Inheritance of Precocity and of Agronomic Characters in Soybean

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ABSTRACT. Precocious soybean cultivars enable crop rotation and low pressure to the biotic and abiotic factors. This study aimed to determinate the inheritance of characters related to precocity and agronomic characters in soybean segregating population, coming from contrasting genitors to cycle. The experiment was conducted at a greenhouse located at Capim Branco farm, belonging to Federal University of Uberlândia. The MG/BR 46 Conquista and UFUS 6901 cultivars were used to bi-parental crossing and acquirement of F1 and F2 populations. The individuals of the genitors, F1 and F2 populations were evaluated to eight characters and the phenotypic, genetic and environmental variances, broad-sense heritability, average degree of dominance and gene number were determined. The average for number of days for flowering and number of days to maturity in the F1 generation was 40.26 and 103.52 days and in the F2 generation was 37.85 and 105.88 days, respectively, which fits into the classification of semi-precocious. The heritability varied from 2.36% for number of grains per pod – controlled by 160 genes, to 85.39% for number of days for maturing – controlled by two genes. On the F2 population, the existence of transgressed segregates was found, except for number of days to maturity, number of nodes and intersection height of the first pod. It was concluded that the genetic variance and heritability of the

agronomic characters of the F2 population, allows the acquirement of selection of superior individuals in terms of precocity, height, number of nodes and compounds of productivity, being promising genotypes in the soybean breeding program.

KEY WORDS: Glycine Max; Generation Analysis; Genetic Parameters.

INTRODUCTION

Soybean [*Glycine max* (L.) Merrill] is one of the most important cultures of Brazil and of the world because of all the production chain and technology developed in this oleaginous production (Cunha et al., 2013). It presents a relevant socioeconomic role due to its different applications in human and animal feeding, as well as impulsion of several agro-industrial complexes, such as the complexes of seeds, fertilizers, agro toxins and agricultural machines (Costa and Santana, 2013).

Brazil is the second biggest producer of soybean in the world, with a production estimated at 103,778.3 thousand tons of soybean and productivity of 3,072 kg/ha at 2016/17 crop (CONAB, 2017). The advance of the cultivated area of soybean in Brazil and the increase of grains productivity results from the contribution of genetics breeding programs, which performs at the development of new cultivars adapted to different areas of the country, as well as the development of production technologies (Val et al., 2014). In front of this crescent growth of the soybean market, the use of more precocious cultivars is required, which makes possible the anticipation of the harvest, the integrated soybean system on first cropping season and maize on second cropping season, and the lowest pressure by abiotic and biotic stresses as leaf diseases and end-of-cycle diseases (Finoto et al., 2011; Meotti et al., 2012).

There are ten unknown genes that acts in characters linked to soybean cycle. Those are the genes E1/e1, E2/e2, E3/e3, E4/e4, E5/e5, E6/e6, E7/e7, E8/e8, E9/e8 e J/j (Bernard, 1971; Bernard and Weiss, 1973; Buzzeli and Voldeng, 1980; McBlain and Bernard, 1987; Bonato and Vello, 1999; Cober and Voldeng, 2001; Cober et al., 2010; Kong et al., 2014; Watanabe et al., 2012). The knowledge of these genes, along with the study of the inheritance for the soybean cycle, brings information that contributes to the development of more precocious cultivars. The analysis of segregant populations demonstrates essential estimative of genetic parameters, such as broad-sense and narrow-sense heritability, the number of genes, heterosis and average degree of dominance (Vasconcelos et al., 2010; Baldissera et al., 2014).

The achievement of estimative of genetic and phenotypic parameters is relevant in the genetics breeding programs for it makes possible choosing methods and characters used at initial and advanced selection stages, allowing, still, the study of mechanisms, genetics values and variability to the character (Vasconcelos et al., 2010). Gatut_Wahyu et al. (2014) studied the inheritance of genes that control soybean maturity in a population understood by parental, F_1, backcrossing, and F_2 on Indonesia, and affirmed that knowledge about genetic inheritance of soybean precocity, especially in tropical areas, are still limited. This way, the objective of the study was to determinate the inheritance of characters related to precocity and agronomic characters in soybean segregating population, coming from contrasting genitors to cycle.

METHODS AND MATERIAL

The experiment was conducted at the Capim Branco farm belonging to Federal University of Uberlândia (UFU), at the municipality of Uberlândia, Minas Gerais, Brazil, which geographic coordinates are 18° 52' S; 48° 20' W and 872 m of altitude. The temperature data during the experiment conduction are presented at Figure 1.
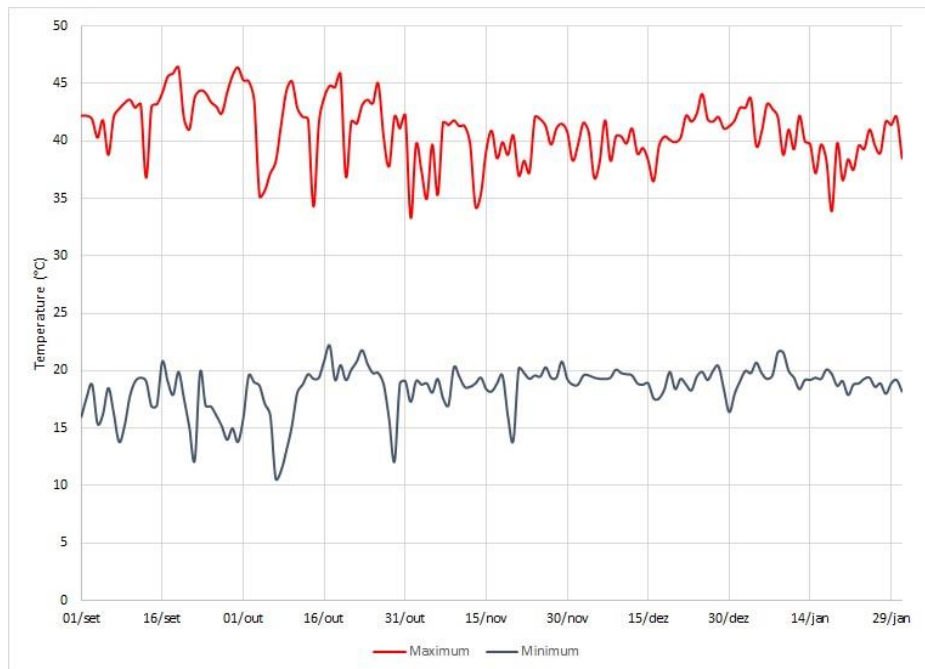
Figure 1. The maximum and minimum temperature in the greenhouse of Capim Branco Farm in Uberlândia-MG, 2016/17 crop, during September 2016 to January 2017. Source: Meteorology station of Capim Branco Farm and IMET.

Two soybean cultivars were used to bi-parental crossing which formed the analyzed populations in the present work. These cultivars were selected for being contrasting to cycle.MG/BR46 Conquista cultivar was developed by EMBRAPA, has a medium late cycle, belongs to maturity cluster linked to 8.1, purple hypocotyl, purple flower, brown pubescence, determined type of growth, black hilum, and tolerance to roots nematodes.

UFUS 6901, in its turn, was developed by the Soybean Breeding Program of UFU, it has a precocious cycle, belongs to the maturity group related to 7.0, green hypocotyl, white flower, bright brown pubescence, undetermined type of growth, medium brown hilum, resistant to bacterial searing and mildew, moderately resistant to powdery mildew, mark stain, and end-of-cycle diseases. The block of crossing has been installed, which genitors sowing have been phased every three days, aiming to make possible the synchrony of flowering of parental. The sowing was made in pots with 3 dm ^{3}, previously filled with 2/3 of soil and 1/3 of organic matter. There were sowed five seeds per pot, each pot with 3 cm depth.

When the plants were at stadium V1, they were thinned, and it was kept two plants per pot. At the stadium V5, the apical meristems of the plants were removed to avoid its stultifying and also help the ramifications. Periodically, watering and recommended cultural treats have been made for the soy culture (EMBRAPA, 2013). Artificial crossings were made adopting UFUS 6901 as the feminine genitor and MG/BR 446 Conquista as the masculine genitor. After the development of the pod on the flower where was accomplished the crossing, a pod with hybrid seeds was obtained, that were confirmed by the sowing of F_1 seeds and evaluation of the hypocotyl color. F_1 generation was conducted to acquisition of F_2 seeds. From the sampling of 24 individuals of each genitor, 24 individuals from F_1 generation and 127 individuals from F_2 generation, an experiment has been taken to proceed the study of analysis of generations.

The sowing of generations P_1, P_2, F_1 and F_2 took place on September 17, 2016, on greenhouse of the Soybean Breeding Program of UFU. The pots used had 5 dm ^{3} and were previously filled with 2/3 of soil and 1/3 of organic matter, sowed with four seed per pot with 3 cm depth. The cultural treats in the conduction of the experiment followed the technical recommendation to soybean cultivation of Minas Gerais state (EMBRAPA, 2013). Furthermore, it has been done two daily watering to guarantee positive experimental conditions for the plants.

The plants were evaluated with the following characters:
a) Number of days for flowering (NDF): period of days elapsed between stadium VE until the emergence of the first flower (R1);
b) Number of days to maturing (NDM): period of days elapsed between stadium VE until maturing (R8);
c) Plant height (PH): measurement, in centimeters (cm), starting from the surface of the soil until the last node on the rod of the main plant, on stage R8.
d) Number of nodes (NN): were counted all the nodes on the main maturing rod (stage R8);

e) Intersection height of the first pod (IHP): distance in centimeters (cm), measurement starting from the soil surface until the first pod;

f) Number of pods per plant (NPP): after the harvest, were counted all the pods produced by the plant;

l) Number of grains per pod (NGP): was obtained for the reason between total number of grains and total number of pods;

m) Grain production (YIELD): total weight of grains in gram (g), produced by each plant.

For definition of the plants stadiums, it was used Fehr and Caviness scale (1977).

The phenotypic data from the genitors and the generations F_1 and F_2 were used to estimate the following parameters, by the formulas below:

- Genotypic variance in F_2

$\hat{\sigma}^2_{G(F2)} = \hat{\sigma}^2_{F(F2)} - \hat{\sigma}^2_{E(F2)}$ (Equation 1)

In which:

$\hat{\sigma}^2_{G(F2)}$: genetic variance of population F_2;

$\hat{\sigma}^2_{F(F2)}$: phenotypic variance of population F_2;

$\hat{\sigma}^2_{E(F2)}$: environmental variance of population F_2.

- Environmental variance

$\hat{\sigma}^2_E = \frac{1}{2}\left[\hat{\sigma}^2_{(P1)} + \hat{\sigma}^2_{(P2)}\right]$ (Equation 2)

In which:

$\hat{\sigma}^2_E$: environmental variance;

$\hat{\sigma}^2_{(P1)}$: phenotypic variance of parental 1;

$\hat{\sigma}^2_{(P2)}$: phenotypic variance of parental 2.

- Broad-sense heritability

$h^2_a = \frac{\hat{\sigma}^2_{G(F2)}}{\hat{\sigma}^2_{F(F2)}}$ (Equation 3)

In which:

h^2_a: broad-sense heritability;

$\hat{\sigma}^2_{G(F2)}$: genetic variance of population F_2;

$\hat{\sigma}^2_{F(F2)}$: phenotypic variance of population F_2.

- Average degree of dominance based in averages

$k_m = \frac{2\overline{F}_1 - (\overline{P}_1 + \overline{P}_2)}{\overline{P}_1 - \overline{P}_2}$ (Equation 4)

In which:

k_m: average degree of dominance based in averages;

$\overline{P}_1$: phenotypic avarage of parental 1;

$\overline{P}_2$: phenotypic average of parental 2;

$\overline{F}_1$: phenotypic average of population F_1.

- Number of involved genes in character determination

$n = \frac{R^2(1 + 0,5k^2)}{8\hat{\sigma}^2_G}$ (Equation 5)

In which:

n: number of genes;

R: range between the averages of progenitors or R: $\overline{P}_1 - \overline{P}_2$;

$\hat{\sigma}^2_G$: genetic variance.

- Prediction of gains per selection

$\Delta G = DS\, h^2$ and $\Delta G\% = \frac{\Delta G}{\overline{X}_O}$ (Equation 6)

In which:

ΔG: selection gain;

h^2 : herdability;

DS: differential of selection, given by the formula $DS = \overline{X}_S - \overline{X}_O$;

$\overline{X}_O$: observed average;

$\overline{X}_S$: average of the selected ones.

The genetic-statistical analysis was achieved using the Computational Program in Genetic and Statistic - Program GENES (Cruz, 2013).

RESULTS AND DISCUSSION

The estimations of the average and variance parameters are useful to the upgrade specialist because they allow inferring about the genetic potential of the segregating population (Baldissera et al., 2014). There are presented on Table 1 the averages of agronomic characters of the generations P_1, P_2, F_1 and F_2, and the estimations of phenotypic variance.

Table 1. Estimations and averages of phenotypic variance of agronomic characters obtained on generations P_1, P_2, F_1 and F_2 in cultivated soy on the greenhouse of crop 2016/2017 on the municipality of Uberlândia - MG.

Generations	NDF		NDM		PH		NN	
	$\overline{X}$	$\hat{\sigma}_F^2$	$\overline{X}$	$\hat{\sigma}_F^2$	$\overline{X}$	$\hat{\sigma}_F^2$	$\overline{X}$	$\hat{\sigma}_F^2$
P_1	36.13	0.90	100.75	2.37	99.75	359.76	15.50	7.57
P_2	42.21	0.52	118.38	8.51	93.92	85.01	13.00	4.09
F_1	40.26	20.66	103.52	20.41	99.83	378.87	14.74	10.12
F_2	37.85	17.91	105.88	37.22	98.57	406.99	14.46	7.04
Generations	IHP		NPP		NGP		YIELD	
	$\overline{X}$	$\hat{\sigma}_F^2$	$\overline{X}$	$\hat{\sigma}_F^2$	$\overline{X}$	$\hat{\sigma}_F^2$	$\overline{X}$	$\hat{\sigma}_F^2$
P_1	20.75	37.52	24.33	66.23	2.27	0.06	8.50	11.30
P_2	32.52	64.55	30.25	78.28	2.35	0.01	10.92	7.47
F_1	19.78	50.54	36.81	447.08	2.44	0.02	14.59	42.56
F_2	22.14	44.02	31.29	181.56	2.44	0.03	12.77	24.99

Note: P_1: UFUS 6901; P_2: MG/BR 46 Conquista; F_1: P_1xP_2; F_2: auto fecundation of F_1; NDF: number of days for flowering; NDM: number of days to maturing; PH: plant height; NN: number of nodes on the main stalk; IHP: intersection height of the first pod; NPP: number of pods per plant; NGP: number of grains per pod; YIELD: grain production; $\overline{X}$: average; $\hat{\sigma}_F^2$: phenotypic variance.

The averages of the genitors P_1 and P_2 have made possible to check that the cultivars UFUS 6901 and MG/BR 46 Conquista were contrasting for the evaluated characters (Table 1). According with Cruz et al. (2012) on heritage studies, the contrast occurrence between parental is necessary to an accurate estimation of the genetic parameters. In addition, Baldissera et al. (2014) claim that crossing between contrasting homozygotes genitors to one character allows inferring about its genetic control.

The cultivar UFUS 6901 presented a shorter cycle (36.13 for flowering and 100.75 day to mature), higher plant height (99.75 cm) and number of nodes (15.50). On the other hand, MG/BR 46 Conquista cultivar presented a longer cycle (42.21 days for flowering and 118.38 days to maturing), and phenotypic average superior to the characters number of pods per plant (30.25), number of grains per pod (2.35), and grain production (10.92 g) (Table 1). The number of days for flowering and maturity are characters that reflect the precocity in soybean genotypic. Those are classified in maturity groups, being the precocious cycle until 100 days, semi precocious between 101 until 110 days, medium from 111 to 125 days, medium late between 124 until 145, and late bigger than 145 days (Sediyama et al., 2016). Notwithstanding, it is worth to highlight that the classification of soybean cultivars as for cycle, must be considered the latitudinal band, by reason of the sensibility of soybean genotypes over the photoperiod.

The cultivar UFUS 6901 presents precocious cycle and the results found are according to that classification, with an average of 100.75 days NDM. While MG/BR 46 Conquista cultivar has a medium late cycle and its average was 118.38 days NDM. The reduction in the cycle of MG/BR 46 Conquista happened because of the high temperature observed during the experimental period.

Major et al. (1975) evaluated the effect of the day length and temperature in soy and checked that colder temperatures and longer days provoke delayed effects in flowering, and higher temperatures induce opposite effects. In concordance with Sediyama et al. (1996) the increase of medium temperatures superior to 24 °C, especially night temperatures, cause fast vegetative growth.

In accordance with Rocha et al. (2012), the temperature influences all the phenological phases of the soybean, since high temperatures curtail the flowering period, which is more accented in short days. These authors observe the precocious flowering and the reduction on the cycle of cultivars exposed to temperatures around 26 °C, in which the medium cycle of MG/BR 46 Conquista was 102 days. The temperature effect did not influence in such way the cycle of the cultivar UFUS 6901, being justified by the work of Major et al. (1975), who identified that cultivars of late maturity are more sensitive to the increase of temperature and length of the day than the precocious cultivars. Kumagai and Sameshima (2014) studied the soybean production answers over the increase of temperature and affirm that the precocious cultivars are less sensitive to the variations on the photoperiod when compared to late cultivars, which are more sensitive. The average to the number of days for flowering and the number of days to maturity in the F_1 generation was 40.26 and 103.52 days and in the F_2 generation was 37.85 and 105.88 days, respectively (Table 1). The averages of both generations presented intermediary values between the parental. These results are compared to the ones obtained by Gatut Wahyu et al. (2014) upon evaluating the gene inheritance which controls soybean maturity, for they have found that F_1 generation had a lower number of days to maturity than the parental with the biggest time of maturity.

The characters of plant height and intersection height of the first pod are important to the adaptation to the mechanized harvest. The ideal height of soybean is between 60 and 110 cm, to make easier the harvest and avoid lodging. About the intersection height of the first pod, the value considered suitable is above ten centimeters, so that values under present possible casualties (Sediyama et al., 2016). The average of the PH was 93.92 cm in the population P_2, inferior to the values found in the populations P_1, F_1 and F_2 with 99.75, 99.83 and 98.57 cm respectively. The averages of intersection height of the first pod were close in the populations P_1, F_1, F_2 with 20.75, 19.78 and 23.08 cm, respectively, and superior to P2, which average was 35.52 cm (Table 1). All the generations P_1, P_2, F_1 and F_2 presented averages of values inside the ideal limits for soybean culture.

The number of nodes is an important character on soybean breeding because there is the predominance of positive correlations with grain productivity (Nogueira et al., 2012). The average of the number of nodes was bigger to P_1 (15.50) and lower to P_2 (13.00), with intermediary values for generations F_1 (14.74) and F_2 (14.46) (Table 1).
The number of pods in the populations P_1, P_2, F_1 and F_2 (Table 1) were 24.33, 30.25, 36.81, 31.29, respectively. It should be emphasized that the low values of this character probably happen because of this study which was achieved in a greenhouse. In a study of the diversity of agronomic characteristics in soybean cultivated in greenhouses, Glasenapp et. al (2015) also found low average to the character number of pods per plant. There has been proximity among the averages of the character number of grains per pod on the populations P_1, P_2, F_1 and F_2. For the character of grain production, it has been noticed that the averages of generations F_1 and F_2 overcame the parental (Table 1), pointing the potential of generation F_2 for the selection of individuals with higher productive potential.

Evaluating the inheritance of grain production and the compound of the production in soybean, based in analysis conducted to field, Castro (2008) found averages for the number of pods per plant equal to 206.56, 206.16, 283.49 and 256.10 and grain production equal to 59.47, 49.73, 86.50 and 68.46 in grams per plant for generations P_1, P_2, F_1 and F_2 respectively. These values are superior to the ones found in the present study, and one of its motives are the differences between field conditions and the greenhouse. The genetic control knowledge of a character is essential to succeed in a breeding program because it allows defining the adequate selection method (Baldissera et al., 2014). Variance estimations, broad-sense heritability, average degree of dominance and number of genes to agronomic characters are presented in Table 2.

Table 2. Estimations of variance compounds, broad-sense heritability, average degree of dominance and number of genes of agronomic characters obtained on generation F_2 in cultivated soybean on a greenhouse, at crop 2016/2017 on Uberlândia-MG.

Parameters	Characters							
	NDF	NDM	PH	NN	IHP	NPP	NGP	YIELD
$\hat{\sigma}^2_F$	17.91	37.22	406.99	7.04	44.02	181.56	0.03538	24.99
$\hat{\sigma}^2_G$	17.20	31.78	184.61	1.22	0.00	109.30	0.00093	15.60
$\hat{\sigma}^2_E$	0.71	5.44	222.39	5.83	51.04	72.26	0.03445	9.39
h^2_a	96.04	85.39	45.36	17.29	null	60.20	2.63	62.43
gm̂d	-0.36	0.69	1.03	0.39	1.16	-3.22	-3.16	-4.04
Number of genes	2.10	1.73	11.62	17.35	-	6.26	159.39	6.28

Note: NDF: number of days for flowering; NDM: number of days to maturing; PH: plant height; NN: number of nodes on the main stem; IHP: intersection height of the first pod; NP: number of pods per plant; NGP: number of grains per pod; YIELD: grain production; $\hat{\sigma}^2_F$: phenotypic variance; $\hat{\sigma}^2_G$: genetic variance; $\hat{\sigma}^2_E$: environmental variance; h^2_a: broad-sense heritability; gm̂d: average degree of dominance.

Hamawaki et al. (2012) affirm that the variance estimations are important for decision-making in a breeding program. On this study, the phenotypic variance oscillated from 0.03 to 406.99 from NGP to HP, respectively. The genetic variance had amplitude from zero (IHP) to 184.61 (PH). Negative estimations of genetic variance indicate an absence of variability to the character. In accordance with Cruz (2005), the resulting variance of the environmental effects influences on the selective process, because it raises difficulties to the recognition of superior genotypes. The environmental variance went from 0.03 to 222.39 for NGP and PH, respectively (Table 2). A predominance of genetic variance higher than the environmental variance has been noticed for the characters NDB, NDM, NP, and YIELD.

Studying genetic parameters and agronomic evaluation in soybean F_2 progeny on Distrito Federal, Santos (2016) determined the phenotypic, environmental and genetic variance for agronomic characters. The estimations were higher than the ones found in this study for the number of days to maturity, ($\hat{\sigma}_F^2$: 45.33, $\hat{\sigma}_E^2$: 4.56 and $\hat{\sigma}_G^2$: 40.77) and the number of pods per plants ($\hat{\sigma}_F^2$: 200.19, $\hat{\sigma}_E^2$: 84.99 and $\hat{\sigma}_G^2$: 115.21). And lower for plant height ($\hat{\sigma}_F^2$: 67.46, $\hat{\sigma}_E^2$: 6.28 and $\hat{\sigma}_G^2$: 61.17), intersection height of the first pod ($\hat{\sigma}_F^2$: 1.27, $\hat{\sigma}_E^2$: 0.68 and $\hat{\sigma}_G^2$: 0.59) and yield of grains per plant ($\hat{\sigma}_F^2$: 9.54, $\hat{\sigma}_E^2$: 4.05 and $\hat{\sigma}_G^2$: 5.49). Castro (2008) found higher environmental variance than the present study for the number of pods per plant (2150.84) and grain production (252.62). Lower estimation was observed for the number of seeds per pod (0.0155).

Heritability is an important genetic parameter for the breeding, because it reflects the proportion of phenotypic variation attributed to genetic variation, which reflects the reliability of the phenotypic value as an indicator of genetic value and interferes on the selection profit (Falconer and Mackay, 1996). The values of heritability can range from zero to one, and estimations above 0.70 are considered in vegetal species (Cruz et al., 2012). It is important to highlight that the heritability is not just the property of one character, it is also of the population under the environmental circumstances to which it has been exposed (Baldissera et al., 2014).
On this study, the heritability went from zero to IHP to 96.04% from NDF (Table 2). The characters NDM, NPP, and YIELD have had heritability values of 85.39%, 60.20%, and 62.43%, respectively, indicating the possibility of selection based on phenotype. Santos (2016) found broad-sense heritability values equals to 0.90 for the number of days to maturity, o.91 for the plant height, 0.46 for the intersection height of the first pod, 0.57 for the number of pods per plant and 0.57 for the yield of grains per plant. These estimations were superior to the observed on the present study, except for grain production.

Bizari et al. (2017), analyzing soybean segregate populations, checked that the characters of the number of days to maturity and yield of grains were between the characters with higher heritability, 91.7% and 71.31%, respectively. The authors also observed the lower estimations were for the characters of the number of pods (54.19%) and plant height at maturity (65.73%). Divergent results to the ones observed in this study were found by Kuswantoro et al. (2011) who, on an inheritance study for character NP with population coming from two soybean combinations, estimated broad-sense heritability equals 0.53 and 0.57. Moreover, estimations of heritability for the productivity and grain production compounds were determined by Castro (2008), who found heritability for the number of pods per plants, the number of seeds per pod and grain production of 0.33, 0.42 and 0.16, respectively.

Evaluating the generations F_2 and F_3 in soybean, coming from six bi-parental combinations, Costa et al. (2008) checked estimations of broad-sense heritability superior to characters of the number of pods and grain productivity, whereas, for the character of the number of days to maturity the estimations were inferior. Average degree of dominance expresses the relation between the genotypic value codified of the heterozygote and the genotypic value codified of the homozygote. If the average degree value is equal to one, it indicates the existence of complete dominance, if it equals to zero there is an absence of dominance and less than one, the occurrence of partial dominance (Cruz, 2005).

On the present study, the average degree of dominance had -4,04 to 1,16 amplitude for grain production and the intersection height of the first pod, respectively (Table 2). There is an effect of the absence of dominance for the characters NDB, NP, NGP and GP, partial dominance for NDM and NN, full dominance to the character PH, and over dominance for IHP. Assunção Filho (2016), evaluating the potential diallel cross of soybean for precocity, grain productivity, and tolerance to rust, obtained gm̂d equal to 0.725 for the number of days to maturity, 1.17 to plant height and 3.71 to grain productivity, showing the effects of partial dominance, complete dominance, and over dominance, respectively.

The estimation of gene number indicates the type of inheritance that controls a character, which can be monogenic, oligogenic or polygenic (Lobo et al., 2005). The qualitative characters are governed by one or few genes that constitute distinct phenotypic classes and little influenced by the environment. However, most characters of

agronomic importance present quantitative inheritance, and they are conditionate by the expression of several genes (Baldissera et al., 2014), as verified in this study.

The concern of the number of genes brings information about the size of the necessary population to recover certain genotype. The higher the number of involved genes, the bigger will be the number of possible genotypic combinations in one population and the bigger will be the number of necessary generations to achieve the complete homozygosis. It is difficult to obtain the number of genes when there is a great influence of the environment on character manifestation, and when there are many genes of small effects involved (Baldissera et al., 2014).

The number of days for flowering and the number of days to maturity was influenced by around two genes. The plant height and number of nodes were characters governed by 12 and 18 genes, respectively. For the number of pods and grain production, it was involved around six or seven grains. And the number of grains per pod presented the influence of 160 genes (Table 2).

Considering the existence of genetic variance for the agronomic characters on population F_2 and, also the occurrence of segregants transgressive (Table 3), it has become appropriate the selection of superior individuals.

Table 3. Maximum and minimum values for parentals and F_2, and the presence of transgressive segregants.

Parameters	Characters							
	NDF	NDM	PH	NN	IHP	NP	NGP	YIELD
Maximum at parents	45	123	130	25	54	48	2.75	17
Minimum at parents	35	99	64	10	10	07	1.71	03
Maximum at F_2	49	120	195	23	44	79	2.89	29
Minimum at F_2	32	99	64	10	10	05	1.80	01
Transgressive	Yes	No	Yes	No	No	Yes	Yes	Yes

Note: NDF: number of days for flowering; NDM: number of days to maturity; PH: plant height; NN: number of nodes; IHP: intersection height of the first pod; NP: number of pods; NGP: number of grains per pod; GP: grain production.

Transgressive segregants are inferior or superior individuals to parental. The occurrence of transgressive segregants happens when there is bigger segregation in recombination, obtained from crossings between adequate genitors for acquisition of hybrids with bigger heterotic effect (Hamawaki et al., 2012). On the present study, there are transgressive segregants to agronomic characters of economic importance, such as NDF, NP, NGP and YIELD (Table 3).

The characters numbers of days for flowering and to maturity are determined for the vegetative and total cycle, which is important for predictions about genotypes precocity, usually desired in soybean breeding programs. The use of precocious cycle cultivars allows using the system of culture succession, which enables the harvest in the ideal time and installation of corn on the second crop after the harvest of soybean, on the main cereal producers of the country (Meotti et al., 2012).

The genotypes of precocious cycle remain less time on the field, and they are subordinate to lower biotic and abiotic effects. They are exposed to a lower pressure of diseases on the end of soybean cycle, which provoke considerable reductions in culture yield (Finoto et al., 2011), and can escape from drought impacts (Gatut_Wahyu et al., 2014). Embracing 30% selection intensity, it has been selected 38 individuals to each one of the evaluated characters, as shown on Tables 4 and 5. The number of days for flowering varied from 32 to 35 and average of 33.87 days. As for the number of days to maturity, the selected individuals presented from 99 to 102 days, average of 100.92 (Table 4). It demonstrates that the selected individuals are more precocious than the genitors, and attend the interest of the current market.

The average of selected individuals for PH, NN, IHP, NP, NGP, YIELD was 121.66 cm, 17.82 nodes, 30.17 cm, 47.92 pods, 2.64 grains and 18.82 grams, respectively (Tables 4 and 5). All the selected individuals have superior characteristics to the genitors UFUS 6901 and MG/BR46 Conquista (Table 1) and are potential genotypes to the advance in soybean breeding programs and development of new cultivars with favorable characteristics.

Table 4. Selected individuals in soybean population F$_2$, coming from the cross UFUS 6901 X MG/BR46 Conquista, average of selected individuals ($\overline{X}$s) and selection gains (GS %) of agronomic characters.

Selected individuals	NDF	Selected individuals	NDM	Selected individuals	PH (cm)	Selected individuals	NN
1	32	1	101	1	113	11	16
2	33	2	101	7	110	27	16
3	32	3	101	11	109	31	19
4	33	4	101	20	110	33	16
5	33	5	101	31	110	43	17
6	33	6	102	43	127	44	16
7	33	7	101	44	120	45	18
8	32	8	102	45	110	46	21
9	33	9	102	51	109	51	17
10	32	10	102	60	110	61	17
11	32	11	102	61	110	62	20
12	33	12	102	62	136	64	17
13	32	13	102	67	110	67	18
14	35	14	102	68	123	68	19
15	35	15	102	70	113	70	19
16	35	16	102	72	116	72	20
17	35	17	102	85	115	75	16
18	35	19	101	88	111	85	16
19	35	41	101	89	111	89	16
20	35	42	99	92	115	94	17
21	35	43	99	93	111	95	17
22	35	45	101	94	128	97	16
27	35	48	100	96	113	102	20
28	35	49	100	97	112	103	18
41	32	50	100	102	145	104	16
42	32	52	100	103	114	106	20
43	35	71	101	106	132	108	16
49	35	81	101	112	137	111	18
50	35	83	101	113	195	112	23
53	35	84	100	114	135	113	22
57	35	86	100	115	111	114	19
58	35	87	100	118	119	118	19
60	35	90	101	120	118	120	16
61	35	93	101	123	113	123	17
65	35	94	101	124	124	124	16
66	35	95	100	125	110	125	16
81	33	96	100	126	145	126	18
82	32	97	100	127	173	127	19
$\overline{X}$s	33.87	$\overline{X}$s	100.92	$\overline{X}$s	121.66	$\overline{X}$s	17.82
GS%	-10.10	GS%	-4.00	GS%	10.62	GS%	4.02

Note: NDF and NDM: number of days for flowering and to maturity; PH: plant height and NN: number of nodes on the main stem.

Table 5. Selected individuals in soybean population F$_2$, coming from the cross UFUS 6901 X MG/BR46 Conquista, the average of selected individuals ($\overline{X}s$) and selection gains (GS %) of agronomic characters and grain production.

Selected individuals	IHP	Selected individuals	NP	Selected individuals	NGP	Selected individuals	YIELD
8	29	6	51	17	2.57	6	14
10	31	7	43	19	2.67	8	16
13	25	11	35	20	2.89	33	16
14	35	27	39	23	2.57	43	15
20	26	31	37	33	2.68	44	18
29	27	33	44	36	2.65	55	15
30	27	43	51	38	2.60	57	15
32	29	44	37	41	2.57	59	23
37	31	45	49	44	2.57	60	20
38	25	57	39	46	2.59	62	26
39	25	59	79	51	2.61	64	20
44	33	60	44	53	2.69	65	16
45	39	61	45	56	2.62	67	16
53	33	62	71	59	2.61	70	18
64	26	64	56	64	2.61	72	24
66	26	65	39	67	2.61	75	17
68	30.5	70	50	68	2.69	77	16
72	30	72	55	73	2.61	80	15
85	28	77	41	74	2.76	86	15
91	31	86	39	75	2.73	89	16
94	26	94	36	78	2.58	94	20
101	26	98	38	81	2.78	98	15
102	44	99	42	82	2.65	99	15
104	33	101	39	89	2.59	101	17
105	34	102	45	90	2.59	102	17
106	33	103	50	91	2.63	103	18
107	30	106	54	93	2.65	104	15
111	26	108	62	99	2.83	106	27
112	31	111	48	104	2.62	108	19
113	29	112	60	106	2.59	111	20
114	35	113	76	109	2.57	112	29
115	34	114	49	112	2.63	113	29
119	29	115	50	113	2.66	114	20
123	30	118	46	117	2.65	115	25
124	30	122	38	119	2.75	118	22
125	27	123	37	120	2.62	123	17
126	34	126	43	125	2.57	126	16
127	29	127	64	126	2.60	127	23
$\overline{X}s$	30.17	$\overline{X}s$	47.92	$\overline{X}s$	2.64	$\overline{X}s$	18.82
GS%	-5.79	GS%	31.99	GS%	0.22	GS%	29.54

Note: IHP: intersection height of the first pod; NP: number of pods per plant: NGP: number of grains per pod and YIELD: grain production.

Evaluating 79 progenies of soybean in generation F$_5$ on the municipality of Uberlândia - MG, Cunha et al. (2013) found a variation in the number of days for flowering from 42 to 87 days, and amplitude from 92 to 127 days for the character number of days to maturity, and oscillation of 34.10 cm to 68.80 cm for plant height. The selected genotypes on the present study are more precocious and with higher height.

Santos (2016) found the average for the number of days to maturity between 107 and 132 days, plant height between 87.10 and 53.91 cm, intersection height of the first pod changing from 7.11 to 11.08 cm, number of pods

from 52.34 to 98.75, and grain production from 9.17 to 21.69 g per plant. It was checked the highest height of the plants, besides of the compound values of similar productivity.

The possibility of prediction of the selection gain is one of the principal contributions of quantitative genetic for breeding. Based on these data, it is possible to efficiently guide the breeding program, predict success of the selection mode adopted and scientifically determinate which techniques can be more effective (Hamawaki et al., 2012). The biggest selection gains were found for the characters of the number of pods and grain production, with values from 39.10% and 30.27%, respectively. So these characters are important and selected to the soybean productivity. The smaller selection gain was obtained for the character of the number of grains per pod, with 0.22%, because of the proximity between the average of the selected individuals and the average of the original population (Table 1). For the characters NDF and NDM, it was selected the individuals with smaller values, because of that the selection gain is negative.

The most important facts that interfere, directly or indirectly, on selection gains are selection intensity, genetic properties of the population and environmental conditions. The gain is directly connected with the difference of the average of the selected group and the average of the original population. The more different the population, the bigger the chances of gain with the selection, once it is based on genetic differences. However, a high pressure involves a bigger risk of genetic variability reduction, which can compromise the gain in successive cycles (Hamawaki et al., 2012). Among the selected individuals, stand out the genotypes 43 and 94. The genotype 43 was selected for the characters number of days for flowering and to maturity, plant height, number of nodes, number of pods and grain production. And the genotype 94 was selected for the characters number to maturity, plant height, number of nodes, number of pods, intersection height of the first pod and grain production. These genotypes reunite characteristics related to precocity and to grain productivity (Tables 4 and 5).

In accordance with Lopes et al. (2002), there are difficulties in acquisition of productive and precocious genotypes. The genotypes 44, 106, 112, 113 and 126 were selected in all of the characters, except for the number of days for flowering and number of days to maturity. It indicates that they are productive material, but they are not among the most precocious. In conclusion, the character number of days to maturity was high heritability and influenced by two genes, with partial dominance between them. The number of pods per plant and grain production presented high heritability, polygenic inheritance with around seven genes involved in the character and absence of dominance. The population F_2 have transgressive segregates for involved characters on precocity, compound of productivity and grains production. The hybridization between MG/BR 46 Conquista and UFUS 6901 allows the acquisition of selection gains of superior individuals in terms of precocity, height, number of nodes and compound of productivity, making them promising genotypes in breeding programs.

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