

Genetic parameters of earliness and plant architecture traits suitable for mechanical harvesting of cowpea (*Vigna unguiculata*)

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Abstract

The development of cowpea (*Vigna unguiculata*) cultivars more suitable for mechanical harvesting is currently a major breeding objective aiming to reduce production costs as well as to address the problem of the labor force shortage observed in the last decade in the main cowpea-producing regions of Brazil. In this context, genetic parameters of key traits related to more efficient mechanical harvesting and earliness were estimated in segregating and non-segregating generations of a cross between two contrasting cowpea genotypes 'BRS Carijó' and 'BR14 Mulato'. The differences between the parents ranged from 1.13 to 2.70 times for the traits main branch length (MBL); secondary vegetative branch length (SVBL); number of secondary vegetative branches (NSVB); number of nodes (NN), and number of days to grain maturity (NDGM). Broad and narrow sense heritability estimates were either close to or above 50% for all traits under evaluation. The parental average and additive gene effects accounted for more than 78% for MBL, NN, and NDGM, while the combination of additive and epistatic effects was important for SVBL and NSVB. The minimum number of genes controlling the five traits ranged from two to 17. Genetic analysis showed a segregation ratio consistent with a monogenic dominant model for the traits indeterminate growth habit and climbing growth pattern. Therefore, our overall results indicate that the development of cultivars combining a set of traits more suitable for mechanical harvesting can be relatively straightforward via classical breeding strategies employed in self-pollinated crops.

Keywords: gene number, heritability, inheritance, mechanical harvesting, plant architecture.

Abbreviations: MBL_main branch length; SVBL_secondary vegetative branch length; NSBV_number of secondary vegetative branches; NN_number of nodes; NDGM_number of days to grain maturity; GP_Growth pattern; GH_Growth habit; BC_backcross.

Introduction

Significant increases in cowpea [*Vigna unguiculata* (L.) Walp.] yield and economic sustainability have been achieved after the release by public breeding programs of improved cultivars adapted to distinct crop management systems and environmental conditions (Pandey, 2007). Currently, the development of cultivars more suitable for mechanical harvesting is a major breeding objective aiming to reduce production costs as well as to address the problem of the labor force shortage observed in the last decade in major cowpea-producing regions of Brazil (Freire Filho et al., 2005). In Northern Brazil, manual harvesting comprises up to 30% of the total cowpea crop production cost, whereas in semi-mechanical harvesting systems this value might drop to 13% (Gazeta Mercantil, 2001). The highland areas of Central Brazil ('Cerrado') are already contributing with around 20% of total cowpea grain production in the country (Freire Filho, 2011). In these large scale production areas, mechanization has been used in all farm operations. However, the currently available cowpea cultivars were developed for hand harvesting, which drastically reduces the mechanical harvesting efficiency. The conversion of cowpea to an entirely mechanized crop is a major breeding challenge. This endeavor will demand the

development of cultivars with a combination of traits, including determinate growth habit, more erect plants associated with more compact (bush-type) canopy, short internodes and short secondary branches as well as lodging resistance (Ehlers & Hall, 1997). According to Singh (2007), the new generation of improved cowpea cultivars must combine high grain yield, erect growth habit, determinate growth pattern, an early to medium maturity cycle and branches with pods located above the plant canopy. Genetic analyses dealing with traits related to the cowpea plant architecture have been reported in the literature, providing estimates of genetic parameters for characteristics related to a more efficient mechanical harvesting. For example, Santos et al. (2005) estimated the number of genes and heritability for the length of the main stem and days to flower initiation, two key traits related to plant architecture. Matos Filho et al. (2009) examined the length of the main branch and number of nodes in combination with traits related to yield. Rocha et al. (2009) carried out a genetic analysis of the peduncle length trait in cowpea and they found that an additive-dominant model was adequate to explain the observed variation. In another study, a collection of 22 cowpea genotypes was evaluated with regard to earliness, plant

architecture, and grain yield and it was concluded that the combination of early, erect, and high-yield traits in a single genotype is possible through crosses between contrasting genotypes (Machado et al., 2008). However, few of these studies were carried out analyzing genetic parameters in populations segregating simultaneously for multiple traits of interest for mechanical harvesting of cowpea. In this context, estimates of genetic parameters for key traits related to more efficient mechanical harvesting were carried out in segregating and non-segregating generations of a cross between two contrasting cowpea genotypes ('BRS Carijó' and 'BR14 Mulato'). The elucidation of the genetic control of important traits related to more compact plant architecture and earliness is expected to give the methodological support necessary for the development of new cowpea varieties more suitable for mechanical/semi-mechanical harvesting.

Results

Generation analyses of the cross 'BRS Carijó' x 'BR 14 Mulato'

The differences between the parental lines 'BR14 Mulato' and 'BRS Carijó' ranged from 1.13 to 2.70 times for the set of five traits under evaluation (Table 1). All the traits evaluated in the F₂ population exceeded the parental averages, with the exception of the trait NDGM, which was inferior. The largest variances for all evaluated traits were found in the F₂ generation (Table 1). This result was somewhat expected, since the F₂ generation is where occurs the largest segregation due to the maximum linkage disequilibrium (Mather and Jinks, 1982).

Genetic parameter estimates

All variances were positive, as expected, with the exception of the variance due to the dominance of SVBL and NSVB (Table 2), that showed negative values and, for practical purposes, were considered as zero. Negative values due to the dominance and additive variance (resulting in zero values) were also observed in previous studies using segregating populations of wheat (Bakarati, 1996). The values of the components of genetic variance for all the examined traits were greater than that observed for the environmental variance (Table 2). The additive variance was the most important component of the genetic variance in all traits under evaluation (Table 2). Values for broad sense heritability (h^2_a) were either close or superior to 50% for all traits (Table 2). Heritability values on this scale indicate that there are abundant possibilities for genetic improvement of these traits through selection in this cowpea germplasm. Similar values were obtained for the narrow sense heritability (h^2_r) for SVBL and NSVB. This was mainly due to the dominance variance ($\hat{\sigma}_d^2$) that has been reduced to zero.

Slightly inferior values were found for the traits NN and NDGM and inferior values for the trait MBL. From the breeding standpoint, there is an optimal situation for the accumulation of favorable alleles that contribute to the improvement of at least four out of the five mechanical harvesting-related traits (Table 2). Transgressive values were found in the F₂ generation in relation to the maximum values of the parents, only for MBL and SVBL (Table 2). These results indicate the possibility of pure line selection for smaller MBL and SVBL values, which are important components of plant architecture in cowpea.

Analysis of variance by non-orthogonal decomposition

The relative contribution of the effects of the parental average (m) and the additive effect of the genes (a) (Table 3) were important for the traits MBL, NN, and NDGM. For the SVBL and NSVB, apart from these effects, there also was detected a contribution of the additive-dominant epistatic effects (ad).

Inheritance of growth habit and growth pattern

The analyses of the F₂ and BC₂ generations for growth habit and growth pattern showed that the calculated chi-square was non-significant (at a probability of 5%) for both traits. The observed frequencies in the F₂ generation adjusted to the expected frequency of 3 indeterminate/climbing to 1 determinate/erectoid. The frequencies observed in BC₂ generation adjusted themselves to the expected frequencies of 1 indeterminate/climbing: 1 determinate/erectoid (Table 4). Therefore, these genetic analyses showed a segregation ratio consistent with a monogenic dominant model for the traits indeterminate growth habit and climbing growth pattern.

Gene number estimates

The estimated values indicated that the traits MBL, SVBL, NSVB, NN, and NDGM are controlled by a relatively small number of genes. The bootstrap confidence interval (at 5% of probability) indicated that 1.4 to 16.3 genes are controlling the phenotypic expression of this set of traits (Table 5). These minimal gene numbers indicate that few selection cycles would be necessary to obtain the required accumulation of the favorable alleles controlling these five traits.

Discussion

Field assays were carried out aiming to estimate genetic parameters, allelic interactions as well as the minimal number of genes controlling important cowpea traits related to mechanical harvesting. This collection of traits includes short main branch length, short secondary vegetative branch length, number of secondary vegetative branches, number of nodes, and number of days to grain maturity. In addition, the populations derived from the cross 'BRS Carijó' x 'BR14 Mulato' also allowed us to study the genetic control of determinate/indeterminate growth habit and erectoid/climbing growth pattern. The overall averages of all these traits in the parental lines 'BRS Carijó' and 'BR14 Mulato' showed the required contrast to carry out all these genetic analyses reported in the present study. According to Mather and Jinks (1982), the phenotypic contrast between the parental lines is of the utmost importance for inheritance studies, aiming to obtain the most precise estimates of genetic parameters. Therefore, to our knowledge, the work reported here is so far the most comprehensive genetic analysis of a set of key traits directly related to cowpea plant architecture. The means of backcross generations for each trait were between the F₁ mean and the mean of the backcrossed parent, reinforcing the notion that the estimates presented here are reliable and also that these genetic parameters will play an important role in the breeding efforts to develop cultivars more suitable for mechanical harvesting.

The F₁ and F₂ averages for the majority of the variables examined here were intermediate in comparison with the parental averages, which suggests that the predominant type of allelic interaction is additive. In cowpea, Matos Filho (2006) evaluated the length of the main branch and number of nodes in two crosses. The results indicated that in the first

Table 1. Number of plants (N), average ($\bar{\chi}$) and variance ($\hat{\sigma}^2$) with and without transformation by square root +1 (Sqrt) of the following traits: main branch length (MBL) in cm; secondary vegetative branch length (SVBL) in cm; number of secondary vegetative branches (NSVB); number of nodes (NN), and number of days to grain maturity (NDGM), obtained from plants in six cowpea populations (P₁, P₂, F₁, F₂, BC₁ e BC₂) of the cross ‘BRS Carijó’ x ‘BR14 Mulato’, evaluated in Petrolina, PE, 2011.

Traits		Original data						Original data with Sqrt transformation					
		‘BRS Carijó’	‘BR14 Mulato’	F ₁	F ₂	BC ₁	BC ₂	‘BRS Carijó’	‘BR14 Mulato’	F ₁	F ₂	BC ₁	BC ₂
MBL	N	41	34	41	180	89	77	41	34	41	180	89	77
	$\bar{\chi}$	50.26	134.88	108.75	111.57	113.31	83.6	7.13	11.55	10.26	10.22	10.36	8.85
	$\hat{\sigma}^2$	64.65	1342.59	1814.28	3497.65	3211.39	2347.43	0.30	2.37	4.50	8.03	6.96	6.31
SVBL	N	42	35	43	180	87	82	42	35	43	180	87	82
	$\bar{\chi}$	46.19	124.74	91.76	98.1	113.75	57.03	6.82	11.07	9.44	9.58	10.51	7.28
	$\hat{\sigma}^2$	103.18	1694.49	1342.75	2907.8	1949.48	1641.61	0.56	3.19	3.68	7.17	4.27	5.09
NSVB	N	44	44	49	185	100	89	44	44	49	185	100	89
	$\bar{\chi}$	2.20	5.65	3.14	3.98	4.81	2.73	1.77	2.56	2.01	2.19	2.39	1.91
	$\hat{\sigma}^2$	0.72	2.04	1.33	2.83	1.87	1.15	0.05	0.07	0.08	0.15	0.08	0.07
NN	N	42	43	45	183	98	82	42	43	45	183	98	82
	$\bar{\chi}$	11.09	22.81	16.48	18.60	20.65	14.54	3.47	4.87	4.17	4.38	4.63	3.91
	$\hat{\sigma}^2$	1.50	5.29	4.34	26.04	16.70	14.25	0.03	0.05	0.06	0.34	0.19	0.22
NDGM	N	43	46	50	187	102	90	43	46	50	187	102	90
	$\bar{\chi}$	61.46	69.58	61.6	63.67	62.2	61.5	8.83	9.34	8.84	8.97	8.88	8.84
	$\hat{\sigma}^2$	1.20	1.27	1.87	5.22	2.93	4.18	0.01	0.01	0.01	0.02	0.01	0.02

cross the additive variance was the most important component only for the trait length of the main branch. In the second cross, the dominance variance contributed to a greater and lesser degree to genotypic variance for the traits length of the main branch and number of nodes, respectively. Lopes et al. (2003) and Rocha et al. (2009) also reported averages for F_1 and F_2 that were intermediate in comparison to the parental averages for cowpea seed size and peduncle length, respectively. Similar genetic studies have been previously conducted with other leguminous crops. For example, Santos and Vencovsky (1986) reported in beans (*Phaseolus vulgaris* L.) that, apart from the presence of dominance, the additive effect was the prevalent component in the genetic control of the length of the internodes and number of nodes of the main stem, which contributed to increase the phenotypic value. Ibarra (1966) concluded that the length of the main branch in common bean is controlled by dominant factors. However, the influence of other genetic factors also occurs with possible additive action, which is in accordance with our observations reported in the present study for cowpea. Heritability in the narrow sense is of greater importance for plant breeders because the alleles with additive effects can be accumulated after selection for the next generation (Falconer and Mackay, 1996). On the other hand, heritability in the broad sense is the result of the sum of the additive effect and the dominance deviation (which is broken in the next generation due to the independent segregation of the alleles). Heritability is a population-specific parameter for which the estimates are based upon a specific genetic background (Falconer and Mackay, 1996). This was the case of the present study which involved crosses derived from two cultivars adapted to Brazilian conditions. In this context, differences in heritability values are somewhat expected since the previous studies employed distinct genetic materials with distinct genetic backgrounds and also with evaluations carried out in distinct environmental circumstances. For example, Shimelis and Shiringani (2010) reported broad sense heritability values of 53% for the NDGM and 66% for NSVB in ten cowpea inbred lines evaluated in distinct environments in South Africa. Interestingly, their heritability estimates of NDGM and NSVB were close to our estimates reported here. In other study, Fery and Singh (1997) reported a broad heritability average of 57% for the number of branches per plant, using ten published estimates as reference. This value was also quite similar to the average value found for this trait in our present study. On the other hand, Matos Filho (2006), through analysis of generations in two crosses, of cowpea reported values of h^2_r of 51.6% and 37.1% for MBL and 10.9% and 42.0% for NN. These estimates displayed similar values to MBL and were significantly inferior to NN as reported here. Matos Filho (2006) reported that the parental average effect (m) and the additive effect (a) explained about 75% of the total variation of the traits MBL and NN in segregating generations of two cowpea crosses. These values are similar to our estimates in the present study. Work carried out with two crosses of common beans, underlined the importance of the additive component in the growth habit and the dominant interaction x dominant for the length of the fourth to the seventh node (Teixeira et al., 1999). In addition, it was found that for the traits SVBL and NSVB, the additive-dominant (ad) and epistatic effect was predominant, corresponding to about 40% of the total variation while for NDGM, the average effect of the parents (m) was the component with the highest value, followed by the additive effect. Lopes et al. (2003) found an expressive additive effect for the seed weight, pointing out its importance for cowpea improvement programs. Rocha et al.

(2009) also reported additive effect (a) as being the most important component, followed by the average (m), emphasizing the contribution of these effects for the observed variation in the peduncle length trait of the cowpea. For the traits growth habit and growth pattern, our results showed that these traits possess monogenic dominant inheritance for indeterminate growth pattern and climbing growth habit. Our results are in agreement with that reported by Matos Filho (2006) for cowpea growth pattern. However, our results are slightly different from Uguru and Uzo (1991) that reported two pairs of genes controlling cowpea growth habit. Matos Filho (2006) found, in two cowpea crosses, that five to nine genes are involved in the expression of for the main branch length trait and about 19 genes are associated with the trait number of nodes. Santos et al. (2005) reported that one to three genes are controlling the length of the main stem and days to flowering in cowpea. Apart from the estimates of the number of genes via classical biometric procedures, the information reported here is important to establish effective platforms for quantitative trait loci (QTLs) mapping. This information is crucial for an effective application of molecular marker-assisted selection, aiming to monitor the incorporation of all traits of interest for mechanical harvesting into elite cowpea breeding lines. In this context, these parameter estimates can serve as a guide for the molecular mapping of cowpea genomic regions carrying the genetic factors associated with MBL, SVBL, NSVB, NN, and NDGM as well as for the major genes coding for the traits growth habit and growth pattern traits. The clarification about the genetic control of important traits related to more compact plant architecture and earliness is expected to give the methodological support necessary for the development of new cowpea varieties more suitable for mechanical/semi-mechanical harvesting. The overall predominance for this set of mechanical harvesting-related traits of additive variances, moderate broad and narrow heritability values, the presence of parental average effects and additive effects as well as the reduced number of genes (some of them with monogenic inheritance) will facilitate the breeding work. Cowpea is a crop with an enormous potential to become a new grain commodity. In fact, cowpea has some interesting attributes that may help to increase its worldwide production and human consumption such as its nutritional quality related to protein and mineral content (Santos and Boiteux, 2013) as well as its ability to withstand water stress in semiarid regions (Freire Filho, 2011; Santos et al., 2012). The water stress tolerance of cowpea may also be an interesting trait in rain fed crops as well as in farming systems with high technological input such as the Brazilian 'Cerrado' (Freire Filho, 2011). The highland savanna-like ('Cerrado') region is currently the agricultural frontier responsible for more than 40% of the Brazilian grain production and cowpea could be easily included as an alternative in crop rotation systems together with other major commodity crops such as cotton, soybean and corn. In fact, the cowpea cultivation is increasing very fast mainly in the high technological farming systems at the Brazilian 'Cerrado', accounting for around 20% of total grain production of the country (Freire Filho, 2011). In these large scale production areas, mechanization has been used in all farm operations. However, the currently available cultivars were developed for hand harvesting, which drastically reduces the mechanical harvesting efficiency. The genetic parameter estimates reported here clearly indicate that this scenario may change and new improved cowpea cultivars, specifically developed for mechanical harvesting, might be released in a large number in the near future. This new generation of cowpea cultivars

Table 2. Estimates of genetic parameters based upon averages and variances of the following traits: main branch length (MBL); secondary vegetative branch length (SVBL); number of secondary vegetative branches (NSVB); number of nodes (NN), and number of days to grain maturity (NDGM), obtained from plants in six cowpea populations (P₁, P₂, F₁, F₂, BC₁ e BC₂) of the cross ‘BRS Carijó’ x ‘BR14 Mulato’, evaluated in Petrolina, PE, 2011. Original data was transformed by the square root +1.

Parameters	Estimates				
	MBL	SVBL	NSVB	NN	NDGM
Phenotypic variance	8.031	7.176	0.154	0.342	0.0205
Environmental variance	2.921	2.783	0.076	0.053	0.0062
Genotypic variance	5.109	4.392	0.078	0.288	0.0143
Additive variance	2.784	4.975	0.147	0.266	0.0121
Dominance variance	2.325	-0.583	-0.071	0.022	0.0021
Broad sense heritability (%)	63.62	61.21	49.44	84.31	69.73
Narrow sense heritability (%)	34.66	61.21	49.44	77.71	59.28
Parents maximum values	223*	218*	8*	28*	72*
Parents minimum values	37*	27*	1*	8*	59*
Maximum value in the F ₂	257*	231*	7*	29*	68*
Minimum value in the F ₂	33*	20*	1*	10*	59*

*Original data without square root transformation+1.

Table 3. Root sums (Sq) and coefficient of determination (R²) in the analysis of variance showing the non-orthogonal decomposition of the sum of squares of parameters by the Gaussian elimination method, based on the averages of the following traits: main branch length (MBL); secondary vegetative branch length (SVBL); number of secondary vegetative branches (NSVB); number of nodes (NN), and number of days to grain maturity (NDGM), obtained from plants in six cowpea populations (P₁, P₂, F₁, F₂, BC₁ e BC₂) of the cross ‘BRS Carijó’ x ‘BR14 Mulato’, evaluated in Petrolina, PE, 2011.

Variation source ¹	MBL		SVBL		NSVB		NN		NDGM	
	Sq	R ²	Sq	R ²	Sq	R ²	Sq	R ²	Sq	R ²
M	101.7	23.1	123.8	23.7	259.5	33.9	435	24.3	30038	94.5
A	252.4	57.2	172	32.9	202.5	26.4	966	53.9	1181.2	3.8
D	2.6	0.6	5.6	1	0.5	0.1	0.9	0.1	134.3	0.4
Aa	4.51	1	7	1.4	1.5	0.2	4.3	0.2	70.8	0.2
Ad	77.1	17.5	208.5	40	301.3	39.3	385	21.5	244.1	0.8
Dd	2.8	0.6	5.5	1	0.1	0.1	0	0	103.9	0.3
Total	441	100	522	100	765	100	1790	100	31772	100

⁽¹⁾m = average of the parental populations; a = measure of genetic additive effect; d = measure of dominance deviation; aa =additive epistatic interaction x dominant; dd = dominant epistatic interaction x dominant.

adapted for entirely mechanized farming operations will help to put the cowpea crop in a stronger position as a potential tropical/subtropical grain commodity.

Material and Methods

Plant materials

The following cowpea genotypes were used as parental lines: (P₁) the cultivar ‘BRS Carijó’ with erect growth habit, determinate growth pattern, black-eye seeds and a cycle of 58 days from sowing to the first harvesting and (P₂) the cultivar ‘BR14 Mulato’ which shows a climbing growth habit, indeterminate growth pattern, grains with a brown coat and a cycle of 75 days from sowing to the first harvest. The experiment was subdivided into two stages. In the first stage the F₁ generation was obtained (P₁ x P₂) and in the second stage the F₂, BC₁ (F₁ x P₂) and BC₂ (F₁ x P₁) segregating generations were obtained.

Experimental design of the field assays

The parental genotypes (P₁ and P₂) and the F₁, F₂, BC₁ and BC₂ generations were evaluated in a field experiment carried out at the Bebedouro Experimental Station, Embrapa Semiárido (09°09’S, 40°22’W, and altitude of 365.5 m) in the first semester of 2011. The seed samples of the six generations were planted in lines with spacing of 1.5 m x 0.2 m between the rows and between the holes, respectively. The ‘Canapu’ variety was used as external guard row. Drip

irrigation and standard crop management practices for the region were used.

Traits under evaluation

The following traits were examined: (a) number of days to grain maturity (NDGM) – Number of days from sowing to the maturity of 50% of the pods; (b) main branch length (MBL) – length between the stem base of the plant and the apex of the main branch; (c) secondary vegetative branch length (SVBL) – Length between the base and the apex of the of the largest secondary branch; (d) number of secondary vegetative branches (NSVB) – Number of branches inserted into the stem of the plant; e) number of nodes (NN) – Number of nodes starting at the insertion node of the unifoliar leaves until the last node of the main branch; (f) Growth pattern (GP) – (GP1) Determinate: growth stop of the main branch after emission of the flower buds and (GP2) Indeterminate: continuous growth of the main branch after emission of the flower buds; (g) Growth habit (GH) – (GH1) Erect: secondary branches in relation to the main branch forming a type of shrub, not touching the soil and (GH2) Climbing: secondary branches in relation to the main branch forming a type of prostrate plant with its branches touching the soil.

Statistical analysis

Statistical analyses were carried out based upon averages and variances to obtain genetic parameters for main branch length (MBL); secondary vegetative branch length (SVBL); number

Table 4. Segregation for the traits growth habit and Growth habit obtained from plants in six cowpea populations (P₁, P₂, F₁, F₂, BC₁ e BC₂) of the cross ‘BRS Carijó’ x ‘BR14 Mulato’, evaluated in Petrolina, PE, 2011. Estimates of the χ^2 for testing segregation hypotheses 3:1 (indeterminate/climbing) in the F₂ generation, and 1:1 in the BC₂ generation.

Generation	Total # of plants	Growth Pattern		χ^2	Growth Habit		χ^2
		Determinate	Indeterminate		Erect	Climbing	
‘BRS Carijó’ (P ₁)	44	44	0	-	44	0	-
‘BR14 Mulato’ (P ₂)	46	0	46	-	0	46	-
F ₁ (P ₁ x P ₂)	50	0	50	-	0	50	-
F ₂ (F ₁ x F ₁)	187	48	139	0.04 ^{ns}	54	133	1.49 ^{ns}
BC ₁ (F ₁ x P ₁)	102	0	102	-	0	102	-
BC ₂ (F ₁ x P ₂)	90	52	38	2.17 ^{ns}	53	37	2.84 ^{ns}

^{ns}Non-significant (P<0.05).

Table 5. Estimate of the minimum number of genes (original) and with transformation (Sqrt) for the square root +1 that control following traits: main branch length (MBL); secondary vegetative branch length (SVBL); number of secondary vegetative branches (NSVB); number of nodes (NN), and number of days to grain maturity (NDGM), obtained from plants in six cowpea populations (P₁, P₂, F₁, F₂, BC₁ e BC₂) of the cross ‘BRS Carijó’ x ‘BR14 Mulato’, evaluated in Petrolina, PE, 2011.

Variables	Original data		Data with Sqrt transformation	
	Without bootstrapping	With bootstrapping	Without bootstrapping	With bootstrapping
MPL	4.36	5.72 (2.3;15.2)*	4.7	5.82 (2.4;16.3)*
SVBL	2.5	3.7 (1.5;9.1)*	2.8	3.5 (1.6;10.0)*
NSVB	1.7	-	1.7	-
NN	2.1	2.2 (1.5;4.1)*	2.2	2.4 (1.4;4.1)*
NDGM	3.0	3.4 (1.9;7.6)*	3.2	3.7 (1.9;8.9)*

*Confidence interval at 5% of probability.

of secondary vegetative branches (NSVB); number of nodes (NN), and number of days to grain maturity (NDGM) traits. The effects of the genes that are attributed to the additive and dominance effects were also estimated by a weighted least squares analysis of generation means (Mather and Jinks, 1982). All calculations were performed in the ‘Genes’ software (Cruz, 2006). All the estimates of the genetic parameters were obtained with the original data transformed by square root +1 to obtain additive genetic variation, essentially as recommended by Lande (1981). The segregation of the growth habit (GH) and the growth pattern (GP) traits displayed two distinct phenotypic classes. Thus, the inheritance of both traits was studied by means of the chi-square goodness-of-fit test (χ^2) using the Microsoft Office 2007 Excel program.

Conclusions

Genetic parameters of key traits related to more efficient mechanical harvesting and earliness were estimated in segregating and non-segregating generations of a cross between two contrasting cowpea genotypes ‘BRS Carijó’ and ‘BR14 Mulato’. The overall results suggested that the development of cowpea cultivars suitable for mechanical or semi-mechanical harvesting can be relatively straightforward by applying classical breeding methods used in autogamous plant species such as cowpea.

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