Genetic parameters estimate and characters analysis in phenotypic phase of soybean during two evaluation periods

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ABSTRACT

Recent studies have shown the need to identify new potential additional descriptors for the soybean culture to contribute to cultivars differentiation. Thus, the objective of this study was to estimate generic parameters and analyze characters in the soybean plants in phenotypical phase, during two evaluation periods. The study analyzed 28 genotypes under greenhouse conditions, during two evaluation periods (October and December, 2017), in two stages of development (V2 and V3), regarding hypocotyl and epicotyl length and plant height. Experimental units (an average of two plants) were displayed in randomized blocks with four replicates. An individual and joint analysis of variance were conducted, and coefficients of experimental variation and genotypic determination were estimated for each character analyzed as well as the ratio between the experimental and genetic variation coefficients. Next, mean tests and the analysis of the phenotypic and genotypic correlation were carried out. Results showed that the genotypes analyzed differed in regard to hypocotyl and epicotyl length and plant height, at the V2 and V3 stages of development. In addition, the estimated magnitude of the genetic parameters and genotypic correlations showed genetic influence on the phenotypic expression of the hypocotyl and epicotyl length and plant height at the V2 and V3 stages of development.

Keywords: *Glycine max*, plant breeding, morphological marker.

INTRODUCTION

Soybean crops (*Glycine max* (L.) Merr.) have played a leading role in grain production increase in the country due to their greater liquidity and the possibility for better profitability compared to other crops, which motivates growers to cultivate this plant (CONAB, 2018). Reports have shown that yield estimates for the 2017/2018 season is of 3,258 Kg/ha, which agrees with the technological packages used, becoming the second greatest average productivity in the country. Part of this success is the result of genetic improvement programs developed by Brazilian research institutes and universities (Bortolotto et al., 2015; Camargos, Campos, Alves, Ferreira, & Matsuo, 2019; Harada, Gonçalves, Kiihl, & Destro, 2015; Oda et al., 2015; Silva et al., 2017).

The Cultivars Protection Law (Law 9,456), regulated by Decree 2,366 of November 5, 1997, guarantees the rights of breeders of new plant varieties (Campos, Machado, Viana, & Azevedo, 2009). Cultivar protection is granted based on three basic requirements: it must be distinct, homogeneous and stable (DHS) (Viana, 2013). These trials, in Brazil, according to the above mentioned author, are responsibility of the breeder and a distinct cultivar is that which clearly distinguishes from any other and whose existence, at the protection request date, is recognized by the criteria established by a competent body, presented in the instructions for soybean cultivars DHS trials (Ministério da Agricultura, Pecuária e Abastecimento [MAPA], 2009). Descriptors (mandatory and additional) to differentiate soybean cultivars are, according to Nogueira et al. (2008), insufficient to distinguish cultivars, making evident the need to expand the list of descriptors used.

For characters evaluated during the soybean plant vegetative stages, Nogueira et al. (2008) analyzed 11 soybean cultivars. They identified genetic variability for hypocotyl and epicotyl length, petiole length of the unifoliate leaf, base shape coefficient of the unifoliate leaf, base width coefficient of the unifoliate leaf, petiole length of the first trifoliate leaf, and rachis length of the terminal leaflet in the first trifoliate leaf.

Matsuo, Sediyama, Cruz, Oliveira and Cadore (2012) analyzed 85 soybean genotypes, in four experiments, and indicated the presence of genetic variability for hypocotyl and epicotyl length. Silva et al. (2016) analyzed 10 soybean cultivars and identified genetic variability between several characters such as hypocotyl and epicotyl and plant height evaluated at the V3 stages of development.

The knowledge of genetic parameters is of great importance for breeders, since it helps them to determine the best breeding method for the crop (Cruz, Carneiro, & Regazzi, 2004). Several studies have been conducted to estimate genetic parameters for soybean crops (Costa et al., 2008; Leite, Pavan, Matos Filho, Alcantara Neto, Oliveira, & Feitosa, 2016; Santos, Spehar, Capone, & Pereira, 2018; Vasconcelos, Reis, Sediyama, & Cruz, 2012; Zambiazzi et al., 2017) and specifically with characters under the vegetative stages (Charles et al., 2017; Matsuo et al., 2012; Nogueira et al., 2008; Silva et al., 2016). Another genetic aspect of great value for plant breeding, which should get special attention from breeders, is the correlations between characters estimates. The association between characters, when present, can be beneficial to population breeding, since its estimate can give an idea about changes to be expected from some characters during the selection of a determined characteristic (Falconer 1981).

Characters such as hypocotyl and epicotyl length and others already analyzed are promising candidates, i.e., potential additional descriptors of soybean culture. Therefore, studies involving other genotypes are important to consolidate this knowledge and to guide evaluation activities at different stadia of development and plant evaluation periods. Thus, the objective of this work was to estimate genetic parameters and analyze characters during the soybean plants phenotypic phases, at two evaluation periods.

MATERIALS AND METHODS

Experiments were conducted under greenhouse conditions (19° 11' 39'' S; 46° 14' 37'' W, 1133m of altitude) at the Federal University of Viçosa - Rio Paranaíba Campus, in the city of Rio Paranaíba, State of Minas Gerais. Twenty-eight (28) conventional soybean genotypes were analyzed during two evaluation periods (October and December 2017) (BRS Candeia, BRS Carnaúba, BRS Tracajá, BRS 283, BRS 284, MG/BR 46 (Conquista), P98C81, BRS 313 [Tieta], TMG 803, M-SOY 8757, BRSGO 8660, FTM Tucunaré, TMG 4185, BRS 8381, BRSGO 8360, TMG 801, TMG 4182, AN 8500, BRSMG 810C, BRSMG 68 (Vencedora), BRSGO 7960, BRS 7980, BRSGO 7560, BRSMG 752S, FT Cristalina, TMG 401, CD 201 and the CD 202).

Seeds of random sizes were used during planting and sown 3.0 cm deep in a substrate (2/3 of soil and 1/3 of organic matter) and displayed in a pot with the capacity for 3.0 dm^3. After germination, plants were managed according to crop recommendations. Each experiment was conducted in a randomized blocks design with four replicates (blocks), and each experimental unit consisted of two cultivated plants per pot, on average. Each experimental unit evaluated the hypocotyl length (the distance between the soil surface and the cotiledonar node), the epicotyl length (the distance between the cotiledonar node and the insertion of the first trifoliate leaf) and plant height (the distance between the soil and the last visible node) (Figure 1). Evaluations took place at the V2 and V3 stages of development (Fehr, & Caviness, 1977), using a millimeter ruler.

Initially, an individual variance analysis was conducted for each evaluation period to verify genotype effect by the F test and to estimate experimental variation ($CVe_{(\%)}$) and genotypic determination ($H^2_{(\%)}$) coefficients for each character analyzed.

The experimental variation coefficient was obtained by:

$$CVe_{(\%)} = \frac{100\sqrt{QMR}}{\bar{X}}$$

Where:

QMR: Square residual mean of analysis of variance

$\bar{X}$: Experiment general mean

The genotypic determination coefficient was obtained according to Cruz (2005):

$$H^2_{(\%)} = \frac{\hat{\phi}_g}{QMG/r}$$

Where:

$\hat{\phi}_g$: Quadratic componente

QMG: Genotype square mean of analysis of variance

r: Number of replications

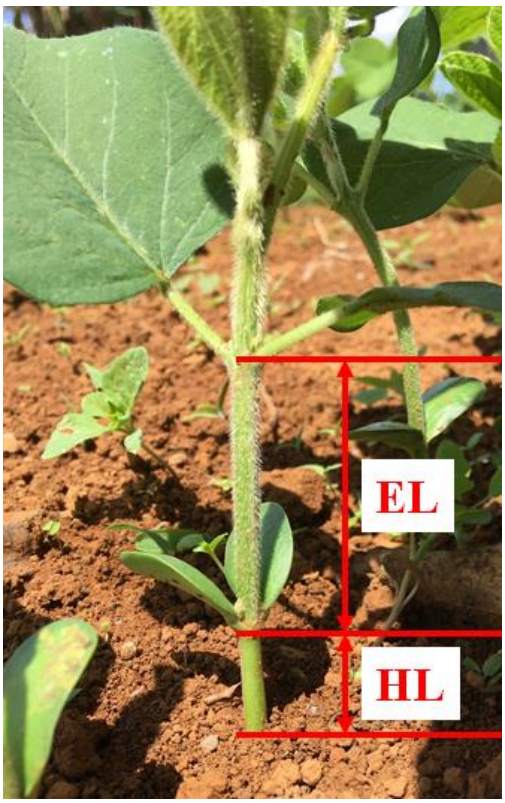

Figure 1. Illustrative image of the hypotyl (HL) and epicotyl (EL) lengths of a soybean plant. Photographed on November 21, 2019, at UFV-CRP.
Photo: Éder Matsuo.

To proceed with the experiments joint analysis, the study verified the presence of homogeneity of residual variance through the Higher(QMR):Lower(QMR) relation of the individual variance analysis, adopting the maximum value of 7:1 (Cruz, Regazzi, & Carneiro, 2012). By taking the effects as fixed, the experiments joint analysis verified the genotypes effect, evaluation period and the interactions between these two factors by the F test. In addition, the analysis estimated experimental variation ($CVe_{(\%)}$) and genotypic determination ($H^2_{(\%)}$) coefficients and the ratio between the experimental variation and genetic coefficients (CVg/CVe).

The genetic variation coefficient was obtained according to (Cruz, 2005):

$$CVg_{(\%)} = \frac{100\sqrt{\hat{\phi}_g}}{\bar{X}}$$

Where:

$\hat{\phi}_g$: Quadratic componente

$\bar{X}$: Experiment general mean

Next, whenever necessary, the means for the genotypes and for the unfolding of the genotype interaction for each period were grouped by the Scott-Knott clustering test at 5% of significance. The F test results, at 5% of significance, was analyzed to identify the difference between the means for the periods and for the unfolding of the period interaction within each genotype. In addition, the phenotypic and genotypic correlations among the characters analyzed were estimated separately, for each evaluation period, according to Cruz, Regazzi and Carneiro (2012). The phenotypic correlation estimates were testes by the t test and the genotypic correlations by the bootstrap method (with 5000 simulations). The statistical analysis

was carried out according to the Genes Program (Cruz, 2013).

RESULTS AND DISCUSSION

The summary of the analysis of variance for each evaluation period, the relative precision for each experiment and the homogeneity of residual variances for each character were showed in Table 1. A significant effect of 1% of probability for the genotype was identified for all characters analyzed by the F test during the analysis of variance. This shows the presence of genetic variance between the genotypes studied. This is a necessary condition for a character to become useful to character differentiation (Chaves et al., 2017; Nogueira et al., 2008; Silva et al., 2016).

Table 1. Summary of the analysis of variance and genetic parameters estimates for the characters (hypocotyl length (HL), epicotyl length (EL) and plants height (PH)) in the V2 and V3 stages of development), from 28 soybean genotypes evaluated in two periods (October and December, 2017), under greenhouse conditions, Rio Paranaíba, State of Minas Gerais.

Variables	October				December				HRV[2]
	GMS	Mean	$H^2_{(\%)}$	C.V. (%)	GMS	Mean	$H^2_{(\%)}$	C.V. (%)	
HL-V2	1.168**	2.33	85.54	17.67	0.943**	2.59	75.69	18.47	1.36
HL-V3	1.074**	2.31	80.48	19.85	0.885**	2.91	74.93	16.17	1.06
EL-V2	4.117**	4.58	80.83	19.41	2.712**	4.18	90.91	11.87	3.13
EL-V3	3.359**	4.56	78.00	18.85	2.298**	4.59	89.74	10.58	3.13
PH-V2	10.012**	9.78	79.48	14.65	7.508**	9.53	84.11	11.47	1.72
PH-V3	22.161**	15.73	79.61	13.51	5.752**	11.24	81.18	9.26	4.17

[1] **: Significant by the F test at 1% of probability, GMS: Genotypes mean square of analysis of variance; Mean: General mean for each character, in centimeters, $H^2_{(\%)}$: Genotypic Determination Coefficient, in %, and C.V. (%): Coefficient of variation, in %;
[2] HRV: Homogeneity of residual variance obtained by the Higher(QMR):Lower(QMR) proposed by Cruz et al. (2012).

Estimates for genotypic determination coefficient ($H^2_{(\%)}$) were superior to 74%, 78% e and 79% for hypocotyl and epicotyl length and plant height, respectively, regardless of the evaluation period. Estimates above 70% indicate high genetic influence on the phenotypic expression (Chaves et al., 2017). Thus, results from the present work show great genetic influence for characters in the two evaluation periods. Matsuo et al. (2012), Nogueira et al. (2008) and Silva et al. (2016) obtained similar results. The genotypic determination coefficient is related to inheritability; thus it makes the inference about genotypes possible (for the cases with fixed effects) (Vasconcelos et al., 2012). These authors identified the genotypic determination coefficient of 43.12% for seeds germination and of 57.12% for seedlings emergence in sand beds and reported that from all variations observed approximately half of them of genetic origin and the other half may be related to experimental deviations.

The range of the experimental coefficient variation ($CVe_{(\%)}$) for hypocotyl and epicotyl length and plants height was 16.17-19.85%, 10.58-19.41% and 9.26-14.65%, respectively. The coefficient of variation values for hypocotyl length identified by Matsuo et al (2012), Nogueira et al. (2008) and Silva et al. (2016) were inferior to 16%, 19% and 12%, respectively. For epicotyl length, these same authors identified CVe magnitudes below 15%, 14% e 15%, respectively. As for plant height, the values identified by Silva et al. (2016) were below 12%. Thus, the experimental precision obtained by the present work was compatible with that found in other published works. The coefficient of variation gives an idea of the experiment precision, considering that the higher the CVe the lower the experiment precision (Ribeiro Júnior, & Melo, 2009). In addition, they reported that a high CVe value might be due to the low quality of the environmental control, i.e., a high experimental error or the instability of the variable response or even the instability of the treatments evaluated, thus recommending the analysis of each case separately. According to Chaves et al. (2017) and Silva et al. (2016) high CVe values may be associated with the non-homogenization of the characters during the cultivars development process.

The analyses of variance for each environment are very important since they make possible the evaluation of the genetic variability magnitude and discrepancies between the residual variances obtained for each environment (Cruz et al., 2012). During the joint analysis, these authors suggest gathering in the same trial group experiments whose residual square means are below the approximate relation of 7:1. Results obtained in the present work thus show the possibility of carrying out a joint analysis of the evaluation periods for all characters analyzed, since the Higher(QMR):Lower(QMR) relation of higher magnitude was 4.17 for plants height at the V3 stage of development.

The joint analysis of variance (Table 2) showed significant effect ($p<0.05$, teste F) for epicotyl length, at V2 and V3. This indicates a differentiated behavior of a determined genotype in relation the evaluation period variation. Values for $H^2_{(\%)}$ were superior to 87%, also indicating great genetic influence for characters and values. Experimental variation coefficient were inferior to 19% and 16%, for hypocotyl and epicotyl length, respectively.

Table 2. Summary of the joint analysis of variance and genetic parameters estimates for the characters (hypocotyl length (HL), epicotyl length (EL) and plants height (PH)) in the V2 and V3 stages of development, from 28 soybean genotypes evaluated in two periods (October and December, 2017), under greenhouse conditions, Rio Paranaíba, State of Minas Gerais.

FV	GL	QM[1]					
		HL-V2	EL-V2	PH-V2	HL-V3	EL-V3	PH-V3
Block/Periods	6	0.301	2.292	5.689	0.266	2.588	10.186
Genotypes (G)	27	1.911**	5.862 **	15.381**	1.697 **	4.803**	22.602 **
Periods (E)	1	3.967 *	8.556 ^{ns}	3.677 ^{ns}	20.600 **	0.043 ^{ns}	1130.043 **
G x E	27	0.200 ^{ns}	0.966 **	2.138 ^{ns}	0.261 ^{ns}	0.852 *	5.310 **
Residue	162	0.199	0.517	1.623	0.215	0.487	2.801
General mean		2.45	4.37	9.65	2.60	4.57	13.48
$H^2_{(\%)}$		89.58	91.16	89.44	87.29	89.85	87.61
C.V.e $_{(\%)}$		18.14	16.42	13.19	17.79	15.26	12.40
CVg/CVe Ratio		1.04	1.14	1.03	0.93	1.05	0.94

[1] **,*: Significant by the F test at 1% and 5% of significance, respectively; $^{ns:}$ non-significant.

A CVg/CVe ratio higher than the unit was obtained for hypocotyl length (at V2) and plants height. According to Leite et al. (2016), whenever the coefficient estimated for ≥ 1, the genetic variation available is the most responsible for the estimated variation of the experimental data and that the CVg/CVe ratio can be adopted as an indicative index for the degree of selection facility of genotypes for each character. Results from this work corroborate with those of Matsuo et al. (2012) who reported on the variation of the CVg/CVe ratio value in function of the stadia of development during which the hypocotyl length was measured.

Table 3 shows the Genotypes x Periods interaction decomposition for epicotyl length (at V2 and V3) and plants height (at V3 stage). Four homogeneous groups were obtained for epicotyl length at V2 during the experiment conducted in October/17. The group with the highest means included genotypes MG/BR 46 (Conquista), BRSGO 7560 and BRSMG752S, while the group with the lowest means included genotypes BRS 283, BRSGO 8660, BRS 8381, BRSGO 8360, FT Cristalina, TMG 401, CD 201 and CD 202. In December/2017, the group with the highest means included genotypes BRS Carnaúba, MG/BR 46 (Conquista), P98C81, TMG 803, TMG 4185, BRSGO 7560 and BRSMG752S. On the other hand, the group with the lowest means included genotypes BRS 283, BRSGO 8360, BRS 7980, FT Cristalina and TMG 401. The epicotyl length evaluation carried out at V3 showed a trend like that observed in the results obtained at V2.

Table 3. Epicotyl length means, in centimeters, evaluated at V2 and V3 (EL-V2 and EL-V3) and plants height, in centimeters, at V3 (PH-V3) in function of two evaluation periods and 28 soybean genotypes, under greenhouse conditions, Rio Paranaíba, State of Minas Gerais[1].

Genotypes	EL-V2		EL-V3		PH-V3	
	OCT	DEC	OCT	DEC	OCT	DEC
BRS Candeia	5.07 Ab	4.37 Ab	4.92 Ab	4.80 Ab	16.62 Ab	12.13 Ba
BRS Carnaúba	5.16 Ab	5.03 Aa	4.88 Ab	5.18 Aa	16.51 Ab	11.30 Ba
BRS Tracajá	4.58 Ac	3.50 Bc	4.40 Ac	4.15 Ac	14.16 Ac	10.50 Bb
BRS 283	3.45 Ad	2.57 Ad	3.71 Ad	3.00 Ac	13.90 Ac	9.83 Bb
BRS 284	5.06 Ab	4.32 Ab	4.95 Ab	4.66 Ab	16.48 Ab	10.61 Bb
MG/BR 46 (Conquista)	6.10 Aa	4.85 Ba	5.88 Aa	5.21 Aa	19.71 Aa	12.76 Ba
P98C81	5.27 Ab	5.32 Aa	5.25 Ab	5.65 Aa	16.13 Ab	12.43 Ba
BRS 313 Tieta	4.31 Ac	4.01 Ac	4.22 Ac	4.42 Ab	16.23 Ab	9.93 Bb
TMG 803	3.88 Bc	5.48 Aa	4.13 Bc	5.82 Aa	15.31 Ac	12.86 Ba
M-SOY8757	4.70 Ab	4.30 Ab	4.61 Ac	4.58 Ab	15.86 Ab	11.00 Bb
BRSGO 8660	3.52 Ad	3.86 Ac	3.82 Ac	4.22 Ac	15.68 Ab	10.52 Bb
FTM Tucunaré	4.46 Ac	3.87 Ac	4.40 Ac	4.28 Ac	16.62 Ab	11.56 Ba
TMG 4185	5.63 Ab	5.11 Aa	4.78 Ab	5.42 Aa	19.86 Aa	13.06 Ba
BRS 8381	3.76 Ad	4.31 Ab	3.96 Ac	4.73 Ab	14.96 Ac	10.72 Bb
BRSGO 8360	3.56 Ad	3.00 Ad	3.56 Ad	3.41 Ac	13.27 Ac	9.78 Bb
TMG 801	5.41 Ab	4.17 Bb	5.32 Ab	4.58 Ab	16.48 Ab	11.61 Ba
TMG 4182	5.11 Ab	4.07 Bb	4.92 Ab	4.51 Ab	18.23 Aa	12.45 Ba
AN 8500	4.53 Ac	4.48 Ab	4.27 Ac	4.88 Ab	15.27 Ac	10.68 Bb
BRSMG 810C	4.30 Ac	4.40 Ab	4.35 Ac	4.80 Ab	13.45 Ac	11.68 Aa
BRSMG 68 (Vencedora)	4.88 Ab	4.33 Ab	4.93 Ab	4.73 Ab	17.68 Ab	11.55 Ba
BRSGO 7960	5.08 Ab	4.23 Ab	5.11 Ab	4.61 Ab	15.76 Ab	11.57 Ba
BRS 7980	4.12 Ac	3.21 Ad	4.31 Ac	3.62 Ac	14.96 Ac	9.88 Bb
BRSGO 7560	6.65 Aa	5.96 Aa	6.70 Aa	6.21 Aa	17.57 Ab	13.28 Ba
BRSMG752 S	6.63 Aa	4.93 Ba	6.65 Aa	5.36 Ba	19.97 Aa	12.73 Ba
FT Cristalina	2.57 Ad	2.65 Ad	2.57 Ad	3.30 Ac	8.90 Ad	8.63 Ab
TMG 401	3.68 Ad	3.23 Ad	4.16 Ac	3.75 Ac	13.82 Ac	9.56 Bb
CD 201	3.32 Ad	3.61 Ac	3.38 Ad	4.06 Ac	12.35 Ac	10.58 Ab
CD 202	3.21 Ad	3.90 Ac	3.43 Bd	4.42 Ab	14.72 Ac	11.48 Ba

[1]Means followed by the same lowercase letter in the column form a homogeneous group by the Scott-Knott (α = 0,05) clustering method and means followed by the same uppercase letters in the line for each variable do not differ among themselves at 5% of significance by the F test.

Analysis of the epicotyl length variation against the evaluation periods variation at V2 showed that 82.1 % of the genotypes did not differ in regard to evaluation periods, 17.9% of the genotypes showed superior means in October/2017 and only the TMG 803 crops showed higher mean in December/2017. Evaluation at

V3 showed that genotype BRSMG752S had the highest mean in October/2017 and genotype TMG 803 in December/2017.

For plant height, four homogeneous groups were developed during the October/2017 evaluation and only two groups in December/2017. The analysis of each genotype behavior against the two evaluations periods showed that genotypes BRSMG 810C, FT Cristalina and CD 201 presented statistically equal means, while the other genotypes analyzed showed a difference between the periods of evaluation, with greater values observed in October.

Genotypes MG/BR 46 (Conquista) and BRSMG752S showed higher means in the two evaluation periods and two stages of development for epicotyl length and plants height (V3), while FT Cristalina showed the lowest mean. The other genotypes showed inconsistent behavior regarding the sowing period. Chaves et al. (2017) evaluated eight soybean cultivars and reported epicotyl length inconsistency in the two different sowing periods, predominantly between cultivars with low and average means.

Table 4 shows the genotypes isolate effect in regard to hypocotyl length, at V2 and V3, and plants height at V2, showing the development of four homogeneous groups for these characters. Analysis of the hypocotyl length showed that only 46.1 % of the genotypes allocated in the group with the highest means were similar between the two stadia of development.

The evaluation period effect on hypocotyl length resulted in a distinct behavior in regarding the means at V2 and V3 stages of development. At V2, means for October and November were 2.32 cm and 2.59 cm, respectively and at V3 means were 2.36 cm and 2.91 cm (Table 5).

Estimates of the phenotypic ($r_{(fe)}$) and genotypic ($r_{(g)}$) correlation coefficients between character pairs and separately for October and December are shown in Table 6.

The CH-V2 x CH-V3, CE-V2 x AP-V2, CE-V2 x CE-V3, CE-V2 x AP-V3, AP-V2 x CE-V3, AP-V2 x AP-V3 and CE-V3 x AP-V3 combinations showed significant correlations ($p<0.05$, t test), both positive and of acceptable magnitude. Lopes, Vello, Pandini, Rocha and Tsutsumi (2002) reported that there is a trend among plant breeders to value the signal (positive or negative) and the magnitude of the values during the applied interpretation of the correlations, valuing estimates below -0.5 and above 0.5. The genotypic correlations, for these combinations, were superior to the phenotypic correlations and of the same signal. This suggests that plant selection based on the longest hypocotyl and epicotyl and plant height, at V2, would result in plants with greater character values at V3. According to Nogueira et al. (2012), when genotypic correlations are higher than the phenotypic and of the same signal, they indicate lower environment influence on the characters expression (Nogueira et al., 2012). According to Falconer and Mackay (1996) one of the causes of these high correlations is pleiotropism, in which the same gene has an influence on the expression of more than one character. Cecon, Morais and Sediyama (1993) identified superior genotypic correlations to the corresponding phenotypic correlations between the pairs of characters analyzed. This indicates, according to these authors, that the phenotypic association between the variables is reduced by the influences of the environment.

The positive and high correlations, both phenotypic as well as genotypic, between hypocotyl and epicotyl lengths and plants height evaluated in the two stadia of development (≥0.90) indicate that genotypes could be selected, for these characters, at the V2 stage of development, once time for the realization of the experiment would be shorter.

Correlations were equal or superior to 0.82 (at V2 and V3, for the two evaluation periods) for epicotyl length and plants height, indicating that plants with high mean for epicotyl length tend to, on average, show high mean for plants height, considering the two soybean stages of development (V2 e V3). Selection based on epicotyl length has the evaluation facilitated compared to plants height evaluation, since it measures specific delimitations at the main stem, i.e., the main stem between the unifoliate leaves insertion node and the first node of the trifoliate leaf.

Results showed that for the CH-V2 x CE-V2, CH-V2 x CE-V3, CE-V2 x CH-V3, CH-V3 x CE-V3 combinations an alteration in magnitude and t test significance between the estimates obtained between the two evaluation periods. When analyzing soybean production with its components, Carvalho, Arias, Toledo, Oliveira and Vello (2002) reported that the degree of association between these components and production depended on the crossing, sowing period and year of the experiments. Nogueira et al. (2012) analyzed the correlations among number of flowering days, number of days for maturation, plants height at flowering and plants height at maturation with the grain yield character and also with their primary components and found and expressive alteration in magnitude and in relation to the two sowing periods.

Table 4. Hypocotyl length means**,** in centimeters, evaluated at V2 and V3 (HL-V2 and HL-V3) and plants height, in centimeters, at V2 (PH-V2) in function of 28 soybean genotypes, under greenhouse conditions, Rio Paranaíba, State of Minas Gerais[1].

Genotypes	HL-V2	HL-V3	PH-V2
BRS Candeia	3.30a	3.36a	10.58b
BRS Carnaúba	1.90c	2.01c	10.24b
BRS Tracajá	2.08c	2.27c	8.90c
BRS 283	2.53b	2.81a	7.31d
BRS 284	2.92a	3.09a	9.72b
MG/BR 46 (Conquista)	3.31a	3.22a	12.36a
P98C81	2.40c	2.44b	10.39b
BRS 313 Tieta	2.91a	3.06a	9.15c
TMG 803	2.03c	2.39b	10.37b
M-SOY8757	2.97a	3.05a	9.89b
BRSGO 8660	2.60b	2.61b	8.93c
FTM Tucunaré	2.76b	2.86a	9.86b
TMG 4185	2.25c	2.60b	11.27a
BRS 8381	2.78b	3.00a	9.38c
BRSGO 8360	2.72b	2.81a	8.18c
TMG 801	2.64b	2.85a	10.23b
TMG 4182	2.34c	2.49b	9.87b
AN 8500	1.97c	2.08c	9.23c
BRSMG 810c	2.20c	2.16c	9.33c
BRSMG 68 (Vencedora)	2.48b	2.67a	10.23b
BRSGO 7960	2.36c	2.55b	9.78b
BRS 7980	2.40c	2.51b	8.48c
BRSGO 7560	3.10a	3.19a	12.0a
BRSMG752 S	2.83b	3.05a	12.3a
FT Cristalina	1.32d	1.36d	6.28d
TMG 401	2.11c	2.21c	7.99c
CD 201	1.90c	2.16c	8.50c
CD 202	1.62d	2.08c	9.31c

[1]Means followed by the same lowercase letter in the column form a homogeneous group by the Scott-Knott clustering method ($\alpha = 0.05$).

Table 5. Hypocotyl length means, in centimeters, evaluated at V2 and V3 (HL-V2 and HL-V3) in function of two evaluation periods (October and December, 2017), under greenhouse conditions, Rio Paranaíba, State of Minas Gerais[1]

Evaluation periods	HL-V2	HL-V3
October	2.32b	2.36b
December	2.59a	2.91a

[1]Means followed by the same lowercase letters in the column for each variable do not differ among them at 5% of probability by the F test.

Table 6. Estimates of the phenotypic ($r_{(fe)}$) and genotypic ($r_{(g)}$) correlation coefficients corresponding to the combination of six characters, analyzed in 28 genotypes, in two evaluation periods (October and December, 2017), under greenhouse conditions, Rio Paranaíba, State of Minas Gerais[1].

Characters[2]	October		December	
	$r_{(fe)}$	$r_{(g)}$	$r_{(fe)}$	$r_{(g)}$
HL-V2 x EL-V2	0.52 **	0.56 ++	0.27 ns	0.35 ns
HL-V2 x PH-V2	0.61 **	0.68 ++	0.45 *	0.46 +
HL-V2 x HL-V3	0.90 **	0.94 ++	0.99 **	0.99 +
HL-V2 x EH -V3	0.55 **	0.61 ++	0.24 ns	0.31 ns
HL-V2 x PH-V3	0.53 **	0.56 ++	0.39 *	0.39 +
EL-V2 x PH-V2	0.91 **	0.95 ++	0.90 **	0.98 ++
EL-V2 x HL-V3	0.47 *	0.53 ++	0.27 ns	0.36 ns
EL-V2 x EL-V3	0.97 **	0.99 ++	1.00 **	1.00 ++
EL-V2 x PH-V3	0.84 **	0.90 ++	0.86 **	0.95 ++
PH-V2 x HL-V3	0.60 **	0.67 ++	0.45 *	0.47 +
PH-V2 x EL-V3	0.89 **	0.94 ++	0.90 **	0.97 ++
PH-V2 x PH-V3	0.87 **	0.96 ++	0.97 **	0.99 ++
HL-V3 x EL-V3	0.50 **	0.60 ++	0.24 ns	0.32 ns
HL-V3 x PH-V3	0.59 **	0.69 ++	0.40 *	0.41 +
EL-V3 x PH-V3	0.81 **	0.90 ++	0.87 **	0.95 ++

[1] **: Significant at 1% of significance by the t test; ++ e + : Significant at 1 and 5% of significance - respectively – by the bootstrap method with 5000 simulations; ns: non-significant; [2] HL: Hypocotyl length, EL: Epicotyl length , PH: plants height, V2: V2 stadia of development and V3: V3 stadia of development.

Chaves et al. (2017) concluded that the estimates for the phenotypic and genotypic correlation between sowing periods for the hypocotyl and epicotyl length were of low magnitude (≤0.36), corroborating, according to the authors, with the complex nature of the interaction detected by the genotypes x environments decomposition.

CONCLUSIONS

The genotypes analyzed differed in regard to hypocotyl and epicotyl length and plants height, at the V2 and V3 stages of development. The magnitude of the estimated genetic parameters and the genotypic correlations showed genetic influence on the phenotypic expression of the hypocotyl, epicotyl and length and plants height, at the V2 and V3 stages of development.

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