean) with the *Fin/fin* alleles in the lines/cultivars of common bean. The segregation of marker was also analyzed in the F<sub>2</sub> of MDRK × V225 and in the RILs Xana × Cornell 49-242. Bmd45-AIA showed co-dominant segregation in both populations, mapping at 4.1 cM (RF = 4.1%; LOD = 9.2) from the *fin* gene in the MDRK × V225 population, and at 3.3 cM (RF = 3.3%; LOD = 16.2) from the *fin* gene in the Xana × Cornell 49-242 population (Pañeda et al., 2008). The Xana line was obtained from the cross Andecha (*Fin*) and V203 (*fin*), followed by a selection during seven generations of selfing, using the Bmd45-AIA marker in the *fin* gene introgression proceeding from V203. The demonstrated linkage between marker Bmd45-AIA and the *fin* gene is in agreement with previous studies conducted by Blair et al. (2003, 2006). These authors using the recombinant inbred line population DOR 364 × G19833, mapped the BMD45 microsatellite in a distal position on linkage group Pv01. Later, Blair et al. (2006), using an advanced backcross inbred line population created from ICA Cerinza (determinate growth habit) crossed with G24404 (indeterminate growth habit), mapped the *fin* gene in an equivalent position on Pv01. Thus, molecular markers linked to genes of agriculturally useful traits can be used to indirectly identify genotypes that have desirable characteristics, supporting thus the process of introducing favorable characteristics into elite genotypes,

favoring the development of new commercial cultivars at different species (Grisi et al., 2007). Pañeda et al. (2004) used several lines of beans with similar morphological characteristics. These lines carry different genes for resistance to anthracnose and have different growth habits. Developed new lines were phenotypically identical to the parental cultivars. All of these materials with different genetic combinations can not be easily distinguished. Therefore, molecular markers provide a useful tool for rapid differentiation rather than rely solely on morphological differentiation. The microsatellite Bmd45-AIA marker is highly polymorphic, co-dominant and highly informative for characterizing common bean plants growth habit. This study further establishes the relevance of the molecular analysis validating the linkage between Bmd45-AIA and the *Fin/fin* locus, which controls the growth habit of the common bean, being efficient for identifying plants with determinate and indeterminate growth habits. The linkage between the Bmd45-AIA marker and the *Fin/fin* locus will be of great importance for marker-assisted introgression of this gene into commercial cultivars and elite cultivars.

## Materials and Methods

### Plant materials

Experiments were conducted under greenhouse conditions at the Laboratório de Melhoramento de Feijão Comum e de Biologia Molecular of the Núcleo de Pesquisa Aplicada à Agricultura (Nupagri) of the Universidade Estadual de Maringá (UEM), Paraná, Brazil. Two F<sub>2</sub> populations were obtained from the Jalo-UEM × Cornell 49-242 and Jalo-UEM × Michelite crosses, with 144 and 138 individuals, respectively. The Jalo-UEM cultivar exhibits a determinate growth habit and was obtained by selecting pure lines following two rearing cycles of the cultivar Jalo EEP558

grown under greenhouse conditions. The parents of this cultivar were developed in 1980 at the Instituto de Pesquisas e Experimentação Agropecuárias do Centro Oeste/Estação Experimental de Patos de Minas (IPEACO/EEP-MG). The Jalo EEP558 cultivar is resistant to fusarium wilt disease, caused by the fungus *Fusarium oxysporum*, and to angular leaf spot, caused by the fungus *Pseudocercospora griseola*. Due to the Andean origin of this cultivar, it is adapted to growing conditions in Brazil (Vieira et al., 2000). The Michelite mesoamerican cultivar (indeterminate growth habit) was obtained from the breeding program at Michigan State University, USA, and was derived from a cross between the Early Prolific and Robust cultivars. Michelite has a higher yield and better seed quality than the parental cultivar Robust. Michelite is resistant to common mosaic, which is caused by the common mosaic virus (BCMV) (Down and Thayer, 1938), and is considered one of the twelve anthracnose differential cultivars, possessing the *Co-11* resistance gene (Gonçalves-Vidigal et al., 2007). Finally, mesoamerican cultivar Cornell 49-242 (indeterminate growth habit) from Venezuela has the *Co-2* anthracnose resistance gene (*Are*) discovered by Mastenbroek (1960) which is located on linkage group Pv11 (Freyre et al., 1998). One hundred forty-four F<sub>2</sub> individuals from the Jalo-UEM × Cornell 49-242 cross and 138 F<sub>2</sub> individuals derived from the Jalo-UEM × Michelite cross were obtained. The segregating populations derived from crosses between Jalo-UEM × Cornell 49-242 and Jalo-UEM × Michelite were analyzed phenotypically and using molecular markers to characterize the indeterminate and determinate growth habits.

### Phenotypic analysis

The phenotypic data were obtained from 144 and 138 F<sub>2</sub> individuals from the Jalo-UEM × Cornell 49-242 and Jalo-UEM × Michelite crosses, respectively. When flowering ceased, the plants were evaluated and classified as exhibiting an indeterminate or determinate growth habit (Pañeda et al., 2008). Whether the terminal meristem was reproductive (determinate) or vegetative (indeterminate) (Fig 1), the number of nodes and the internode length were used for this classification (Repinski et al., 2012).

### Molecular analysis

#### DNA extraction

Molecular marker analysis was conducted using DNA extracted from the central leaflet of the first trifoliate leaf from 144 and 138 F<sub>2</sub> individuals from the Jalo-UEM × Cornell 49-242 and Jalo-UEM × Michelite crosses, respectively. DNA extractions were performed according to the method described by Afanador et al. (1993) with the following modification: DNA was extracted from the central leaflet of the first trifoliate leaf using 400 mL of CTAB extraction buffer.

#### Molecular marker analysis

A total of 21 molecular markers were used to identify polymorphisms among the parents (Jalo-UEM and Michelite and/or Cornell 49-242), determinate and indeterminate bulks and in segregating populations. Bulked segregant analysis (BSA) was used to identify markers linked to the *Fin/fin* alleles. Of the 21 tested molecular markers, only BMD45-AIA exhibited polymorphisms characterized by contrasting amplification patterns in the parental materials and the

determinate versus indeterminate bulks or individuals and were chosen for further studies. This marker amplified bands of 245 bp and 207 bp in the genomic region of interest for growth habits. The two alleles of marker BMD45-AIA differ in a single base pair and in a deletion of 38 bp.

Microsatellites BMD45 and AIA, previously located on linkage group Pv01 were amplified by different oligonucleotide pairs (developed by Blair et al. 2003 and by Guerra-Sanz 2004, respectively) directed to the same sequence (Genbank entry AF293023). The BMD45-AIA marker was obtained by combining two microsatellite primers, BMD 45 and AIA, previously used by Pañeda et al. (2008), the BMD 45 forward primer (5'-GGTTGGGAAGCCTCATAACAG-3') and AIA reverse primer (5'-TAGTCCTTGCTTTCTTTTGC-3'). These authors suggested that fragments of 207 and 245 bp were indicative of indeterminate and determinate growth, respectively. The molecular markers were PCR-amplified by polymerase chain reaction (PCR) in a total volume of 20 µL containing 10 ng of total DNA, 0.2 mM of each dNTP, 1.5 mM of MgCl<sub>2</sub>, 1X enzyme buffer, 0.2 µM of forward and reverse primers and 1 unit of *Taq* DNA polymerase in 20 µL total volume. All PCR reactions were performed in a thermal cycler model TC-412 (M.J. Research Inc., Waltham, M.A.). The amplification conditions for the SSR were as follows: 3 min at 95°C and 34 cycles of 30 s at 92°C, 1 min at 50°C and 60 s at 72°C, followed by a 5 min extension at 72°C and 4°C for 4 min. Following amplification, 2 µL of loading buffer (30% glycerol and 0.25% bromophenol blue) were added to each sample, and the PCR products were analyzed on 3% MetaPhor agarose gels stained with 0.02% SYBR Safe (Invitrogen, Eugene, Oregon, EUA). The DNA bands were visualized under ultraviolet light; digital images were recorded using an L-PIX Image EX (Loccus Biotecnologia-Loccus do Brasil, Cotia, SP, Brazil).

### Statistical analysis

Segregation analysis of the growth habit phenotype from 144 F<sub>2</sub> plants from the Jalo-UEM × Cornell 49-242 cross and 138 F<sub>2</sub> plants from the Jalo-UEM × Michelite cross was performed using a chi-square ( $\chi^2$ ) test, with the assumption of Mendelian segregation of 3*Fin* (dominant):1 *fin* (recessive). A goodness-of-fit test for the segregation hypothesis of 1:2:1 (*Fin/Fin:Fin/fin:fin/fin*) was performed using the co-dominant molecular marker BMD45-AIA. Linkage analysis was performed using the software Genes (Cruz, 2013). The efficiency of the microsatellite marker BMD45-AIA was calculated by molecular analysis based on the method of Beraldo et al. (2009).

### Conclusion

In conclusion, the results obtained in this study and in previous studies suggest that the linkage between the BMD45-AIA microsatellite marker and the *Fin/fin* locus was efficient for identifying plants with determinate and indeterminate growth. This marker, in particular, will reduce the team is useful for rapid differentiation rather than rely solely on morphological differentiation. This suggests that this marker can be used in marker-assisted selection for plant architecture and high productivity. Therefore, the data obtained from this research should allow common bean breeders to use the BMD45-AIA marker in breeding programs to improve the architecture of plants through the process of introgression of determinate and indeterminate alleles in future common bean cultivars.

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