Selection strategies in agronomic characters in progenies $F_{3:4}$ of transgenic soy RR

Estratégias de seleção em caracteres agronômicos em progênies $F_{3:4}$ de soja transgênica RR

Anna Regina Tiago Carneiro[1]*, Osvaldo Toshiyuki Hamawaki[1], Ana Paula Oliveira Nogueira[1], Arthur Felipe Eustáquio e Silva[1], Raphael Lemes Hamawaki[2], Cristiane Divina Lemes Hamawaki[1]

[1]Universidade Federal de Uberlândia/UFU, Uberlândia, MG, Brasil
[2]Cargill Agrícola, São Paulo, SP, Brasil
*Corresponding author: anna-regina@hotmail.com

ABSTRACT

The selection indexes aggregate information to multiple characters and, with this, they are able to carry out the selection of a set of variables simultaneously. The objective was to verify the genetic potential of agronomic traits and to select soybean $F_{3:4}$ progenies based on different selection strategies. 123 progenies and the parents were sown in randomized blocks with two replications. The gains of direct selection by the indexes, the sum of "ranks" and the genotype-ideotype were lower for all characters when compared to the gains of direct and indirect selection. The rank sum index stood out for achieving the highest total gain with 37.11%. The index of the genotype-ideotype obtained a lower gain (-0.48%) for the character number of days for flowering compared to the sum index of "ranks" (-0.54%) and reached a negative gain for the attribute insertion height of the first pod with -1.82%. The genetic potential of the $F_{3:4}$ population is high and allows different selection strategies to be applied to reach superior genotypes. The progenies UFU 72, UFU 116, UFU 86, UFU 45, UFU 117, UFU 56, UFU 5, UFU 106, UFU 6, UFU 4, UFU 73, UFU 101, UFU 96, UFU 90, UFU 123, UFU 116, UFU 88, UFU 65, UFU 70, UFU 3, UFU 69 and UFU 37 were selected by both selection indexes. The UFU 72, UFU 90, UFU 88 and UFU 69 progenies are agronomically superior both in direct and indirect selection, as in Mulamba and Mock (1978) sum of "ranks" selections and genotype-ideotype.

Index terms: *Glycine max*; selection index; genetic gain.

RESUMO

Os índices de seleção agregam informações de múltiplos caracteres e, com isto, conseguem realizar a seleção simultaneamente de um conjunto de variáveis. Objetivou-se verificar o potencial genético de caracteres agronômicos e selecionar progênies $F_{3:4}$ de soja com base em diferentes estratégias de seleção. Foram semeadas 123 progênies e os genitores, em blocos casualizados com duas repetições. Os ganhos de seleção direta pelos índices, soma de "*ranks*" e do genótipo-ideótipo, foram inferiores para todos os caracteres quando, comparados aos ganhos da seleção direta e indireta. O índice de soma de *ranks* se destacou por alcançar o maior ganho total com 37,11%. O índice do genótipo-ideótipo obteve menor ganho (-0,48%) para o caráter número de dias para o florescimento comparado ao índice de soma de "*ranks*" (-0,54%) e, alcançou ganho negativo para o atributo altura de inserção da primeira vagem com -1,82%. O potencial genético da população $F_{3:4}$ é elevado e permite aplicar distintas estratégias de seleção no alcance de genótipos superiores. As progênies UFU 72, UFU 116, UFU 86, UFU 45, UFU 117, UFU 56, UFU 5, UFU 106, UFU 6, UFU 4, UFU 73, UFU 101, UFU 96, UFU 90, UFU 123, UFU 116, UFU 88, UFU 65, UFU 70, UFU 3, UFU 69 e UFU 37 foram selecionadas por ambos índices de seleção. As progênies UFU 72, UFU 90, UFU 88 e UFU 69 são agronomicamente superiores tanto na seleção direta e indireta, quanto nos índices de seleção de soma de "*ranks*" de Mulamba and Mock (1978) e do genótipo-ideótipo.

Termos para indexação: *Glycine max*; índice de seleção; ganho genético.

INTRODUCTION

Soy (*Glycine max* (L.) Merrill) is one of the most consumed grains in the world and its demand continues to expand. In 2019/20 the world consumption of this legume was 353.9 million tons and the estimate for 2020/21 is to consume 368.9 million tons. Brazil is the third largest consumer estimated to consume 49.4 million tons of soy in 2020/21 (United States Department of Agriculture - USDA, 2021). In order to meet all this demand, it is essential that breeding programs constantly develop superior genotypes, therefore, successful selection is necessary.

In plant breeding, success lies in the existence of genetic variability that makes it possible to select superior genotypes. The selected individuals must simultaneously combine a series of favorable attributes such as agronomic

superiority, high grain yield, wide adaptability, and stability (Vianna et al., 2019). One of the strategies that provide this type of selection is the use of selection indexes.

The selection indexes aggregate the information related to multiple characters of agronomic importance with the genetic properties of the evaluated population, and with this, they are able to carry out the selection of a set of variables simultaneously, regardless of the existence or not of correlation between them (Cruz; Regazzi; Carneiro, 2012). By achieving this, the selection indexes identify quickly and efficiently the progenies that may be more adequate to the breeder's purposes, increasing the chance of success of the genetic improvement program (Leite et al., 2016; Bizari et al., 2017; Teixeira et al., 2017; Leite et al., 2018).

In soybeans, several authors have already demonstrated the potential of this selection strategy. Teixeira et al. (2017) used selection indexes to carry out the selection of soybean genotypes in the city of Uberlândia - MG. The authors used the indexes of Smith (1936) and Hazel (1943); Sum of ranks of Mulamba and Mock (1978); Willians (1962) and the genotype-ideotype distance in ten soybean characters and obtained total selection gains of 42.44%; 49.56%; 47.81% and 59.38% for each index, respectively.

Bizari et al. (2017) compared different selection strategies such as direct and indirect selection; classical index of Smith (1936) and Hazel (1943); index based on sum of Mulamba and Mock (1978); Willians index (1962); index based on Pesek's and Baker (1969) and the genotype-ideotype distance index (Cruz, 2013) in seven segregating soybean populations in F_5 generation. The authors concluded that the Smith and Hazel and Willians indexes showed the smallest variations in terms of gains and that the sum of ranks index provided the most favorable gains.

Thus, due to the high demand and the relevance of this culture, it is essential to distinguish the best strategy for selecting genotypes with high yields and with the greatest genetic gains. Based on the above, the objectives of this work were to verify the genetic potential of agronomic traits and to select soybean $F_{3:4}$ progenies based on different selection strategies.

MATERIAL AND METHODS

The experiment was conducted in the field at the experimental farm Capim Branco, belonging to the Federal University of Uberlândia - UFU, located in the municipality of Uberlândia - MG, located at latitude 18°53'19''S, longitude 48°20'57''W, with altitude of 835 mm (Instituto Brasileiro de Geografia e Estatística - IBGE, 2020).

123 $F_{3:4}$ progenies originated from artificial hybridization between BRS256RR (♀) x TMG1179RR (♂) plus the two parents were evaluated, in randomized blocks (RBD) with two replications. Each plot consisted of a 1.5 m long line represented by an $F_{3:4}$ progeny of the study population or by the parent, with an interline spacing of 0.5 m and an average density of 10 plants every 0.5 m.

The sowing took place on September 15, 2019 in a field on a Dystrophic Dark Red Latosol soil. The soil was previously prepared in a conventional manner, with deep plowing and two harrows. Fertilization was carried out directly in the sowing furrows, using 400 kg ha^{-1} of the formula NPK 4–20–20.

The seeds were previously treated with fungicide with the active ingredient Fludioxonil in the dosage of 200 mL 100 kg^{-1} of seed. The inoculation was carried out in the sowing furrow with a 20L backpack sprayer with liquid inoculant containing CEPAS 5079 and 5080 of the bacterium *Bradyrhizobium japonicum* with a dose of 300 mL ha^{-1}.

The sowing was manual and for the distribution of genetic material in the field, the scheme of plots of progenies with plots of the interleaved parents was used. For each 15 plots of $F_{3:4}$ progenies, one plot of the parent was placed, totaling five plots of each parent per block.

Two phenotypically superior plants, which entered the R1 reproductive phenological stage (Fehr; Caviness, 1977), were sampled and identified with colored satin ribbon (Fehr; Caviness, 1977) for evaluations of the following agronomic traits:
- Number of days to flowering (NDF): period of days between the VE (emergence) stage in which the cotyledons are above the surface of the soil until the appearance of the first flower on the main stem (reproductive phenological stage R1);
- Number of days to maturity (NDM): period of days between the VE stage (emergency) until maturity when 95% of soybean pods reach the color of a mature pod (reproductive phenological stage R8);
- Plant Height at Flowering (PHF): height measured in centimeters (cm), with the aid of a ruler, from the soil surface on the main stem to the end of the main stem (apical meristem) when the plants reach flowering (R1);
- Plant Height at Maturity (PHM): height measured in centimeters (cm), with the aid of a ruler from the soil surface on the main stem to the end of the apical meristem, at maturity (R8);
- Height of insertion of the first pod (HIP): height measured in centimeters (cm), with the aid of a ruler, from the ground until the insertion of the first pod in the main stem;

- Number of Nodes at Maturity (NNM): obtained by counting all nodes on the main stem from the cotyledon node at maturity (R8);
- Number of Productive Nodes (NPN): obtained by counting all the nodes or branches on the main stem that had the presence of pods (R8);
- Number of Branched Nodes (NBN): obtained by counting all the nodes that had branches of the main stem (R8);
- Number of pods (TNP): after harvest, all pods produced by the plant were counted;
- Grain production per plant (GP): mass of grains in grams (g), produced by the two plants in the useful parcel;
- Grain production per line (GPL): mass of grains in grams (g), produced by all plants in the plot.

To define the vegetative and reproductive phenological stages of the plants, the Fehr and Caviness (1977) scale was used.

The data for each of the evaluated agronomic characters were subjected to analysis of variance (ANOVA), considering the effects of random genotypes, according to the statistical model below: $Y_{ij} = \mu + G_i + B_j + \varepsilon_{ij}$, where Y_{ij} is value of each character in a plot comprising the i-th genotype in the j-th block; μ is general mean of the character; G_i is effect of the genotype considered random i; B_j is effect of the block considered random j and ε_{ij} is effect of the error considered random.

The genotype means were submitted to the Scott-Knott cluster test at the level of 1% and 5% probability. The genotypic variation coefficient parameter (CV_g) was estimated $CV_g = \dfrac{\hat{\sigma}_g}{m} x100$ where: CV_g is coefficient of genetic variation; $\hat{\sigma}_g$ is estimate of the genotypic standard deviation and m is observed mean of the character.

In addition, the heritability parameter was estimated in the broad sense based on the following equation: $H^2 = \dfrac{\sigma_g^2}{QMT/r}$ and $\sigma_g^2 = \dfrac{QMT - QMR}{r}$ where: H^2 is heritability; σ_g^2 is genetic variance; QMT is mean square of the treatment in ANOVA; QMR is average square of the residue in ANOVA and r is number of repetitions.

The selection gains estimates were obtained by different selection strategies: 1) Direct and indirect selection (Cruz, 2006); 2) Mulamba and Mock (1978) ranks sum index and 3) genotype-ideotype distance index (Cruz, 2006). The selection criterion used was to reduce the NDF characters and increase the PHF, HIP, NPN, NBN, TNP, GP and GPL characters.

The expected gain from direct selection (Cruz, 2006) on the i-th character (GS_i) was estimated based on the selection differential, using the formula: $GS_j = (X_{si} - X_{oi})h_i^2 = DS_j h_i^2$ where X_{si} is average of the progenies selected for character i; X_{oi} is original average of the population; DS_i is selection differential practiced in the population and h_i^2 is heritability of character i.

The indirect gain of character j, by selection in character i, was given by: $GS_{j(i)} = DS_{j(i)} \, x \, h_i^2$ where $GS_{i(j)}$ is indirect selection differential obtained as a function of the average character of those individuals whose superiority was verified based on another character, on which direct selection is practiced.

For the Mulamba and Mock (1978) ranks sum index, the orders of each progeny were added, resulting in the selection index, as described below: $I_i = r_{i1} + r_{i2} + \ldots + r_{in}$ where I_i is index value for the progeny; r_{ij} is classification (or "rank") of progeny i in relation to the j-th character and n is number of characters considered in the index.

Weights were given by: $I_i = p_{i1}r_1 + p_{i2}r_2 + \ldots + p_{in}r_n$ where Op_j is economic weight attributed to the j-th character.

In the genotype-ideotype distance index (GID) (Cruz, 2006), the average, maximum and minimum values for each variable were calculated. X_{ij} was considered as the average phenotypic value of the i-th genotype in relation to the j-th characteristic. We also considered the value Y^{ij}, which represents the mean transformed phenotypic value, and C_j, a constant relative to the depreciation of the mean of the genotype. Thus, we had: LI_j as the lower limit to be presented by the genotype, relative to the characteristic j; LI_j as the upper limit to be presented by the genotype and; VO_j as the optimal value to be presented by the genotype, under selection. If $LI_j \leq X_{ij} \leq LS_j$, then $Y_{ij} = X_{ij}$ and if $X_{ij} < LI_j$, $Y_{ij} = X_{ij} + VO_j - LI_j - C_j$ and if $X_{ij} > LI_j$, $Y_{ij} = X_{ij} + VO_j - LI_j - C_j$.

In the procedure, $C_j = LS_j - LI_j$ was considered. The C_j value ensured that any value of X_{ij} within the range around the optimum would result in a value of Y_{ij} with a magnitude close to the optimal value (VO_j), as opposed to the values X_{ij} of outside that range. Thus, the X_{ij} transformation was performed to guarantee the depreciation of phenotypic values outside the range. The Y_{ij} values obtained by transformation were later standardized and weighted by the weights assigned to each characteristic, obtaining the y_{ij} values, as specified below: $y_{ij} = \sqrt{a_j} \dfrac{Y_{ij}}{S(Y_j)}$ where $S(Y_j)$ is standard deviation of the mean phenotypic values obtained by the transformation and a_j is weight or economic value of the characteristic.

For the calculation, standardization and weighting of the following were also required VO_j, as specified: $VO_{ij} = \sqrt{a_j}\, \dfrac{VO_j}{S(Y_j)}$. Then, the values of the genotype-ideotype distance index (GID) were calculated, expressed by the distances between the genotypes and the ideotype, as shown below: $I_{DGI} = \sqrt{\dfrac{1}{n} \sum_{j=1}^{n} (Y_{ij} - VO_j)^2}$. From these indices, the best progenies are identified and the selection gains are calculated.

In direct and indirect selection, a decrease was considered for the number of days for flowering and an increase for the other characters. For the GID index, the optimal values, lower and upper limits were defined as ideal for soybean cultivation.

For all methodologies, the negative selection sense was used as favorable for NDF, in order to select progenies with less vegetative cycle. For PHF, HIP, NBN, NNR, NVT, PGP and GPL the positive selection direction was adopted, for selection of progenies with the highest values for these characters.

All statistical-genetic analyzes were performed using the Computational Program in Genetics and Statistics - GENES (Cruz, 2006).

RESULTS AND DISCUSSION

A significant effect was found by the F test, at the level of 1% and 5% probability, among the $F_{3:4}$ progenies for most of the analyzed agronomic traits. This indicates the existence of genetic variance, an essential factor for the successful selection of superior genotypes. For the characters number of days to maturity (NDM), plant height at maturity (PHM) and number of nodes at maturity (NNM), there was no statistical difference between the progenies (Table 1).

Heritability (h^2) is one of the most significant parameters in genetic improvement, being used by breeders for successful selection. This is because this parameter participates in the expression of the gain with the selection and, with this, it allows to evaluate the selection possibilities before they are carried out (Ramalho; Bruzi; Teixeira, 2017).

The heritability coefficient varies from 0 to 100%, being considered ideal when higher than 70% (Cruz; Regazzi; Carneiro, 2012; Ramalho et al., 2012). When the coefficient is equal to 100, the phenotype is completely determined by the genotype, with the environment having no influence on the character's manifestation. A coefficient equal to zero suggests that the variability of the character has no genetic origin (Silveira et al., 2006).

Table 1: Medium squares, genetic parameters, coefficient of variation and mean for 11 agronomic traits in soybean $F_{3:4}$ progenies, in Uberlândia - MG.

Characters	GMS	(%)	CVg (%)	CVe (%)	Average
NDF	7.973**	40.26	2.91	5.02	43.4
NDM	25.02 ns	23.07	1.29	3.34	131.3
PHF	79.31**	37.01	9.15	16.88	41.8
PHM	107.82 ns	13.50	4.43	15.88	60.7
HIP	22.37 *	30.48	18.05	38.55	10.2
NNM	1.80 ns	5.16	1.71	10.36	12.6
NPN	2.91 *	27.31	6.46	14.9	9.7
NBN	1.92 **	41.72	20.06	33.54	3.1
TNP	155.21 **	60.64	17.88	20.37	38.6
GP	14.84 *	26.36	8.33	19.7	16.7
GPL	6386.03*	30.68	12.69	26.97	246.6

NDF and NDM: number of days for flowering and maturity, respectively; PHF and PHM: plant height at flowering and maturity (cm), respectively; HIP: insertion height of the first pod (cm); NNM, NPN and NBN: number of mature, productive and branched nodes, respectively; TNP: total number of pods; GP: grain production per plant (g); GPL (g): grain production per row. GMS: genotype mean square; h_a^2 (%): heritability in the broad sense; CV(g) (%):genetic variation coefficient and CVe (%):general coefficient of variation.** and *: significant at the level of 1% and 5% probability for the F test, respectively; ns: not significant for the F test.

For this study, in general, heritabilities in the broad sense ranged from 5.16% for the number of nodes in maturity (NNM) to 60.64% for the number of total pods (TNP) (Table 1). Low amplitude heritability is common in polygenic inheritance characters, due to a large number of loci that control it, also leading to a great influence of the environment (Costa et al., 2008; Bárbaro et al., 2009; Hamawaki et al., 2012).

Silva et al. (2018), when analyzing soybean F_5 progenies, achieved heritabilities in the broad sense above those obtained in this research, with 44% for PHM; 80% for HIP; 60% for NBN and 88% for TNP.

When researching 202 soybean genotypes in the F_6 generation, in the 2013/2014 harvest, in Jaboticabal – SP, Andrade et al. (2016) obtained heritabilities below those obtained in this study for the characters: NDF (27%); HIP (29.5%) and TNP (45.69%) and above for the characters: NDM (75%); PHF (26.54%); PHM (38.47%); NNM (34.73%); NBN (46%) and GP (36%).

When estimating heritabilities in two F_4 populations of soybean, Hakim and Suyamto (2012) found for the population 1 values of 30.3% (NDF); 39.8% (NDM); 53.7% (PHM); 33.5% (NNM); 20.6% (NPN); 55.4% (TNP) and 18.3% (GP). For population 2, heritabilities were 36.1% (NDF); 42.6% (NDM); 58.2% (PHM); 26.7% (NNM); 18.3% (NPN); 47.6% (TNP) and 21.1% (GP).

The CVg genetic variation coefficient (%) is an indicator of the genetic potential of the study population, that is, of the genetic variability. The lowest CVg (%) was obtained by the NDM character with 1.29% and the highest for the number of branched nodes (NBN) with 20.06% (Table 1).

The coefficient of variation shows the degree of experimental precision. According to Pimentel-Gomes (2009) they are considered low when CVe values are below 10%, average when they are between 10 to 20% and high when they are above 30%. For most characteristics, this coefficient was less than 20% (3.34% - NDM; 5.02% - NDF; 10.36% - NNM; 14.9% - NPN; 15.88% - PHM; 16.88% - PHF and 19.7% - GP), which indicates good environmental accuracy. However, for the TNP (20.37%); GPL (26.97%); NBN (33.54%) and HIP (38.55%) characters, this parameter was greater than 20% (Table 1). These CVe values (%) are in accordance with that presented in the literature for these characters in agricultural experiments in soybean culture (Bizari et al., 2017; Silva et al., 2018; Bianchi et al., 2020; Luiz et al., 2020; Mattos et al., 2020).

Table 2 shows the maximum and minimum averages and the Scott-Knott average cluster test for each character.

For the NDF, the average of the progenies were below 50 days, with the lowest vegetative phase of 38 days and the largest of 48 days. Still, for this character the formation of two groups was observed. For group "a", the earliest progeny had an average duration of the vegetative period of 43.5 days and the latest of 48.0 days. For group "b", the amplitude for days for flowering was 38.0 to 43.0 days. The parents, BRS256RR and TMG1179RR, obtained averages of 44.5 and 43.0 days and were in group "a" and "b", respectively (Table 2).

Table 2: Minimum and maximum averages of eight agronomic characters of $F_{3:4}$ progenies of soybean and parents in the city of Uberlândia – MG.

| Characters | Progenies $F_{3:4}$ | | | | Parents | |
| | Group "a" | | Group "b" | | | |
	Minimum	Maximum	Minimum	Maximum	BRS256$_{RR}$	TMG1179$_{RR}$
NDF	43.5	48.0	38.0	43.0	44.5 a	43.0 b
PHF	40.5	62.0	26.5	40.0	41.0 a	38.5 b
HIP	11.5	22.0	5.5	11.0	11.5 a	11.0 b
NPN	10.0	12.0	6.0	9.5	9.5 b	10.5 a
NBN	3.5	6.0	0.0	3.0	3.0 b	3.0 b
TNP	39.5	62.5	21.0	39.0	37.0 b	35.5 b
GP	17.5	25.0	11.0	17.0	16.5 b	15.5 b
GPL	110.0	419.5	-	-	196.0	249.0

NDF: number of days for flowering; PHF: plant height at flowering (cm); HIP: insertion height of the first pod (cm); NPN and NBN: number of productive and branched nodes, respectively; TNP: total number of pods; GP: grain production per plant (g); GPL (g): grain production per row (g). Group "a" and "b" refers to the means that presented the same letter by the Scott-Knott test at 10% significance.

Sousa et al. (2020), when evaluating the genetic diversity of 35 soybean genotypes with the aid of microsatellites, also obtained the formation of two groups and an average of 47.29 days for the character number of days for flowering. In contrast, Oliveira et al. (2017), in a study of agronomic characters with 24 soybean genotypes in the 2011/2012 agricultural year in Uberlândia-MG, formed four distinct groups and found an average above that obtained at this research, with 65.62 days for flowering.

The induction of flowering in soybean is a characteristic determined by the photoperiod and genetically controlled (Gazzoni et al., 2018). The critical photoperiod is specific for each cultivar and thus, each cultivar has its adaptation in a specific range of latitude (Sediyama et al., 2016).

Soybeans with this adaptation (PJL), do not flower during the juvenile period, even under conditions of inductive photoperiod (Silva et al., 2017). Thus, it is possible for the plant to grow and develop, produce biomass in an adequate volume and express high yields (Gazzoni et al., 2018). This was observed in this study, plants that obtained the highest NDF also presented the highest values for the characters NPN, TNP, GP and GPL (Table 2).

Still, although the analyzed parents (BRS256RR and TMG1179RR) are not recommended for Uberlândia, which has a low latitude (18°), the values are in accordance with those found in the literature for this region (Sousa et al., 2020), due to the cultivars have LJP.

As for the plant height at flowering (PHF) two groups were formed. Group "a" presented plants with a height of 40.5 cm to 62.0 cm, and the parent BRS256RR fit this group with 41.0 cm in height. The second, group "b", obtained values from 26.5 cm to 40.0 cm, in which the parent TMG1179RR was inserted at a height of 38.5 cm (Table 2).

According to Sediyama, Silva and Borém (2015) in soybeans the insertion height of the first pod (HIP) must be between 10 and 15 cm, so that it avoids damage and loss of grains and allows a maximized and efficient mechanized harvest. The progeny averages were below (5.5 cm) and above (22.0 cm) in height, considered ideal for soybean culture, and constituted two groups. In the first group, the minimum value was 11.5 cm and the maximum 22.0 cm. For the second group, the lowest average was 5.5 cm and the highest was 11.0 cm. As for the parents, both were within the recommended for soybeans, with BRS256RR with HIP of 11.5 cm belonging to group "a" and TMG1179RR to group "b", with 11.0 cm of HIP (Table 2).

Silva et al. (2018), in research with agronomic characters in F_5 progenies, observed averages between 12.0 to 13.0 cm for the height of insertion of the first pod, being within the values obtained in this study. Ribeiro et al. (2016) obtained a range of variability in the approximate means to those obtained in this study. These authors evaluated the agronomic attributes of commercial soybean cultivars in the central region of the state of Tocantins and found averages from 12.30 cm to 18.58 cm for HIP, grouped into four distinct groups.

A soybean plant with high productive capacity should have an average of 17 to 18 knots on the main stem (Sediyama, 2016). Both parents and progenies obtained an average number of productive nodes (NPN) below that indicated as favorable for a genotype with high productivity. Formation of two groups was observed, in which group "a" had a range of averages from 10.0 to 12.0 productive nodes and group "b" from 6.0 to 9.5 nodes. The parent BRS256RR was in the second group with 9.5 nodes and the parent TMG1179RR in the first group with 10.5 productive nodes (Table 2). Meier et al. (2019) obtained an average within the values achieved in this study. When studying the agronomic performance and linear correlation between components of soybean yield in two cultivation sites in the State of Rio Grande do Sul, these researchers found an average of 9.38 productive nodes.

The number of branched nodes (NBN) is indicative of higher pod production in soybeans. According to Ludwig et al. (2010) the greater the number of branched nodes, the greater the conditions for greater formation of flowers and, consequently, pods, since the reproductive structures in the plant are formed in the armpits of the nodes. As for this character, two groups were formed. Group "a" showed an average of 3.5 to 6.0 knots and group "b" from 0.0 to 3.0 branched knots. Both parents obtained an average of 3.0 knots, belonging to the second group (Table 2).

Leite et al. (2018) reached an average within those obtained in this work. In research to select F_5 soybean progenies carrying the RR gene with good agronomic traits through multivariate analysis and selection index, these authors reached an average of 3.18 branched nodes, an average within those found in this research.

The number of total pods per plant (TNP) is an important character, since it is one of the components of the grain yield in soybeans, which contributes the most to the achievement of higher yields. According to Matsuo, Ferreira and Sediyama (2015) national cultivars have a maximum of 80 pods per plant. No progeny or parents reached the average of Brazilian cultivars. Group "a"

obtained an average of 39.5 to 62.5 pods per plant and group "b" from 21.0 to 39.0 pods per plant. The parents BRS256RR and TMG1179RR were in the second group with averages of 37.0 and 35.0 pods, respectively (Table 2).

Zuffo et al. (2018), with the objective of evaluating the influence of some agronomic traits of soybean cultivars, in function of different plant densities, and the contribution of these characteristics in the grain yield, reached an average of 50.1 pods, being within the averages obtained in this study. Bizari et al. (2017), in a research with 386 F_5 progenies in the 2012/2013 agricultural year in Jaboticabal-SP, observed a TNP average above this research, with 95.70 total pods per plant.

The reduced values found for the number of productive and branched nodes, respectively, and the total number of pods, probably happened because the parents used are not recommended for Minas Gerais and, consequently, are in different conditions of climate and photoperiod. It is known that the agronomic performance of a cultivar occurs according to its genetic potential, as well as the environment in which they are grown (Barbosa et al., 2013).

Sowing in September, that is, outside the recommended season for soybeans, may also have exposed it to different combinations of photoperiod and temperature, reflecting the reduction of these characters (NPN, NBN and TNP). According to Câmara (2015) sowing a soybean genotype early or late may contribute to phenotypic changes in the plant. Studies by Zanon et al. (2016) demonstrated that the lowest number of nodes in the phenological stage R8 of soybeans occurred due to sowing in September (before the preferred season), due to the fact that the plants were exposed to a short photoperiod in late September and early October.

According to Sediyama et al. (2016) in general, soybean cultivars used for oil and bran production have an average weight between 12 to 20g per 100 seeds. Grain production per plant (GP) obtained a range of variability from 11.0g to 25.0g. The progenies were separated into two groups, in which the first reached averages from 17.5 to 25.0g and the second from 11.0g to 17.0g. As for the parents, both remained in group "b" with 16.5 grams for the BRS256RR and 15.5 grams for the TMG1179RR (Table 2).

Regarding grain production per row (GPL), despite the significant effect of the progenies, there was no distinction between groups. Progeny averages ranged from 110.0 to 419.5 grams. While the parents have an average of 196.0g for the BRS256RR and 249.0g for the TMG1179RR (Table 2).

According to Cruz et al. (2017) quantitative genetics makes numerous practical contributions to plant genetic improvement, among them, the possibility of evaluating the gains to be obtained by different selection strategies.

Knowing the selection gains is of great importance since they allow to better orient the breeders, to predict the success of the adopted selection scheme, to select or discard populations and to concentrate efforts on the evaluation of characters of greater importance and earning potential (Cruz; Regazzi; Carneiro, 2012; Cruz et al., 2017).

Direct selection is based on obtaining maximum gains in a single character in which the selection is practiced and, depending on the relationship of that character with others, positive or negative responses may occur in the characters of secondary importance, which were not analyzed in the process selection criteria (Cruz, 2013).

Table 3 presents the estimates of gains from direct and indirect selection for eight agronomic characters.

The selection criterion used was a decrease for the NDF and an increase for the other characters (PHF, HIP, NPN, NBN, TNP, GP and GPL). The direct selection caused the biggest individual gains in relation to the indirect selection for the characters: NDF (-2.32%); HIP (12.93%); NPN (4.38%); NBN (16.81%) and TNP (18.06%).

In a study to estimate selection gains through direct and indirect selection, several authors also found the greatest individual gains for direct selection when compared to indirect selection (Bárbaro et al., 2009; Akram et al., 2016; Bizari et al., 2017; Teixeira et al. 2017).

The greatest gains in direct selection were obtained for the TNP attribute with 18.06%, followed by NBN with 16.81% and HIP with 12.93%. Meanwhile, the lowest direct gains were achieved for NDF with -2.32% and NPN with 4.48% (Table 3). Bárbaro et al. (2009) estimated the gain of direct and indirect selection in five soybean populations in the F_5 generations in the 2003/2004 agricultural season and in the F_6 generation in the 2004/2005 harvest. For the F_5 generation, the greatest direct gains were for the number of nodes at maturity and height of insertion of the first pod, and for the F_6 generation, the greatest gain was for the number of nodes at maturity.

Zuffo et al. (2017), when estimating the gains of direct selection in soybean genotypes in the municipality of Lavras - MG, obtained results that differ from those achieved in this research. The authors achieved direct gains of: - 0.118%; - 0.005% and 0.107% for PHF, HIP and TNP, respectively.

Table 3: Selection gain estimates (GS%) obtained for eight characters analyzed, by direct and indirect selection, for 123 $F_{3:4}$ progenies, in the city of Uberlândia – MG.

Characters	NDF	PHF	HIP	NPN	NBN	TNP	GP	GPL
NDF	-2.32	0.91	0.9	0.2	-0.5	-0.86	-0.49	0.74
PHF	-2.1	7.22	2.55	0.59	-2.47	-0.82	-0.12	7.42
HIP	-0.88	5.54	12.93	-7.27	-1.33	-5.46	-1.05	2.56
NPN	-0.38	0.49	-2.75	4.38	4.26	3.03	-0.3	1.15
NBN	-0.74	-5.09	-1.26	10.7	16.81	16.53	11.87	5.21
TNP	1.74	-1.25	-3.89	5.63	12.22	18.06	13.68	2.36
GP	-0.02	-0.13	-0.52	-0.39	6.2	9.67	5.55	1.35
GPL	-2.65	11.29	1.79	2.12	3.84	2.36	1.91	9.12

NDF: number of days for flowering; PHF: plant height at flowering (cm); HIP: insertion height of the first pod (cm); NPN and NBN: number of productive and branched nodes, respectively; TNP: total number of pods; GP: grain production per plant (g); GPL (g): grain production per row (g). Values in bold diagonal refer to the gain of direct selection, the other values to the gains of indirect selection.

Likewise, different results of this research were achieved by Akram et al. (2016) that, when analyzing the genetic variability of 11 soybean genotypes, found direct selection gains of -0.995% for the number of days for flowering, 0.0728 for the number of branched nodes, 1.973% for the total number of pods and 2.848% for grain production per plant.

It was observed that the direct selection for the PHF promoted the greatest indirect gain for GPL with 11.29% (Table 3). And the direct selection for the number of total pods allowed the greatest indirect gain for the production of grains per plant with 9.67%, in addition to a gain of 16.53% for the number of branched nodes (Table 3).

Direct selection of plants based on the number of days of flowering is not feasible, since it caused a direct positive gain only for the TNP character (1.74%). For the other characters, indirect gains were negative with -2.1% (PHF); -0.88 (HIP); -0.38 (NPN); (-0.88); -0.74 (NBN); -0.02 (GP) and -2.65 (GPL) (Table 3).

The indirect selection of TNP resulted in direct gain of 13.68% for GP, 12.22% for NBN and 2.36% for GPL. Still, the indirect selection of the GPL attribute is interesting, since it allowed a negative direct selection gain for NDF (-2.65) and positive direct gains for the other characters with 11.29% for PHF; 1.79% for HIP; 2.12% for NPN; 3.84% for NBN; 2.36% for TNP and 1.91% for GP (Table 3).

Table 4 shows the averages of the top 30 soybean $F_{3:4}$ progenies selected by direct selection for the characters number of days to flowering, number of productive nodes, number of total pods, grain production per plant and grain production per row.

When analyzing Table 4, it was noted that all progenies for all characters were superior to parental ones, BRS256RR and TMG1179RR, which is interesting for reaching higher progenies. The UFU 72 progeny stood out compared to the others for gathering the largest amount of positive characters, namely: NDF, NPN, TNP and GP. Other progenies also stood out for grouping favorable characters, which are the progenies: UFU 1, UFU 7, UFU 63 and UFU 102 (NDF, TNP and GP); UFU 69 (NDF, NPN and TNP); UFU 71 (NNP, GP and GPL); UFU 88 (TNP, GP and GPL) and UFU 90 (NDF, TNP and GL).

In breeding programs, selection based on one or a few characters has been shown to be inefficient. This is because it leads to the formation of a superior genotype in relation to the selected characters, but with less favorable performance in relation to the other characters not considered in the selection (Ramalho et al., 2012), making it difficult to select superior genotypes.

According to Nogueira et al. (2012) genetic improvement aims to improve a main character, and to maintain or improve the expression of other characters simultaneously. An option to carry out the selection of a set of characteristics of interest, in a synchronized way, and, with gains in the direction favorable to all of them, is the use of selection indexes.

In the selection indexes, the selection process takes place based on the index values (numerical value), which works as an additional character (super character), theoretical, resulting from the linear combination of all the characters of interest for each unit to be selected, regardless of existence or not of correlation between them (Cruz; Regazzi; Carneiro, 2012). By achieving this, the selection indexes quickly and efficiently identify the progenies that

may be more suitable for the breeder's purposes, increasing the chance of success of the breeding program (Leite et al., 2016; Bizari et al., 2017; Teixeira et al., 2017).

Table 5 shows the selection gain estimates for eight characters using the "ranks" sum index (Mulamba; Mock, 1978) and the genotype-ideotype index (Cruz, 2006).

Table 4: Average of the top 30 soybean $F_{3:4}$ progenies selected by direct selection.

Progenies	NDF	Progenies	NPN	Progenies	TNP	Progenies	GP	Progenies	GPL
UFU 63	33.0	UFU 38	12.0	UFU 101	62.5	UFU 102	25.0	UFU 121	419.5
UFU 32	38.5	UFU 41	12.0	UFU 4	59.5	UFU 86	23.0	UFU 88	400.0
UFU 85	39.5	UFU 71	12.0	UFU 121	57.5	UFU 4	22.5	UFU 23	385.5
UFU 26	40.0	UFU 101	12.0	UFU 7	56.5	UFU 71	22.5	UFU 109	367.0
UFU 107	40.0	UFU 7	11.5	UFU 111	56.5	UFU 7	22.0	UFU 4	362.0
UFU 9	40.5	UFU 11	11.5	UFU 102	54.5	UFU 63	21.5	UFU 26	345.0
UFU 11	40.5	UFU 39	11.5	UFU 72	53.0	UFU 72	21.5	UFU 64	338.5
UFU 72	40.5	UFU 72	11.5	UFU 11	50.5	UFU 11	21.0	UFU 108	338.5
UFU 77	40.5	UFU 91	11.5	UFU 17	50.5	UFU 26	21.0	UFU 117	338.5
UFU 83	40.5	UFU 3	11.0	UFU 44	50.5	UFU 88	21.0	UFU 60	325.0
UFU 92	40.5	UFU 24	11.0	UFU 103	50.5	UFU 70	20.5	UFU 8	324.5
UFU 94	40.5	UFU 26	11.0	UFU 1	50.0	UFU 96	20.5	UFU 19	322.5
UFU 102	40.5	UFU 34	11.0	UFU 37	50.0	UFU 101	20.5	UFU 33	314.5
UFU 1	41.0	UFU 42	11.0	UFU 38	49.5	UFU 1	20.0	UFU 105	313.0
UFU 49	41.0	UFU 49	11.0	UFU 63	49.5	UFU 37	20.0	UFU 81	312.0
UFU 52	41.0	UFU 55	11.0	UFU 90	49.5	UFU 82	20.0	UFU 71	310.5
UFU 98	41.0	UFU 56	11.0	UFU 88	48.5	UFU 121	20.0	UFU 80	308.0
UFU 35	41.5	UFU 57	11.0	UFU 69	47.0	UFU 42	19.5	UFU 112	307.0
UFU 46	41.5	UFU 60	11.0	UFU 117	47.0	UFU 44	19.5	UFU 32	305.5
UFU 53	41.5	UFU 62	11.0	UFU 56	46.5	UFU 73	19.5	UFU 87	302.5
UFU 58	41.5	UFU 69	11.0	UFU 70	46.5	UFU 116	19.5	UFU 93	299.5
UFU 69	41.5	UFU 97	11.0	UFU 77	46.5	UFU 117	19.5	UFU 113	298.5
UFU 90	41.5	UFU 99	11.0	UFU 92	46.5	UFU 8	19.0	UFU 104	297.0
UFU 93	41.5	UFU 103	11.0	UFU 25	46.0	UFU 17	19.0	UFU 18	294.5
UFU 110	4.0	UFU 106	11.0	UFU 30	45.5	UFU 31	19.0	UFU 74	290.5
UFU 7	42.0	UFU 107	11.0	UFU 55	45.5	UFU 36	19.0	UFU 86	289.5
UFU 40	42.0	UFU 113	11.0	UFU 86	45.5	UFU 67	19.0	UFU 56	288.5
UFU 57	42.0	UFU 118	11.0	UFU 91	45.5	UFU 76	19.0	UFU 101	286.5
UFU 59	42.0	UFU 121	11.0	UFU 118	45.5	UFU 87	19.0	UFU 90	286.0
UFU 62	42.0	UFU 123	11.0	UFU 42	45.0	UFU 18	18.5	UFU 13	285.5
P_1	44.0	P_1	10.0	P_1	37.0	P_1	17.0	P_1	196.0
P_2	43.0	P_2	10.0	P_2	36.0	P_2	15.0	P_2	249.0

NDF: number of days for flowering; NPN: number of productive nodes; TNP: total number of pods; GP: grain production per plant (g); GPL (g): grain production per row (g). P_1: BRS256$_{RR}$ and P_2: TMG1179$_{RR}$.

Table 5: Estimates of selection gains (GS%) obtained for eight characters by selection using the Genotype - ideotype Index (Cruz, 2006) and the *Ranks* Sum Index (Mulamba and Mock, 1978) for 123 soybean F$_{3:4}$ progenies, in the municipality of Uberlândia – MG.

Characters	Mulamba and Mock (1978)	Genotype-ideotype distance
NDF	-0.56	-0.48
PHF	2.13	2.09
HIP	1.06	-1.82
NPN	2.19	2.19
NBN	11.38	12.04
TNP	12.57	13.47
GP	3.99	4.25
GPL	3.55	4.42
Total	37.11	36.95
Selected Progenies	UFU 72, UFU 116, UFU 86, UFU 45, UFU 117, UFU 56, UFU 5, UFU 53, UFU 106, UFU 23, UFU 6, UFU 4, UFU 73, UFU 101, UFU 96, UFU 82, UFU 90, UFU 123, UFU 116, UFU 88, UFU 18, UFU 113, UFU 103, UFU 71, UFU 65, UFU 70, UFU 3, UFU 69, UFU 107 and UFU 37.	UFU 121, UFU 90, UFU 101, UFU 117, UFU 91, UFU 72, UFU 86, UFU 5, UFU 45, UFU 96, UFU 56, UFU 77, UFU 55, UFU 106, UFU 88, UFU 6, UFU 4, UFU 116, UFU 73, UFU 90, UFU 37, UFU 123, UFU 70, UFU 69, UFU 3, UFU 65, UFU 60, UFU 81, UFU 109 and UFU 112.

NDF: number of days for flowering; PHF: plant height at flowering (cm); HIP: insertion height of the first pod (cm); NPN and NBN: number of productive and branched nodes, respectively; TNP: total number of pods; GP: grain production per plant (g); GPL (g): grain production per row (g).

When compared to the gains from direct and indirect selection (Table 3), in general, the direct gains from both indexes, the sum of "ranks" and the genotype-ideotype, were lower for all characters (Table 5). This may have occurred since the selection indexes cause a balanced distribution of the selection gains. According to Cruz, Regazzi and Carneiro (2012) in the selection index the gain on the character is reduced, however this reduction is offset by a better distribution of favorable gains in the other characters.

The Mulamba and Mock (1978) *ranks* sum index consists of classifying the genotypes in relation to each of the characters evaluated in the order favorable to improvement, and then the ranks orders or the classification of each genotype are added, resulting in the selection index. For this index the greatest individual gains were for the characters: number of total pods (12.57%), number of branched nodes (11.38%), production of plant grains (3.99%) and production of grains per row (3.55%) (Table 5).

The genotype-ideotype distance index methodology (Cruz, 2006) allows the determination of the optimal values for each variable, as well as the range of values considered adequate for improvement with the mean, maximum and minimum being calculated for each variable of the values. For this index, individual gains were greater and for the same characters as the sum of "ranks" index with 13.57% for TNP, 12.04% for NBN, 4.42% for GL and 4.5% for GP (4.25%) (Table 5).

Results different from those obtained in this study were found by Teixeira et al. (2017), in a study with several soybean selection indexes they found for the sum of ranks gains index of -0.01% (NDF); 4.10% (PHF); 6.42% (NPN) and 7.25% (TNP) and, for the genotype-ideotype index, selection gains of 2.83% (NDF); 4.44% (PHF); 10.29% (NPN) and 6.79% (TNP).

The genotype-ideotype index showed the highest individual gains for the characters, TNP, NBN, GP and GPL. Despite this, the sum of ranks index stood out for reaching the highest total gain with 37.11%, against 36.95% of the genotype-ideotype index (Table 5). In addition, the index of the genotype-ideotype obtained a lower gain (-0.48%) for the NDF character compared to the sum index of "ranks" (-0.54%) and reached a negative gain for the height of insertion of the first pod with -1.82% (Table 5). With this, the sum index of "ranks" is the most suitable for the selection of superior genotypes.

Results similar to this research were found by Bizari et al. (2017) who, when evaluating different selection strategies for agronomic traits in seven segregating soybean populations in the F_5 generation, concluded that the Mulamba; Mock index caused the most favorable gains when compared to the other selection strategies studied.

Leite et al. (2016), in research with different selection indexes, found results that corroborate those obtained in this research. The authors analyzed the selection index methodologies of Smith (1936) and Hazel (1943), Mulamba and Mock (1978) sum of ranks, Willians (1962) and the desired earnings of Pesek and Baker (1969), and obtained the highest total gain for the sum of ranks.

Leite et al. (2018) attested to the efficiency of Mulamba; Mock sum of ranks selection index methodology. When checking the agreement of multivariate techniques and selection index in the selection process of F_5 progenies of RR soy certified that the Mulamba; Mock index selected the same progenies as the multivariate technique, which reinforces its potential for the selection of promising genotypes.

The Mulamba and Mock (1978) ranks sum index was also recommended for causing the best results for reaching promising genotypes in several research with different cultures, such as: popcorn (Santos et al., 2007); alfalfa (*Medicago sativa* L.) (Vasconcelos et al., 2010); yellow passion fruit (*Passiflora edulis*) (Rosado et al., 2012) and papaya (*Carica papaya* L.) (Vivas et al., 2013).

Of the 30 $F_{3:4}$ progenies selected, 22 of them (UFU 72, UFU 116, UFU 86, UFU 45, UFU 117, UFU 56, UFU 5, UFU 106, UFU 6, UFU 4, UFU 73, UFU 101, UFU 96, UFU 90, UFU 123, UFU 116, UFU 88, UFU 65, UFU 70, UFU 3, UFU 69 and UFU 37), were similar in both selection indexes, which reaffirms that these progenies are potentially promising (Table 4).

The progenies UFU 72, UFU 90, UFU 88 and UFU 69 stood out both in the direct and indirect selection (Table 4), as well as in the sum indexes of Mulamba and Mock (1978) ranks and the genotype-ideotype (Table 5) for the NDF and the characters related to grain yield (NPN, TNP, GP and GPL), indicating that the selection of these progenies would bring the reach of superior genotypes.

UFU 72 added an average of 40.5 days for NDF, with TNP of 53 pods and GP of 21.5 grams. UFU 90 combined NDF with 41.5 days, 49.5 TNP and 286.0 grams for GPL. UFU 88 stood out for gathering high averages for characters related to grain yield, with 48.5 for TNP; 21.0 grams for GP and 400 g for GPL. Finally, UFU 69 stood out with 41.5 days for NDF; with 11.0 NPN and 47.0 for TNP (Table 4).

CONCLUSIONS

The genetic potential of agronomic traits of the $F_{3:4}$ population is high and allows different selection strategies to be applied to reach superior genotypes. The progenies UFU 72, UFU 116, UFU 86, UFU 45, UFU 117, UFU 56, UFU 5, UFU 106, UFU 6, UFU 4, UFU 73, UFU 101, UFU 96, UFU 90, UFU 123, UFU 116, UFU 88, UFU 65, UFU 70, UFU 3, UFU 69 and UFU 37 were selected by both selection indexes. The progenies UFU 72, UFU 90, UFU 88 and UFU 69 are agronomically superior both in direct and indirect selection, and in the sum selection indexes of Mulamba and Mock (1978) ranks and the genotype-ideotype.

AUTHOR CONTRIBUTION

Conceptual Idea: Hamawaki, O. T.; Nogueira, A. P. O.; Carneiro, A. R. T. Methodology design: Carneiro, A. R. T.; Nogueira , A. P. O.; Silva, A. F. E. Data collection: Carneiro, A. R. T; Silva, A. F. E.; Hamawaki, C. D. L. Data analysis and interpretation: Carneiro, A. R. T.; Nogueira, A. P. O.; Hamawaki, R. L.; Writing and editing: Carneiro, A. R. T; Nogueira , A. P. O.; Hamawaki, C. D. L.

REFERENCES

ANDRADE, A. C. B. et al. Strategies for selecting soybean genotypes using mixed models and multivariate approach. African Journal of Agricultural Research, 11(1):23-31, 2016.

AKRAM, S. et al. Genetic variability and association analysis of soybean (*Glycine max* (L.) Merrill) for yield and yield attributing traits. Plant Gene and Trait, 7(13):1-11, 2016.

BÁRBARO, I. M. et al. Análises genéticas em populações de soja resistentes ao cranco da haste e destinadas para áreas de canaviais. Colloquium Agrariae, 5(1):8-24, 2009.

BARBOSA, M. C. et al. Desempenho agronômico e componentes da produção de cultivares de soja em duas épocas de semeadura no arenito Caiuá. Semina: Ciências Agrárias, 34(3):945- 960, 2013.

BIANCHI, M. C. et al. Heritability and genotype x environment interactuon in soybean. Agrosystems, Geosciences & Environment, 3(1):e20020, 2020.

BIZARI, E. H. et al. Selection indices for agronomic traits in segregating populations of soybean. Revista Ciência Agronômica, 48(1):110-117, 2017.

CÂMARA, G. M. S. Preparo do solo e plantio. In: SEDIYAMA, T.; SILVA, F.; BORÉM, A. Soja do plantio à colheita. Viçosa: UFV, p. 66-109, 2015.

COSTA, M. et al. Heritability estimation in early generations of two-way crosses in soybean. Bragantia, 67(1):101-108, 2008.

CRUZ, C. D. Programa GENES: Biometria. Viçosa: Editora UFV, 2006. 382p.

CRUZ, C. D. ; REGAZZI, A. J; CARNEIRO, P. C. S. Modelos biométricos aplicados ao melhoramento genético. Viçosa: Editora UFV, 2012. 514p.

CRUZ, C. D. GENES - A software package for analysis in experimental statistics and quantitative genetics. Acta Scientiarum.Agronomy, 35(7):271-276, 2013.

CRUZ, C. D. et al. Biometria aplicada ao melhoramento genético. In: SILVA, F. et al. Melhoramento da Soja. Viçosa: Editora UFV, p. 249-287, 2017.

FEHR, W. R.; CAVINESS, C. E. Stages of soybean development. Ames: Iowa State University of Science and Technology, 1977. 11p. (Special report, 80).

GAZZONI, D. L. A soja no Brasil é movida por inovações tecnológicas. Ciência e Cultura, 70(3):16-18, 2018.

HAKIM, L.; SUYAMTO. Heritability and expected genetic advances of quantitative traits in F_4 progenies of soybean crosses. Journal Penelitian Pertanian Tanaman Pangan, 31(1):22-26, 2012.

HAMAWAKI, O. T. et al. Genetic parameters and variability in soybean genotypes. Comunicata Scientiae, 3(2):76-83, 2012.

HAZEL, L. N. The genetic basis for constructing selection indexes. Genetics, 28(6):476-490, 1943.

INSTITUTO BRASILEIRO DE GEOGRAFIA E ESTATÍSTICA – IBGE. Cidades. 2020. Available in: <https://cidades.ibge.gov.br/brasil/mg/uberlandia/panorama>. Access in: September, 21, 2021.

LEITE, W. S. et al. Estimativas de parâmetros genéticos, correlações e índices de seleção para seis caracteres agronômicos em linhagnes F_8 de soja. Comunicata Scientiae, 7(3):302-310, 2016.

LEITE, W. S. et al. Identification of superir genotyoes and soybean traits by multivariate analysis and selection index. Revista Ciência Agronômica, 49(3):491-500, 2018.

LUDWIG, M. P. et al. Características morfológicas de cultivares de soja convencionais e *Roundup Ready* TM em função da época e densidade de semeadura. Ciência Rural, 40(4):759-767, 2010.

LUIZ, M. C. P. et al. Efeito da época de semeadura e população de plantas sobre o potencial produtivo e caracteres agronômicos em soja. Bioscience Journal, 36(1):161-172, 2020.

MATTOS, T. P. et al. Efect of sowing season on soybean performance. Bioscience Journal, 36(5):1607-1618, 2020.

MEIER, C. et al. Performance agronômica e correlação linear entre componentes de rendimento da soja em segunda safra. Revista de Ciências Agrárias, 42(4):933-941, 2019.

MATSUO, E.; FERREIRA, S. C.; SEDIYAMA, T. Botânica e fenologia. In: SEDIYAMA, T.; SILVA, F.; BORÉM, A. Soja: Do plantio à colheita. Viçosa: Editora UFV, p.27-53, 2015.

MULAMBA, N. N. MOCK, J. J. Improvement of yield potential of the eto blanco maize (*Zea mays* L.) population by breeding for plant traits. Egyptian Journal of Genetics and Cytology, 7(1):40-51, 1978.

NOGUEIRA, A. P. O. et al. Análise de trilha e correlações entre caracteres em soja cultivada em duas épocas. Bioscience Journal, 28(6):877-888, 2012.

OLIVEIRA, M. M. et al. Evaluation of genetic diversity among soybean (*Glycine max*) genotypes using univariae and multivariate analysis. Genetics and Molecular Research, 16(2):2-10, 2017.

PESEK, J.; BAKER, R. J. Desired improvement in relation to selected indices. Canadian Journal of Plant Sciences, 49:803-804, 1969.

PIMENTEL-GOMES, F. Curso de estatística experimental. Piracicaba: Editora Nobel, 2009. 451p.

RAMALHO, M. A. P. et al. Aplicações da genética quantitativa no melhoramento de plantas autógamas. Lavras: Editora UFLA, 2012. 522p.

RAMALHO, M. A. P.; BRUZI, A. T.; TEIXEIRA, R. K. S. Genética quantitativa no melhoramento. In: SILVA, F. et al. Melhoramento da Soja. Viçosa: Editora UFV, p. 147-172, 2017.

RIBEIRO, F. C. et al. Desempenho agronômico de cultivares de soja na região central do Estado do Tocantins, safra 2014/2015. Scientia Plena, 12(7):2-7, 2016.

ROSADO, L. D. S. et al. Simultaneous selection in progênies of yellow passion fruit using selection indices. Revista Ceres, 59(1):95-101, 2012.

SANTOS, F. S. et al. Predição de ganhos genéticos por índice de seleção na população de milho-pipoca UNB-2U sob seleção recorrente. Bragantia, 66(3):389-396, 2007.

SANTOS, E. R. et al. Parâmetros genéticos e avaliação agronômica em progênies F_2 de soja no Distrito Federal, Brasil. Revista Brasileira de Ciências Agrárias, 14(1):1-8, 2019.

SEDIYAMA, T.; SILVA, F.; BORÉM, A. Soja: Do plantio à colheita. Viçosa, MG: Editora UFV, 2015. 333p.

SEDIYAMA, T. et al. A Soja. In: SEDIYAMA, T. Produtividade da Soja. Londrina: Editora Mecenas, 2016. 310p.

SILVA, F. et al. Melhoramento da Soja. Viçosa: UFV, 2017, 563p.

SILVA, F. M. S. et al. Strategies to select soybean segregating populations with the goal of improving agronomic traits. Acta Scientiarum.Agronomy, 40:e39324, 2018.

SMITH, H. F. A. discriminant function for plant selection. Annals of Eugenics, 7(3):240-250, 1936.

SILVEIRA, G. D. et al. Seleção de genótipos de soja para a região de Jaboticabal - Ano agrícola 2003-2004. Revista Científica, 34(1):92-98, 2006.

SOUSA, L. B. et al. Microsatellites and phenotypic characteristics used to select soybean lines in a Brazilian university breeding program. Genetics and Molecular Research, 19(1):2-15, 2020.

TEIXEIRA, F. G. et al. Genetic parameters and selection of soybean lines base do selection indexes. Genetics and Molecular Research, 16(3):2-17, 2017.

UNITED STATES DEPARTMENT OF AGRICULTURE – USDA. World Agricultural Production. 2021. Available in: <https://usda.library.cornell.edu/concern/publications/5q47rn72z?locale=en>. Access in: August, 24, 2021.

VASCONCELOS, E. S. et al. Estimates of genetic progress using different selection criteria in alfafa genotypes. Revista Ceres, 57(2):205-210, 2010.

VIANNA, M. S. et al. Selection of lineages, genetic parameters, and correlations between soybean characters. Bioscience Journal, 35(5):1300-1314, 2019.

VIVAS, M. et al. Predição de ganhos genéticos e seleção de progênies de mamoeiro para resistência à pinta-preta. Tropical Plant Pathology, 38(2):142-148, 2013.

WILLIAMS, J. S. The evaluation of a selection index. Biometrics, 18(3):375-393, 1962.

ZANON, A. J. et al. Efeito do tipo de crescimento no desenvolvimento de cultivares modernas de soja após o início do florescimento no Rio Grande do Sul. Bragantia, 75(4):445-458, 2016.

ZUFFO, A. M. et al. Path analysis in soybean cultivars grown under foliar spraying and furrow inoculation with *Azospirillum brasiliense*. Journal of Agricultural Science, 9(10):137-144. 2017.

ZUFFO, A. M. et al. Correlações e análise de trilha em cultivares de soja cultivadas em diferentes densidades de plantas. Cultura Agronômica, 27(1):78-90, 2018.