SELECTION OF LINEAGES, GENETIC PARAMETERS, AND CORRELATIONS BETWEEN SOYBEAN CHARACTERS

SELEÇÃO DE LINHAGENS, PARÂMETROS GENÉTICOS E CORRELAÇÕES ENTRE CARACTERES EM SOJA

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ABSTRACT: Soybean has great economic importance in the world accordingly, this legume has been exploited in breeding programs aiming to provide cultivars with extensive grain yield, tolerant to pests and diseases, and adapted to different soil and climatic conditions. Therefore, the objectives of this study were to evaluate genetic parameters and correlations between soybean traits to select lineages to increase yield and improve agronomic traits. Experiments were carried out on the Capim Branco farm, of the Federal University of Uberlândia, harvest in 2016/2017. Fifteen morph-agronomic traits were assessed on twenty-two genotypes in a randomized complete block design with three replicates. Agronomic traits related to cycle, height, number of nodes and total pods have shown coefficients of genotypic determination higher than 70%. In addition, coefficients of variation of the number of days to the flowering and number of days to maturity were equal to 3.79% and 4.87%, respectively, indicating high homogeneity of data and low random variation. Among evaluated traits, ten have presented the ratios between the coefficient of genetic variation (CVg) and coefficient of environmental variation (CVe) above one, demonstrating high success likelihood in the selection of these traits. Fifteen genotypes have presented grain yield above the national average of the 2016/2017 harvest, which was 2882 kg h^{-1}. Significant phenotypic correlations between traits ranged from -0.49 to 0.89, however genotype correlation was higher than the phenotypic ones, indicating that genetic factors have contributed more than the environmental factors. Traits related to cycle, height, and the number of nodes in the main stem have presented measures of H^2 and CVg / CVe with extensive magnitudes, evidencing the possibility of selection lineages having superior traits in the Soybean Breeding Program of the Federal University of Uberlândia. To increasing grain yield, the traits Number of pods of three grains and the Total number of pods were identified as appropriated to indirect selection based on the phenotypic and genotypic correlations. The 2lP14, B2P1, B2P28, B1P33 and 2AP11 lineages stand out as superior genotypes to direct selection.

KEYWORDS: *Glycine max*. Plant breeding. Indirect selection.

INTRODUCTION

Soybean (*Glycine max*) has originated in Asia and through the years has become one of the main legumes cropped in the world. Due to the opening of new frontiers, to the development of new technologies of production in Brazilian conditions, to the genetic improvement of the species, availability

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of high grain yield cultivars, tolerance to pests and diseases. Also, well adapted cultivars to different soils and climatic conditions (NOGUEIRA; SEDIYAMA; GOMES, 2015).

Genetics and breeding research programs seek to develop new cultivars with agronomic superiority, high grain yield, wide adaptability, and stability. In addition, parents must be divergent among them and comprising favorable traits, ensuring larger genetic variability among the offspring. Therefore, some breeding programs seek to widen their soybean genetic basis to obtain more combinations on the breeding populations (BORÉM et al., 2015).

Breeding programs usually involve five main steps: parents' selection, crossing and obtaining segregating population advancement of generations through self-fertilization, agronomic performance tests, and selection of superior lineages. Several methods are applied to the improvement of crops aiming for the production of new cultivars, and the increase of grain yield is among the main objectives of these programs. Because it is a quantitative and complex trait, which results from the expression and association of different genetic components, it undergoes great environmental influence (NOGUEIRA, 2011).

The selection of superior genotypes is harder in either trait with low heritability or, traits of difficult assessment. For this purpose, correlations can be used as a tool for indirect selection of superior genotypes; studies of correlations between traits provide information about the changes occurring in one feature when the selection is made in the feature correlated to this (CRUZ; REGAZZI, CARNEIRO, 2012). The objective of this study was to evaluate genetic parameters and correlations between soybean traits, selecting lineages to increase yield and improve agronomic traits.

MATERIAL AND METHODS

Experiments were carried out on the *Capim Branco* farm (18º53’19’’ S; 48º20’57’’ W, 805m altitude), of Federal University of Uberlândia, municipality of Uberlândia, Minas Gerais State, harvest 2016/2017. Twenty lineages developed by the Soybean Improvement Program of the Federal University of Uberlândia and two cultivars (CD 2737 and TMG 2158 IPro) were evaluated in a randomized complete block design with three replications on an area equal to 900 m^2.

Four lines of 5 m in length and spaced 0.5 m apart made up each experimental plot; the two central rows 0.5m at the row ends formed the useful area, resulting in 4m^2 for each plot. Soil preparation was performed as conventional; with one plowing and two harrowings. Previous to the sowing, the surface was grooved and fertilized according to soil analysis.

Regarding cultural practices were used herbicides to control pre and post emergence weeds, also complementing with manual weeding when necessary. Diseases and insect pests were controlled according to appropriate technical recommendations.

The agronomic traits were assessed according to the stages of crop development as Fehr and Caviness (1977) recommendations.

Evaluated traits were: number of day to the flowering (NDF); number of days to maturity (NDM); flowering plant height (APF); plant height at maturity (APM); number of nodes on main stem at the flowering (NNF); number of pods with one grain (NV1); two grains (NV2) and three grains (NV3); total number of pods per plant (NVT); number of pods showing aborted grains (NVCHOCHAS); and grain yield (PROD).

Data were submitted to individual variance analysis to assess phenotypic variability and estimate coefficients of genotypic determination. The data were grouped based on the F test at 5% of probability level. Subsequently, analyses of phenotypic and genotypic correlations were performed and statistical significances were tested by the *t*-test at the 5% probability level. All analyses were performed using the Computational Program in Genetics and Statistics (GENES) (CRUZ, 2016).

RESULTS AND DISCUSSION

Traits assessed have exhibited genetic variability at the 5% probability level by the F test, indicating the possibility of selection of superior lineages (Table 1).

Table 1. Phenotypic variability, genetic parameters and coefficient of variation of morpho-agronomic traits of 20 lines and 2 soybean cultivars sown in 2016/2017, Uberlândia - MG, Brazil.

Traits	QMG	CV (%)	H^2 (%)	CVg/ CVe
NDF	14.30*	3.79	72.55	0.94
APF	423.01*	15.19	77.89	1.08
NNF	7.22*	8.71	86.25	1.44
APV	229.77*	21.75	85.71	1.41
APM	803.08*	9.94	87.92	1.56
NDM	444.53*	4.87	90.84	1.82
NNPROD	24.15*	26.09	48.54	0.56
NNM	17.73*	8.20	88.33	1.59
NV1G	6.35*	75.78	51.82	0.60
NV2G	258.80*	35.01	68.78	0.86
NV3G	135.78*	29.46	87.00	1.49
NVCHOCHAS	377.21*	40.09	86.84	1.48
NVCHOGRAO	270.03*	38.56	87.41	1.52
NTVt	841.95*	26.18	76.02	1.03
PROD	2016003.71*	25.84	61.56	0.73

*: significant at 5% probability, by F test; QMG: mean squares of genotypes; CV (%): coefficient of variation; H^2: coefficient of genotypic determination; CVg / CVe: ratio between coefficient of genetic variation (CVg) and coefficient of environmental variation (CVe); NDF: number of days for flowering, NDM: number of days to maturity; APF: flowering plant height, maturity plant height, APM: maturity plant height. NNF and NNM: Number of nodes on main stem at flowering and at maturity; NNPROD: number of productive nodes in the main stem; NV1G, NV2G and NV3G: number of pods with one, two and three grains; NVCHOCHAS: number of pods showing aborted grains; NVCHOGRAO: number of pods containing no grains; NTVt: sum of all plant pods; PROD: grain yield.

According to the morpho-agronomic analysis results the coefficient of variation ranged from 3.79% to 75.78% regarding the number of days to the flowering and number of pods with one grain, respectively (Table 1). Sousa et al. (2013) evaluating agronomic traits in 71 soybean lineages have found a low CV to the number of days for flowering (5.04) due to environmental influence, thus it is less recommended selecting genotypes based on this attribute.

The coefficient of variation of 25.84% observed to grain yield in this study is justified because it is a trait subject to wide experimental interference. Machado (2017) evaluated the agronomic performance and genetic diversity of soybean lineages and cultivars in the same region and obtained coefficients of variation (CV) ranging between 2.13% to 56.50% for the number of days to maturity (NDM) and the number of pods with three grains (NV3), respectively. Higher CV values for production components are acceptable because these are quantitative traits largely influenced by the environment (LEITE et al., 2015) (DE SOUSA LEITE et al., 2016).

When genotype's effects are fixed, once they have been predetermined, the genotypic variation coefficient (H^2) expresses the proportion of phenotypic variability due to genetic causes (CRUZ; REGAZZI; CARNEIRO, 2012). In this study, H^2 ranged from 48.54% to 90.84% for the number of productive nodes (NNPROD) and the number of days to maturity (NDM), respectively. Values of H^2 above 70% are considered high, therefore NDF, APF, NNF, APV, APM, NDM, NNM, NV3G, NVCHOCHAS, NVCHOGRAO, and NTVt have shown high heritability according to our results, demonstrating that difference between genotypes is predominantly of genetic nature (Table 1).

Traits as number of productive nodes, number of pods with one and two grains, and yield, have shown H^2 values lower than 70%. These results might be justified by the fact that these are quantitative traits, which are driven by many genes and subject to higher environmental influences (HAMAWAKI et al, 2010).

The ratio between the coefficient of genetic variation and the coefficient of environmental variation is a useful quantity in plant breeding since it indicates a chance of success in the selection process. A trait is considered favorable to selection when values obtained by this ratio are equal or superior to one (CRUZ, REGAZZI, CARNEIRO, 2012). In this study, results obtained ranged from 0.56 to 1.82 for NNPRO and NDM, respectively (Table 1). Furthermore, APF, NNF, APV, APM, NDM, NNM, NV3G, NVCHOCHAS, NVCHOGRAO and NTVt traits have presented CVg / CVe results greater than 1 (Table 1).

Table 2 shows that NDF and NDM have separated genotypes into two groups. The NDF ranged from 49.00 to 58.00 for the B2P7 / B2P26 and B2P17 genotypes, respectively. The controls CD 2737 and TMG 2158 IPro were the earliest at 97 days. On the other hand, lineages of the UFU soybean program were late, with a total cycle of 123 to 142 in the genotypes B2P7 and B2P15. Genotypes B2P7, B2P20, B2P28, B2P38, B1P26, and B1P33 were found intermediate, with average taking from 123 to 131 days to reach maturity.

Table 2. Agronomic traits of lineages and soybean cultivars cropped in the 2016/2017 harvest, Uberlândia-MG, Brazil.

Genotypes	NDF (days)	NDM (days)	APF (cm)	APM (cm)	AIPV (cm)
B2P1	51.67 b	138.33 a	66.07 a	116.20 a	24.13 c
B2P7	49.00 b	123.00 b	58.30 a	102.70 b	35.50 b
B2P8	51.67 b	131.00 a	60.20 a	97.20 b	26.27 c
B2P11	57.00 a	140.50 a	68.80 a	116.40 a	47.80 a
B2P12	53.00 b	134.00 a	77.87 a	103.40 b	23.40 c
B2P13	51.00 b	128.50 a	59.40 a	71.40 c	13.70 d
B2P14	53.00 b	138.33 a	74.00 a	105.93 b	36.47 b
B2P15	51.67 b	142.67 a	66.73 a	118.87 a	30.40 b
B2P17	58.33 a	138.33 a	81.93 a	115.33 a	33.67 b
B2P20	50.33 b	130.33 b	57.53 a	103.20 b	32.67 b
B2P26	49.00 b	140.50 a	52.70 b	78.90 c	23.50 c
B2P27	51.00 b	140.50 a	64.40 a	86.80 c	24.33 c
B2P28	53.00 b	128.50 b	70.30 a	111.10 a	18.70 d
B2P33	51.67 b	134.67 a	71.67 a	87.53 c	26.80 c
B2P38	53.00 b	130.33 b	79.47 a	112.53 a	34.67 b

B1P26	53.00 b	130.33 b	62.87 a	114.13 a	24.80 c
B1P33	50.33 b	126.67 b	57.20 a	100.13 b	31.33 b
CD2737	50.67 b	97.00 c	41.50 c	83.00 c	13.13 d
TMG 2158 IPro	53.00 b	97.00 c	30.47 c	64.40 c	13.20 d
2LP14	53.00 b	134.00 a	61.90 a	75.60 c	15.90 d
2AP11	51.50 b	140.50 a	71.20 a	114.70 a	29.50 b
P19 16c	53.00 b	134.67 a	66.20 a	101.60 b	19.67 d

Means followed by the same letter belong to the same group by the Scott Knott test at 5% probability. NDF and NDM: Number of days for flowering and maturity; APF and APM: Plant height at flowering and at maturity; and AIPV: First pod insertion height.

Plant height at flowering has divided genotypes into three groups, however, most genotypes have shown averages ranging from 57.20 to 81.93 cm (Table 2). The average plant height at maturity also has separated assessed genotypes in three groups, the smallest plants have comprised heights between 64 and 87 cm, intermediate plants between 100 and 105 cm, and the tallest plants from 112 to 118 cm.

Both plant height at flowering and plant height at maturity are relevant traits, taller plants are more prone to lodging than smaller ones, and plants higher than 100cm decrease the efficiency of the mechanized harvest. Ideal heights in the soybean cropping range from 40 to 90cm (NOGUEIRA et al., 2009; SEDIYAMA et al., 2015).

First pod insertion height is another important trait during the process of soybean lineage selection. According to Sediyama (2013), to avoid losses and guarantee maximum efficiency in harvesting, the ideal height of insertion to the first pod lay between 10 and 15 cm; the insertion of the first pod determines the height adjustment of the harvester-cutting bar. In this study, the average values for APV ranged from 13.13 to 47.8 cm regarding the genotypes CD 2737 and B2P11, respectively. These results may be higher than the ideal height found in other studies, due to climatic and environmental factors that this experiment has been submitted.

Genotypes B1P13, B2P28, CD2737, TMG 2158 IPro, 2LP14, and P19 16c presented lower estimates of AIPV, varying from 13.13 to 19.67 (Table 2). These results are similar to those found by Dornelas et al. (2011), in which the average height of the insertion of the first pod oscillated from 9 to 16cm in 22 soybean lineages. Higher values of insertion of the first pod may be due to either some type of stress that has caused abortion of lower flowers or plant genetics. In this work, we have used in the F8 generation in the same lineages used by Souza (2013) on his study in the F6 generation, which also presented high insertion values of the first pod.

The number of nodes in the main stem is an important feature for lineage selection because it is directly correlated to grain yield (SEDIYAMA; SILVA; BORÉM, 2015). The results in Table 3 showed the number of nodes in flowering and the number of nodes at maturity ranging from 9.80 to 14.07 and 13.40 to 24.67, respectively. According to Sediyama; Silva and Borém (2015), an ideal soybean plant must have around 18 nodes, therefore, the genotypes P19 16c, B2P33, B2P8, 2AP11, B2P38, B1P33, B2P1, B2P14, and B2P17 were found promising to breeding.

Although results presented in Table 1 indicate the existence of genetic variability regarding NNPROD, Scott Knott test results did not allow the division of genotypes into more than one group (Table 3).

Table 3. The number of nodes in the main stem, number of nodes at flowering and maturity, and number of productive nodes in cultivated soybean lineages and cultivars in the 2016/2017 harvest, Uberlândia-MG, Brazil.

Genotypes	NNF	NNM	NNPROD
B2P1	10.87 b	18.33 b	14.47 a
B2P7	9.80 b	16.80 c	12.60 a
B2P8	11.07 b	16.07 c	12.67 a
B2P11	12.70 a	18.90 b	11.90 a
B2P12	11.73 a	16.67 c	11.07 a
B2P13	10.50 b	13.40 d	11.00 a
B2P14	11.67 a	18.07 b	12.20 a
B2P15	12.00 a	24.67 a	17.93 a
B2P17	14.07 a	17.93 b	12.00 a
B2P20	10.47 b	19.13 b	14.13 a
B2P26	10.40 b	14.80 d	9.40 a
B2P27	11.00 b	15.43 c	11.70 a
B2P28	13.00 a	20.10 b	15.80 a
B2P33	12.20 a	17.00 c	12.73 a
B2P38	13.53 a	18.40 b	13.20 a
B1P26	11.93 a	20.00 b	12.93 a
B1P33	10.93 b	18.47 b	23.27 a
CD2737	7.93 c	16.93 c	15.67 a
TMG 2158 IPro	8.13 c	13.67 d	13.33 a
2LP14	12.70 a	15.60 c	12.80 a
2AP11	13.00 a	18.70 b	13.90 a
P19 16c	11.93 a	17.00 c	12.60 a

Averages followed by the same letter belong to the same group by the Scott-Knott test at 5% probability level. NNF: Number of nodes in the main stem in flowering; NNM: Number of nodes at maturity; NNPROD: Number of productive nodes in the main stem.

Since the number of pods influences the grain yields per plant, taking into account traits NV1G, NV2G, the genotype 2AP11 has shown higher yield averages 5.30 and 44.20 for these respective traits. On the other hand, the genotypes TMG 2158 IPro and 2LP14 stand out for the NV3G, presenting averages of 25.93 and 25.40, respectively. Among the genotypes studied those that produced more pods were 2LP14, 2AP11, B2P15 and B2P28 with averages 98.9, 69.6, 78 and 81.8, respectively (Table 4).

Table 4. Grain yield components and yielding of soybean lineages and cultivars cropped in the 2016/2017 harvest, Uberlândia-MG, Brazil.

Genotypes	NV1G	NV2G	NV3G	NVTt	PROD
B2P1	2.40 b	27.27	20.87 a	58.47 b	4317.99
B2P7	1.20 b	13.70	19.20 a	48.60 b	2831.71
B2P8	2.47 b	21.60	21.87 a	61.40 b	4148.07
B2P11	1.00 b	22.00	6.20 b	35.70 b	2692.48
B2P12	2.87 b	25.47	10.73 b	44.73 b	3552.64

B2P13	1.10 b	25.90	15.30 a	57.50 b	3152.06
B2P14	1.80 b	25.87	6.47 b	47.73 b	1898.97
B2P15	2.33 b	39.60	18.53 a	78.00 a	4290.08
B2P17	1.93 b	29.33	10.53 b	50.77 b	2426.25
B2P20	0.90 b	14.00	4.70 b	26.60 b	2666.42
B2P26	0.20 b	25.70	5.80 b	40.60 b	2476.62
B2P27	1.90 b	29.93	16.88 a	62.30 b	3555.93
B2P28	4.40 a	35.70	21.10 a	81.80 a	3678.25
B2P33	3.87 a	36.87	8.60 b	53.20 b	3423.82
B2P38	3.67 a	32.87	7.73 b	51.67 b	2993.31
B1P26	2.87 a	11.60	12.53 b	35.00 b	2098.51
B1P33	3.33 a	28.53	15.40 a	54.07 b	3848.92
CD2737	0.27 b	12.00	20.83 a	37.47 b	4032.13
TMG 2158 IPro	0.40 b	10.60	25.93 a	46.20 b	4507.19
2LP14	4.70 a	30.10	25.40 a	98.90 a	4785.63
2AP11	5.30 a	44.20	6.60 b	69.60 a	4240.11
P19 16c	1.87 b	22.07 b	12.93 b	53.80 b	3337.76 a

Averages followed by the same letter belong to the same group by the Scott-Knott test at 5% probability. NV1G: Number of pods with one grain; NV2G: Number of pods with two grains; NV3G: Number of pods with three grains; NTVt: Total number of pods. PROD: Yielding.

Increasing grain yield is one of the main objectives of soybean genetic breeding programs. In this study, genotype 2LP14 has shown larger yielding in comparison with other assessed genotypes, including controls CD2737 and TMG 2158 IPro. Among the 20 lines studied, 15 have presented yielding above the national average of 2882 kg h^{-1} (CONAB, 2017) (Table 4). Sediyama et al. (2015) claimed that cultivars are considered superior when its productivity is above 3000 kg ha^{-1}, therefore genotype P19 16c and all genotypes belonging to group 'a' were found productively superior.

Results present in Table 5, have shown that genotypic correlations were bigger than phenotypic correlations for most of the traits, which indicate that genetic factors have contributed more to these traits than the environmental ones (ALMEIDA; PELUZIO; AFFÉRRI, 2010).

Table 5. Results of phenotypic correlation coefficients (rf) above the diagonal, and genotypic correlation coefficients (rg) below the diagonal, regarding 13 agronomic traits assessed in 20 lineages and 2 soybean cultivars, 2016/2017 harvest, Uberlândia- MG, Brazil.

Caracteres	APF	NNF	APV	APM	NDM	NNPROD	NNM	NV1G	NV2G	NV3G	NTVt	PROD
NDF	0,46*	0,59*	0,30	0,36	0,19	-0,18	0,17	0,12	0,10	-0,14	0,01	-0,19
APF		0,89*	0,51*	0,68*	0,76	-0,15	0,41	0,55*	0,62*	-0,49*	0,21	-0,33
NNF			0,44*	0,61*	0,73*	-0,08	0,43*	0,67*	0,67*	-0,39	0,38	-0,20
APV				0,67*	0,50*	0,05	0,47*	0,02	0,15	-0,60*	-0,30	-0,51*
APM					0,51*	0,24	0,81*	0,33	0,3	-0,37	-0,04	-0,27
NDM						-0,20	0,35	0,36	0,62*	-0,49*	0,26	-0,27
NNPROD							0,52*	0,27	0,16	0,27	0,21	0,39
NNM								0,31	0,34	-0,18	0,12	-0,06
NV1G									0,70*	0,03	0,66*	0,34
NV2G										-0,19	0,66*	0,26
NV3G											0,52*	0,70*
NTVt												0,63*

*: Significant at the 5% probability level by the t test; +: significant to 5% by bootstrap with 5 thousand simulations; NDF and NDM: number of days to the flowering and at maturity; APF and APM: plant height at flowering and at maturity; NNF and NNM: Number of nodes at the flowering and at maturity; APV: first pod insertion height; NNPROD: number of productive nodes in the main stem; NV1G, NV2G, NV3G: number of pods with one, two and three grains, respectively; NTVt: total of plant pods; PROD: grain yield.

By evaluating correlations between agronomic traits in soybeans, Sousa et al. (2015) also have observed higher values of genotypic correlations about phenotype correlations to most of the evaluated traits, except plant height at flowering and plant height at maturity. Nogueira et al. (2012) and Leite et al. (2015) also observed higher genotypic correlations than phenotypic for agronomic traits assessed in soybean genotypes.

The plant height at flowering was correlated genetically and phenotypically with plant height at maturity, first pod insertion height and number of pods with one, two and three grains (Table 5). These correlations indicate that the higher one plant is when flowering, the higher this plant will be at maturity and also the insertion of its first pod, as well as larger will be the number of pods.

Plant height at flowering was positively correlated with plant height at maturity and first pod insertion height (Table 5). These correlations are important for breeding programs since plant height at maturity is a determining factor in the mechanized harvest. In this context, it is possible to perform indirect selection (SEDIYAMA; SILVA; BORÉM, 2015).

Phenotypic and genotypic correlations of grain yield concerning the total number of pods and the number of pods with three grains have presented extensive magnitude (Table 5), 0.62 and 0.81, therefore these traits are indicated for indirect selection. Alcântara Neto et al. (2014) applied pathway analysis to soybean yield and found similar results confirming that the number of pods per plant is the component of production having the greatest effect.

CONCLUSIONS

Traits related to the cycle, height and number of nodes in the main stem had shown ample magnitude for coefficients of genotypic determination and CVg/CVe ratio, evidencing the possibility of successes in the selection of superior lineages in the Soybean Improvement Program of the Federal University of Uberlândia.

B2P1, B2P28, B1P33, and 2AP11 lineages stand out among genotypes showing superior grain yield and better agronomic traits.

The extensive magnitude of phenotypic and genotypic correlations between the grain yield and the number of pods with three grains and the number of total pods have evidenced the possibility of indirect selection aiming grain yield increases.

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RESUMO: A soja é uma cultivar de grande importância econômica mundial e por esse motivo essa leguminosa é explorada nos programas de melhoramento, que visam disponibilizar cultivares de alta produtividade de grãos, tolerantes a pragas e doenças e adaptadas à diferentes condições edafoclimáticas. Os objetivos desse trabalho foram selecionar linhagens, avaliar parâmetros genéticos e correlações entre caracteres de soja. O experimento foi conduzido na área experimental da Fazenda Capim Branco pertencente à Universidade Federal de Uberlândia na safra de 2016/2017. Avaliaram-se 22 genótipos em delineamento de blocos completos casualizados com três repetições para 15 caracteres morfo-agronômicos. Os caracteres agronômicos relacionados ao ciclo, altura, número de nós e vagens totais tiveram coeficiente de determinação genotípico superiores a 70%. Obteve-se coeficiente de variação para o caráter número de dias para o florescimento igual a 3,79% e para o caráter número de dias para maturação, 4,87%, indicando maior homogeneidade entre os dados e baixa variação ao acaso. Dos caracteres avaliados, dez apresentaram razão entre coeficiente de variação genético e coeficiente de variação ambiental superiores a um, demonstrando oportunidade de sucesso no processo de seleção para esses respectivos caracteres. 15 genótipos obtiveram produtividade de grãos superior à média nacional de safra 2016/2017, isto é, a 2882 kg h^{-1}. As correlações fenotípicas entre caracteres que foram significativas oscilaram de -0,49 a 0,89, cujas estimativas de correlação genotípica foram superiores à correlação fenotípica, indicando que os fatores genéticos contribuíram mais que os ambientais. Os caracteres relacionados ao ciclo, altura e número de nós na haste principal, tiveram H^2 de elevada magnitude e altas estimativas na razão CVg/CVe, evidenciando a possibilidade de seleção de linhagens superiores no Programa de Melhoramento de Soja da Universidade Federal de Uberlândia. Considerando o caráter produtividade de grãos, foi possível identificar número de vagens de três grãos e número total de vagens para a seleção indireta, com base nas correlações fenotípicas e genotípicas. As linhagens 2lP14, B2P1, B2P28, B1P33 e 2AP11 destacam-se como genótipos superiores na seleção direta.

PALAVRAS-CHAVE: *Glycine max*. Melhoramento genético. Seleção indireta.

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