



Potential of hypocotyl diameter in family selection aiming at plant architecture improvement of common bean

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ABSTRACT. Cultivars of common bean with more erect plant architecture and greater tolerance to degree of lodging are required by producers. Thus, to evaluate the potential of hypocotyl diameter (HD) in family selection for plant architecture improvement of common bean, the HDs of 32 F_2 plants were measured in 3 distinct populations, and the characteristics related to plant architecture were analyzed in their progenies. Ninety-six $F_{2:3}$ families and 4 controls were evaluated in a randomized block design, with 3 replications, analyzing plant architecture grade, HD, and grain yield during the winter 2010 and drought 2011 seasons. We found that the correlation between the HD of F_2 plants and traits related to plant architecture of $F_{2:3}$ progenies were of low magnitude compared to the estimates for correlations considering the parents, indicating a high environmental influence on HD in bean plants. There was a predominance of additive genetic effects on the

determination of hypocotyl diameter, which showed higher precision and accuracy compared to plant architecture grade. Thus, this characteristic can be used to select progenies in plant architecture improvement of common beans; however, selection must be based on the means of at least 39 plants in the plot, according to the results of repeatability analysis.

Key words: Genetic control; *Phaseolus vulgaris* L.; Plant architecture; Repeatability

INTRODUCTION

Carioca-type bean is the most cultivated (52% of the planted area) and consumed bean in Brazil (79%) because of its high yield and disease resistance and it is preferred among consumers (Carneiro et al., 2012). However, cultivars of carioca-type bean present some problems, such as a high degree of lodging. Cultivars with the most suitable plant architecture, particularly the erect cultivars, enable mechanized harvesting, a reduction in production loss, and enhanced grain quality (Cunha et al., 2005; Menezes Júnior et al., 2011; Silva et al., 2009, 2013a; Moura et al., 2013). Thus, selecting plants with more erect plant architecture has received great attention from bean breeders (Kelly and Adams, 1987; Menezes Júnior et al., 2008).

Bean plant architecture is a complex trait that depends on several other factors, such as growth habit, number and angle of branches, number and length of internodes, plant height, pod distribution, and hypocotyl diameter (HD) (Santos and Vencovsky, 1986; Teixeira et al., 1999). Generally, plant architecture of bean is evaluated using a grade scale proposed by Collicchio et al. (1997). However, this evaluation is visual, demands an experienced evaluator, and is difficult to use for individual plants. Thus, in order to identify effective indicators of plant architecture in common bean to support or replace the grade scale and solve these problems, Moura et al. (2013), evaluating 36 common bean lines, observed that branches insertion angle, plant height at harvest, and HD were the main traits related to plant architecture.

Understanding the genetic control of traits associated with plant architecture is very important when starting a bean breeding program, which aims at obtaining upright cultivars. In several studies, although they might disagree at some points, it was observed predominance of additive gene action in relation to dominance for most traits (Nienhuis and Singh, 1986; Santos and Vencovsky, 1986; Kornegay et al., 1992; Teixeira et al., 1999; Silva et al., 2013a). Among the traits related to plant architecture, HD stands out due to its strong association of cause and effect with plant architecture grade, and high accuracy and precision in its evaluation. It is noteworthy that, in this study, the correlations were estimated using the lines, and information regarding evaluation between segregating families were not taken into account (Moura et al., 2013). HD is easier to use in evaluations compared to other methods and enables the evaluation of individual plants. However, a suitable number of plants to be evaluated must be established.

The coefficient of repeatability is used to determine the number of necessary measures on the same genotype in order to repeatedly observe actual trait expression (Resende, 2002). From this estimate, one can increase data reliability and accuracy when selecting for superior genotypes, contributing to genetic gain in bean architecture improvement.

Because of the importance of this trait, the objective of this study was to evaluate the potential of hypocotyl diameter in family selection to improve the plant architecture of bean.

MATERIAL AND METHODS

To evaluate the potential of HD in family selection for plant architecture improvement of common bean, the HDs of 32 F_2 plants were measured in 3 distinct populations, and the characters related to plant architecture were analyzed in their progenies. Ninety-six $F_{2,3}$ families and 4 controls were evaluated (BRSMG Majestoso, L1, BRSMG Madrepérola, and A525). The control named L1 originated from the crossings UTF0013 x Rudá-R. In progenies and controls, in addition to HD, we also evaluated plant architecture grade (PAG) and grain yield (YIELD). The 96 families (32 from each cross) were obtained from three populations derived from the crossings of the BRSMG Majestoso, L1, and BRSMG Madrepérola lines with A525 lines, which have contrasting traits regarding PAG and YIELD compared with the other three lines.

Evaluation of the 96 $F_{2,3}$ families and 4 controls was carried out in a randomized block design with 3 replications, and plots consisted of 3 1-m rows spaced 0.5 m apart. Five pit-holes per row and 3 seeds per pit-hole were used. The cultivation practices were those recommended for bean crops in the region. This experiment was carried out over 2 seasons, including winter 2010 and drought 2011, in the experimental field of Coimbra, belonging to the Horticultural Department of Universidade Federal de Viçosa (UFV) in the municipality of Coimbra, Minas Gerais, located at 20°51'24"S lat, 42°48'10"W long, and 720 m asl.

Regarding the architecture, plants in the plots were evaluated next to the harvest season using a scale from 1 to 5 (Collicchio et al., 1997) as follows: grade 1 refers to type II plants, erect, with a single stem and high first pod insertion; grade 2 refers to type II plants, erect with some branching; grade 3, to the type II or III plants, with many branches and tendency to prostrate; grade 4, to type III plants, semi-erect or medium prostrate; and grade 5, to type III plants, with long internodes and very prostrate.

HD was measured 1 cm below the cotyledonary node, in millimeters, using a digital caliper, after plant harvest. The hypocotyl diameters of 15 plants from the central row of each plot were measured. Data for YIELD in kg/ha were obtained from the lateral rows of each plot.

Initially, data from each season were subjected to analysis of variance using a randomized block design, considering as random all model effects, except mean. Subsequently, the combined analysis of variance for experiments over 2 seasons was carried out considering the effect of random genotypes and seasons as fixed. For HD, we also estimated the additive and dominant components involved in their genetic control as described by Cruz et al. (2012).

We estimated the correlation coefficients between HD measures of F_2 plants with HD, PAG, and YIELD of their derived progenies. We also estimated the correlation between these traits over different seasons. Estimates of correlation coefficients were carried out as described by Cruz et al. (2012).

To determine the minimum number of individuals in the plots in order to have a representative sample of the F_2 populations and parents regarding the HD, repeatability analysis was carried out. To estimate the repeatability coefficient, we used the method of principal components; to determine the minimum number of measures in the plots, we adopted an R^2 value equal to 80% accuracy as described by Cruz et al. (2012).

All statistical analyses were carried out using the GENES software (Cruz, 2013).

RESULTS AND DISCUSSION

Significant effects of families and controls were noted at 1% probability based on the F test for all evaluated traits, including PAG, YIELD, and HD, during the winter 2010 and drought 2011 seasons (Table 1). These results indicate variability between families as well as between controls, i.e., between the parents of these families. Accuracies (heritability at family mean level) for HD and PAG for both seasons were observed; however, HD showed higher precision than PAG, with values below 7% (Table 1). For the evaluation of 36 common bean lines, regarding the traits related to plant architecture, Moura et al. (2013) also reported high precision for HD.

Table 1. Summary of analyses of variance related to the evaluation of 96 $F_{2,3}$ families and 4 controls regarding plant architecture grade (PAG), grain yield (YIELD), and hypocotyl diameter (HD) in the winter 2010 and drought 2011 seasons. Coimbra, MG.

Source of variation	Degrees of freedom	Mean squares					
		Winter 2010			Drought 2011		
		PAG (grade)	Yield (kg/ha)	HD (cm)	PAG (grade)	Yield (kg/ha)	HD (cm)
Blocks	2	3.292500	5229274.33	0.049609	0.332500	10854174.33	0.002361
Treatments (99)		0.722854**	1496804.08**	0.005653**	0.691886**	1155127.53**	0.005738**
Families (F)	95	0.661979**	1401214.03**	0.004973**	0.629788**	1120198.86**	0.005215**
Controls (C)	3	2.888889**	1187288.89	0.028964**	2.888889**	2307411.11**	0.023961**
F vs C	1	0.007812	11506404.01**	0.000312	0.000139	1016500.35	0.000700
Residue	198	0.262197	489929.55	0.001256	0.137214	415135.95	0.001183
CV (%)		17.21	17.78	6.85	11.12	19.57	6.92
F mean		2.98	3897.26	0.52	3.33	3281.29	0.50
Te mean00		3.00	4896.67	0.52	3.33	3578.33	0.49
σ^2		0.133261	303761.49	0.001239	0.164191	235020.97	0.001344
h^2 (%)		60.39	65.04	74.75	78.21	62.94	77.32

***Significant at 5 and 1% probability, respectively, by the F test.

A joint analysis of the seasons (Table 2) showed significant effects ($P < 0.01$) for both families and controls for the evaluated traits, confirming the high variability between these traits, and is fundamental to the study of genetic control of analyzed characters. Breeders exploit family variability in breeding programs with gains in several traits of common beans. Ramalho et al. (2005) evaluated YIELD in inbred families and obtained gains of up to 7.2%. Menezes Júnior et al. (2013) examined $F_{3;5}$ and $F_{3;6}$ families and observed gains of approximately 9, 10, 13, and 33% for YIELD, grain grade, angular leaf spot, and rust, respectively.

There were significant environmental effects ($P < 0.05$) for PAG and YIELD, while the effects for HD were not significant. However, the environment x family effects interaction was significant ($P < 0.01$) for YIELD and HD, but not significant for PAG. These results indicate greater environment influence (effect of season and year) on PAG than on HD, considering the family means, and greater environment effects on HD than on PAG, considering the means of each family. However, environment interactions were not significant for HD when considering the controls (lines). This may be because of the reduced size of the plot used for evaluating HD in $F_{2,3}$ families. A high environmental influence on traits related to plant architecture was also reported in previous studies (Collichio et al., 1997; Ramalho et al., 1998; Menezes Júnior et al., 2008; Silva et al., 2013a).

To estimate environmental variance within families, we used variance means between plots of the parents involved in the cross (Table 3). To evaluate individual plants based on HD considering the $F_{2,3}$ families and controls, we estimated variation between and within plots as described by Cruz and Carneiro (2006). We observed a predominance of estimates of additive variance related to dominance for the 3 populations in the 2 seasons (Table 4). Baldissera et al. (2012) and Silva et al. (2013b) also observed a predominance of additive effects in HD genetic control.

Table 2. Summary of analyses of variance related to the evaluation of 96 $F_{2,3}$ families and 4 controls regarding plant architecture grade (PAG), grain yield (YIELD), and hypocotyl diameter (HD) in the winter 2010 and drought 2011 seasons. Coimbra, MG.

Source of variation	d.f.	Mean squares		
		PAG (grade)	YIELD (kg/ha)	HD (cm)
Blocks/Environments	4	1.812500	8037783.17	0.026010
Treatments (T)	99	1.166713**	1969148.42**	0.009688**
Families (F)	95	1.036838**	1880764.80**	0.008459**
Control (C)	3	5.666667**	2204837.71**	0.051826**
F vs C	1	0.005017*	9658524.43**	0.000035
Environment (E)	1	18.903750*	62137649.28*	0.060803
T x E	99	0.248026	683066.54**	0.001741**
F x E	95	0.254930	641157.72*	0.001775**
Te x E	3	0.111111	1294845.49*	0.000938
(F vs C) x E	1	0.002934	2829067.93*	0.000956
Residues	396	0.199706	452409.29	0.001216
General mean		3.15	3614.98	0.51
Family mean		3.15	3589.08	0.51
Control mean		3.17	4236.54	0.51
CV (%)		14.18	18.61	6.87

***Significant at 5 and 1% probability, respectively, by the F test.

Table 3. Summary of analyses of variance related to the evaluation of the 4 controls regarding plant architecture grade (PAG), grain yield (YIELD), and hypocotyl diameter (HD) in the winter 2010 and drought 2011 seasons. Coimbra, MG.

Source of variation	d.f.	Mean squares							
		Winter 2010				Drought 2011			
		A525	BRSMG MAJESTOSO	BRSMG MADREPÉROLA	L1	A525	BRSMG MAJESTOSO	BRSMG MADREPÉROLA	L1
Within Plots	2	0.04546	0.020041	0.003066	0.018478	0.000646	0.023068	0.001799	0.014757
	39 (36)	0.021182	0.013241	0.003342	0.012313	0.032144	0.007235	0.00525	0.011208
	32 (37)								
	36 (38)								
	39 (39)								
Mean		0.66	0.50	0.43	0.50	0.61	0.45	0.41	0.49
$\sigma^2_{amb.}$		0.001513	0.00115	0.000261	0.000881	0.002473	0.000551	0.000384	0.000802

Values in parentheses refer to the degree of freedom regarding the experiment carried out in the drought 2011 season.

Heritability estimates of family means ranged from 55 to 76% for the 3 populations over the 2 seasons (Table 4). In contrast, heritability estimates in a plant within the plot did not exceed 6%. These results corroborate the high environmental influence on HD. Thus, selection aimed at obtaining plants with higher HD will be more effective if it is based on the mean of the plot rather than on the individual plants within the plot.

Estimates of correlation between the HD of F_2 plants with the HD and PAG of their

$F_{2:3}$ progenies (Table 5) were of low magnitude, reaching values of at most 0.47. HD and PAG of $F_{2:3}$ progenies, between the 2010 and 2011 seasons, also showed low-magnitude correlations of the values, and some were close to zero. However, estimates for the correlation coefficients between the HD of the 4 lines with HD and PAG of progenies of these plants (homozygous), obtained by selfing, were of high magnitude, with values greater than 0.83 in both seasons. Two hypotheses explain these results: i) reduced sample size of $F_{2:3}$ progenies and ii) high environmental influence in the expression of HD and PAG. High estimates of phenotypic correlation between HD and PAG using common bean lines were also observed by Silva et al. (2013b) and Moura et al. (2013).

Table 4. Summary of analyses of variance, with information between and within plot, for the 3 populations evaluated regarding the hypocotyl diameter (HD) in the winter 2010 and drought 2011 seasons. Coimbra, MG.

Source of variation	d.f.	Mean squares					
		Winter 2010			Drought 2011		
		Pop. 1 ^A	Pop. 2 ^B	Pop. 3 ^C	Pop. 1	Pop. 2	Pop. 3
Blocks	2	0.101122	0.288425	0.282766	0.009678	0.00988	0.029915
Families	31	0.069023**	0.058184**	0.058572**	0.048504**	0.050466**	0.062042**
Between Plots	62	0.02064	0.015329	0.01291	0.013207	0.015465	0.019131
Within Plots	1189 (1166) 1201 (1174) 1197 (1191)	0.0095	0.009366	0.009251	0.011724	0.009276	0.010938
CV (%)		7.55	6.77	5.96	6.36	7.35	7.35
Mean		0.52	0.50	0.52	0.50	0.47	0.52
σ^2 between		0.001225	0.001075	0.001149	0.000909	0.000894	0.001076
S^2 ^E within ^D		0.00062037	0.00063804	0.000608	0.0007898	0.0004919	0.00069975
S^2 ^E		0.0012198	0.00100797	0.0011267	0.0006855	0.0008641	0.0009682
S^2 ^{A,F}		0.0000210	0.00026812	0.0000893	0.0008941	0.0001197	0.0004313
h^2 ^D between		0.70	0.69	0.76	0.55	0.67	0.62
h^2 ^r within		0.06	0.05	0.06	0.03	0.05	0.04

**Significant at 1% probability by F test. ^APopulation derived from the cross between A525 and BRSMG Majestoso. ^BPopulation derived from the cross between A525 and VC3. ^CPopulation derived from the cross between A525 and L1. ^DEstimation of genetic variance between individuals within the plot; ^EEstimation of additive variance. ^FEstimation of variance due to dominance deviations. Values in parentheses refer to the degree of freedom regarding the experiment carried out in the drought 2011 season.

To discriminate the 32 $F_{2:3}$ families from each population with 80% accuracy ($R^2 = 0.80$), it was necessary to evaluate the HD of at least 39 plants in each plot (Table 6). However, for the parents only 4 measures were required to achieve this same accuracy. The need to evaluate more than one homozygous plant to discriminate parents regarding the HD also indicated an environmental influence on the expression of this trait. After evaluating a maximum of 12 plants per plot in each $F_{2:3}$ progeny, we found that it was necessary to evaluate at least 39 plants to discriminate these progenies with 80% accuracy. We concluded that the reduced sample size used in the progenies was the main determinant of low correlation between the HD of F_2 plants and HD and PAG of their $F_{2:3}$ progenies.

Because of the demand from producers for more erect cultivars, plant breeders must develop more accurate evaluations that better discriminate superior genotypes in order to maximize gains in a shorter period. Erect cultivars facilitate cultural practices, enable mechanized harvesting, and ensure higher quality grains (Mendes et al., 2009; Silva et al., 2009; Rocha et al., 2013; Zilio et al., 2013). Unfortunately, the evaluation of plant architecture by visual grade (Collichio et al., 1997) is more propitious to error, as it requires the evaluators to have experi-

ence and training. Furthermore, at least 3 evaluators are required to obtain a grade mean (Moura et al., 2013), which are given in the plot. However, HD can be measured using digital calipers on individual plants, and it does not require evaluator training and has a lower chance of errors but highly accurate results. The information obtained reflects each individual within the plot, and is fundamental for identifying superior genotypes, which was not possible in the evaluation by grade.

Table 5. Estimates of the phenotypic correlation between hypocotyl diameter (HD) of F_2 plants, and HD and plant architecture grade (PAG) in their respective $F_{2,3}$ progenies, evaluated in the winter 2010 and drought 2011 seasons. Coimbra, MG.

	Correlations															
	HD of Progenies $F_{2,3}$ 2010				HD of Progenies $F_{2,3}$ 2011				PAG of Progenies $F_{2,3}$ 2010				PAG of Progenies $F_{2,3}$ 2011			
HD of F_2 plants	0.45 ^{1A}	0.17 ²	0.08 ³	0.28 ⁴	0.23	0.01	0.11	0.15	-0.15	0.01	-0.42	-0.32	-0.30	-0.15	-0.27	-0.29
	0.42 ^B	0.26	0.06	0.31	0.19	0.25	0.47	0.39	-0.22	0.25	-0.29	-0.16	-0.29	-0.24	-0.21	-0.30
	-0.05 ^C	-0.05	0.28	0.09	-0.19	0.08	0.06	-0.01	-0.24	-0.10	0.22	-0.01	0.05	-0.11	-0.05	-0.03
	0.33 ^D	0.17	0.19	0.28	0.19	0.21	0.27	0.27	-0.33	-0.10	-0.26	-0.31	-0.21	-0.23	-0.22	-0.26
	0.92 ^E	0.91	0.97	0.96	0.92	0.98	0.97	1.00	-0.99	-0.99	-0.84	-0.98	-0.90	-0.97	-0.83	-0.91
HD of $F_{2,3}$ progenies in 2010					0.41	0.62	0.42	0.71	0.02	-0.22	0.09	-0.46	-0.34	0.02	0.09	0.01
					0.31	0.31	0.40	0.51	-0.53	0.19	-0.18	-0.28	-0.54	-0.05	-0.01	-0.32
					0.43	0.36	0.46	0.65	-0.20	0.02	0.07	-0.16	-0.12	-0.35	-0.33	-0.38
					0.42	0.45	0.44	0.65	-0.29	-0.10	-0.09	-0.38	-0.36	-0.16	-0.12	-0.28
					0.94	0.83	0.91	0.97	-0.89	-0.96	-0.84	-0.99	-0.95	-0.97	-0.89	-0.99
HD of $F_{2,3}$ progenies in 2011									-0.06	-0.16	-0.07	-0.20	0.10	0.24	0.18	0.19
									-0.05	0.01	-0.27	-0.13	-0.29	-0.13	-0.17	-0.26
									-0.38	-0.05	-0.31	-0.45	-0.39	-0.10	-0.42	-0.47
									-0.38	-0.22	-0.36	-0.50	-0.28	-0.11	-0.23	-0.31
									-0.93	-0.96	-0.91	-0.99	-1.00	-0.90	-0.86	-0.93
PAG of $F_{2,3}$ progenies in 2010													0.06	-0.04	0.13	0.34
													0.46	0.28	0.72	0.75
													0.68	-0.02	0.45	0.62
													0.43	0.15	0.50	0.61
													0.90	0.98	0.97	0.96

¹Replication 1; ²Replication 2; ³Replication 3; ⁴Replications mean. ^APopulation 1; ^BPopulation 2; ^CPopulation 3; ^DTotal Families, and ^EParents.

Table 6. Number of observations used to obtain estimates of the repeatability coefficient in the winter 2010 and drought 2011 seasons. Coimbra, MG.

Population	Replication	Number of measurements	
		Winter 2010	Drought 2011
1: A525 x BRSMG MAJESTOSO (32)	1	8 (14)	7 (19)
	2	10 (18)	10 (26)
	3	8 (11)	11 (19)
2: A525 x BRSMG MADREPÉROLA (32)	1	8 (12)	10 (19)
	2	9 (12)	9 (20)
	3	10 (25)	9 (13)
3: A525 x L1 (32)	1	10 (24)	10 (27)
	2	12 (19)	10 (18)
	3	7 (16)	11 (12)
Total Populations (96)	1	8 (18)	7 (39)
	2	9 (23)	9 (30)
	3	7 (13)	9 (16)
Parents (4)	1	13 (02)	13 (02)
	2	9 (04)	10 (03)
	3	10 (02)	13 (02)

Values in parentheses refer to the minimum number of measurements necessary to obtain $R^2 = 80\%$, compared to plant HD, by the method of principal components. Values in brackets refer to the number of genotypes evaluated.

Thus, HD may be used to evaluate families to improve bean plant architecture, particularly given its advantages such as predominance of additive effects in their genetic control and high precision when evaluating the HD mean of at least 39 plants in the plot.

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