



Combining performance and estimated genetic diversity among soybean parents and F₁ populations¹

Samuel Leandro Soares^{2*} , Gustavo André Simon², Renata Cristina Alvares³, Fernando Higino de Lima e Silva⁴

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ABSTRACT

Studies about the combining ability and genetic diversity can provide information on the genetic resources contained in the working collection of germplasm. The objective of this study was to estimate the combining ability of ten soybean parents and their hybrids in the F₁ generation using diallel analysis and genetic diversity analysis to evaluate the dissimilarity between parents and crosses. The experiment was carried out in a greenhouse, in a completely randomized design with five replications, during the 2019/2020 crop season, in the municipality of Rio Verde, State of Goiás, Brazil. Agronomic and physiological variables were evaluated. Data were subjected to analysis of variance. Diallel analysis was performed using the Griffing method 2. Analysis of genetic diversity was performed with the Mahalanobis generalized distance and the hierarchical average linkage clustering. Additive gene effects were predominant in the control of all variables analyzed in the F₁ generation. The parents SYN 1163 RR and CG 7370 RR showed good complementarity for the variable grain yield. The thirty-five genotypes were separated into six groups, and the variable weight of one hundred seeds had the greatest contribution to genetic diversity.

Keywords: *Glycine max*; diallel; general capacity; specific capacity; UPGMA.

INTRODUCTION

Soybean breeding programs require a period of six to eight years for the development of cultivars, consisting of various stages such as hybridizations, conduction of segregating populations, and productivity tests. Given the time required for a breeding cycle, choosing the parents and the design that will be used in the interbreeding are determinant steps for success (Daronch *et al.*, 2014). Therefore, the selection of parents is one of the main steps in plant breeding programs (Bilyeu *et al.*, 2016).

After the selection of parents, hybridizations are carried out to obtain segregating populations with maximum genet-

ic variability and a high potential for extraction of superior lines during the selection process. In this context, the prior assessment of the genetic potential of the parents allows for the expansion of genetic variability and, consequently, greater genetic gains can be achieved (Rocha *et al.*, 2019).

Aiming at increasing the efficiency of breeding programs, biometric techniques such as diallel analysis were developed to help researchers when choosing parents. Diallel analysis allows the prediction of the potential of populations as well as inference about the combining ability of soybean parents (Umar *et al.*, 2017).

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² Universidade de Rio Verde, Programa de Pós-graduação em Produção Vegetal, Rio Verde, Goiás, Brazil. samuelleandro_sc@hotmail.com; simon@univ.br

³ Caraiba Genética, Rio Verde, Goiás, Brazil. renata.alvares@caribagenetica.com.br

⁴ Instituto Federal Goiano, Campus Rio Verde, Rio Verde, Goiás, Brazil. fernando.higino@ifgoiano.edu.br

*Corresponding author: samuelleandro_sc@hotmail.com

Additionally, it is important in a breeding program to infer about the genetic diversity between parents and segregating populations, aiming at the maintenance of alleles that express significant agronomic characteristics for the crop. Studies on genetic diversity in breeding processes allow the germplasm bank systemization, assistance in a core collection generation, and especially the maintenance of genetic resources (Sousa *et al.*, 2015).

Among the methods to assess genetic diversity, the generalized Mahalanobis distance (D2) allows analyzing data with repetitions and can combine hierarchical and non-hierarchical clustering methods (Cruz *et al.*, 2020). The UPGMA hierarchical method calculates the distance between two clusters as the average distance between all pairs of items of two clusters (Oliveira *et al.*, 2017). Methods that group the genotypes based on some similarity or dissimilarity measures aim to separate an original group observed into several subgroups, in a way to obtain intra-subgroup homogeneity and inter-subgroup heterogeneity (Rodrigues *et al.*, 2017).

The objective of this study was to evaluate the effects of the combining ability of ten soybean parents and their hybrid combinations in the F₁ generation in partial diallel crosses and to evaluate the genetic diversity between parents and crosses using the method of the generalized distance of Mahalanobis and the hierarchical clustering method (UPGMA).

MATERIAL AND METHODS

Plant material and hybridizations

Partial diallel crosses were carried out with no reciprocals involving ten soybean cultivars, in February 2019. The cultivars were divided into two parental groups (Table 1), and the purple- and white-flower parents were allocated to groups I and II, respectively. Hybridizations were conducted in a greenhouse, in which ten parent seeds were sown in 12-dm³ pots, in the municipality of Rio Verde, Goiás, Brazil. To ensure flowering synchronism, staggered sowing was done every five days in the four seasons.

Hybridizations were performed mainly with white-flower cultivars as pollen receptor parents. This strategy was

adopted to eliminate plants from self-fertilization in the F₁ generation, since the purple flower has complete dominance over the white flower, that is, in the F₁ generation, all crossed plants must present the purple flower.

Experimental design and procedures

An experiment was conducted with the F₁ generation in a completely randomized design, with thirty-five treatments, in which twenty-five were hybrid combinations and ten were parents, with five replications. Each experimental unit consisted of a pot with two plants, and the value of each treatment was represented by the mean of the two plants.

The treatments were sown in 12-dm³ plastic pots, in greenhouses, on December 12, 2019, in the municipality of Rio Verde, Goiás (17°44'24.9" S and 50°57' 31.4" W, 853 m altitude). To carry out the sowing, two holes three cm deep were made on opposite sides of the pot, and two seeds were planted per hole. To ensure equal number of plants per treatment, thinning was performed at five days after the emergence of the seedlings, leaving one plant per hole.

During the experiment, daily irrigation was applied for providing uninterrupted supply of the water demanded by the soybean crop and preventing the occurrence of water restrictions. Pests and diseases management was carried out following the technical recommendations for the soybean crop.

Analyzed variables

The variables analyzed were: days to flowering - stage R1 (DTF); plant height at flowering (PHF); days to maturity - stage R8 (DTM); and plant height at maturity (PHM). Evaluation of plant development was based on the phenological scales proposed by Fehr & Caviness (1977). Other variables evaluated included first pod insertion height (FPIH); number of nodes per plant (NNP), which was used only for analysis of genetic diversity; the number of pods per plant (NPP); "a" and "b" chlorophyll content (TCab) measured with a Clorofilog Falker 1030 chlorophyll meter, at thirty days after seedling emergence, in the third fully expanded trifoliolate leaf from the apex to the base of the plant, always in the central leaflet as described by Yokoyama *et al.* (2018); weight of one hundred seeds (WHS); and grain yield expressed as grams plant⁻¹ (GY).

Table 1: Description of soybean parents and hybrids used in a partial diallel crossing design (5x5)

*ID	Genotype	Flower color	Group
1	NA 5909 RG x BMX Desafio RR	-	F ₁
2	NA 5909 RG x FMT Anta 82 RR	-	F ₁
3	NA 5909 RG x TMG 7262 RR	-	F ₁
4	NA 5909 R GenotypeG x BRSGO 6959 RR	-	F ₁
5	NA 5909 RG x CG 7370 RR	-	F ₁
6	NS 4823 RR x BMX Desafio RR	-	F ₁
7	NS 4823 RR x FMT Anta 82 RR	-	F ₁
8	NS 4823 RR x TMG 7262 RR	-	F ₁
9	NS 4823 RR x BRSGO 6959 RR	-	F ₁
10	NS 4823 RR x CG 7370 RR	-	F ₁
11	SYN 1163 RR x BMX Desafio RR	-	F ₁
12	SYN 1163 RR x FMT Anta 82 RR	-	F ₁
13	SYN 1163 RR x TMG 7262 RR	-	F ₁
14	SYN 1163 RR x BRSGO 6959 RR	-	F ₁
15	SYN 1163 RR x CG 7370 RR	-	F ₁
16	PRE 6336 RR x BMX Desafio RR	-	F ₁
17	PRE 6336 RR x FMT Anta 82 RR	-	F ₁
18	PRE 6336 RR x TMG 7262 RR	-	F ₁
19	PRE 6336 RR x BRSGO 6959 RR	-	F ₁
20	PRE 6336 RR x CG 7370 RR	-	F ₁
21	CG 7262 RR x BMX Desafio RR	-	F ₁
22	CG 7262 RR x FMT Anta 82 RR	-	F ₁
23	CG 7262 RR x TMG 7262 RR	-	F ₁
24	CG 7262 RR x BRSGO 6959 RR	-	F ₁
25	CG 7262 RR x CG 7370 RR	-	F ₁
26	NA 5909 RG	Purple	I
27	NS 4823 RR	Purple	I
28	SYN 1163 RR	Purple	I
29	PRE 6336 RR	Purple	I
30	CG 7262 RR	Purple	I
31	BMX Desafio RR	White	II
32	FMT Anta 82 RR	White	II
33	TMG 7262 RR	White	II
34	BRSGO 6959 RR	White	II
35	CG 7370 RR	White	II

*ID: Identification code

Statistical-genetic analyses

The analysis of variance was used to evaluate the effect of the treatments. Then, the Griffing's (1956) diallel analysis, model 2, was applied to the variables with significant effect, with adaptation for partial diallel performed by Geraldi & Miranda Filho (1988), according to the model:

$$Y_{ij} = \mu + \frac{1}{2} + (d1 + d2) + gi + gj + Sij + \epsilon$$

Where, Y_{ij} : mean of the cross between the i^{th} parent of group I and j^{th} parent of group II; μ : general mean of the diallel; $d1 + d2$: differences between means of groups I and II and the general mean; g_i : effect of the general combining ability of the i^{th} parent from group I; g_j : general combining ability of the j^{th} parent from group II; S_{ij} : effect of specific combining ability; ϵ : experimental mean error.

The variables with significant effect ($p < 0.05$) were subjected to genetic diversity analysis. The distances between

pairs of genotypes were calculated by the Mahalanobis generalized distance matrix (D2) defined as $D_{ii'}^2 = \delta\psi^1\delta$, and the clustering of genotypes was performed using the hierarchical method of between-group average linkage (UPGMA).

Where: $D_{ii'}$: generalized Mahalanobis distance between i and i' genotypes; ψ : matrix of residual variances and covariances; δ : [d1 d2 ...dv] where $d_j = Y_{ij} - Y_{i'j}$ and Y_{ij} : mean of the i^{th} genotype in relation to the j^{th} variable.

The dendrogram shows the hierarchical clustering of the genotypes. The efficiency of the dendrogram in reproducing the dissimilarity matrix (D2) was calculated by the cophenetic correlation coefficient (CCC). The dendrogram

cutoff point was applied according to Mojena (1977). To verify the contribution of each variable to genetic diversity, the principal component analysis was applied as described by Cruz *et al.* (2012). The variance and diallel analyses were performed using the Genes statistical software (Cruz, 2016), and the Rbio statistical software was used for the other analyses (Bhering, 2017).

RESULTS AND DISCUSSION

The analysis of variance detected a significant effect ($p < 0.01$) of the source of variation and treatments for all variables analyzed (Table 2), indicating the presence of genetic variability between parents and F_1 hybrids.

Table 2: Mean square of the partial diallel variance analysis for days to flowering (DTF), plant height at flowering (PHF), days to maturity (DTM), plant height at maturity (PHM), number of nodes per plant (NNP), number of pods per plant (NPP), “a” and “b” chlorophyll content (TCab), weight of one hundred seeds (WHS), and grain yield as $g\ plant^{-1}$ (GY), evaluated in the F_1 progenies derived from a set of diallel crosses involving ten soybean cultivars. Rio Verde – GO, 2020

SV	DF	Mean squares								
		DTF	PHF	DTM	PHM	NNP	NPP	TCab	WHS	GY
Treatment	34	26.3**	100.3**	87.6**	655.4**	17.3**	706.6**	24.0**	8.6**	353.8**
Groups	1	87.4**	38.0 ^{ns}	206.1**	0.1 ^{ns}	17.1*	5277.8**	9.3 ^{ns}	26.7**	127.4*
GCA ¹ I	4	24.3**	244.9**	255.1**	2457.5**	28.9**	695.9**	35.6*	3.8 ^{ns}	142.4**
GCA ² II	4	2.2 ^{ns}	384.6**	218.8**	426.3**	60.3**	503.7**	25.0 ^{ns}	18.3**	359.1**
SCA ³	25	9.2*	34.1**	35.1*	430.0**	8.5**	558.0**	22.6**	7.1**	395.9**
Residue	105	5.4	11.4	1.7	65.8	3.2	140.3	10.4	1.9	25.8
GCA/SCA		2.9	18.4	13.5	6.7	10.5	2.1	2.7	3.1	1.3
Mean		34.8	22.7	109.6	66.4	15.1	68.9	30.0	16.4	28.0
CV (%)		6.7	14.9	4.1	12.2	11.9	17.2	10.7	8.3	18.2

^{ns}, ** and *, non-significant and significant values at 1 and 5% of probability by the F test, respectively.

¹GCA I: General combining ability of I; ²GCA II: Group II General combining ability; ³SCA: Specific combining ability.

The general combining ability (GCA I) in Group-I was significant ($p < 0.05$) for all variables, except for the weight of 100 seeds (Table 2). In Group-II, the general combining ability (GCA II) was significant ($p < 0.05$) for all variables, except for tdays to flowering and “a” and “b” chlorophyll content (Table 2), suggesting that among the parents in Group-II there was no significant difference in the allelic concentration for the two traits. In cases where GCA is significant, it can be inferred that at least one of the parents differs from the others regarding the concentration of favorable alleles (Pimentel *et al.*, 2013). The source variation SCA showed significant effect for all variables analyzed (Table 2).

The GCA/SCA ratio with the highest GCA estimates

indicates a predominance of additive gene effects in controlling this characteristic. When additive effects are pronounced, gains of greater magnitude will be predicted (Bhering *et al.*, 2017). On the other hand, the highest SCA values indicate a predominance of non-additive gene effects in controlling these traits (Bi *et al.*, 2015).

The additive gene effects were predominant for all the characteristics assessed, with the lowest GCA/SCA ratio found for grain yield (1.3) and the highest GCA/SCA ratio for plant height at flowering (18.4). Rocha *et al.* (2019) demonstrated the importance of additive gene effects in controlling the characteristic grain yield when evaluating F_2 populations from diallel crosses. Similar results were also obtained by Zorzetto *et al.* (2009), who verified the

importance of additive gene effects in the expression of the characteristics number of seeds per plant, number of pods per plant, and weight of 100- seeds.

In contrast, Colombo *et al.* (2018) obtained a greater contribution of non-additive gene effects in the F₁ generation for the expression of number of days to flowering and maturity, and grain yield. The diverged results may be related to the population of interest, since estimates of genetic parameters are intrinsic to the target population. Furthermore, the complexity of inheritance of quantitative

traits and the effect of the genotype x environment interaction may explain the divergence of the results obtained (Goksoy *et al.*, 2019).

Because precocity is one of the primary objectives of breeding programs, parents that contribute to the reduction of the cycle must be inserted in new crossing blocks. Thus, the parents NS 4823RR (DTF: -1.7 and DTM: -4.0) and FMT Anta 82 RR (DTF: -0.5 and DTM: -0.4) presented negative GCA estimates or both days to flowering and days to maturity (Table 3).

Table 3: Estimates of general combining ability for: days to flowering (DTF), plant height at flowering (PHF), days to maturity (DTM), plant height at maturity (PHM), number of nodes per plant (NNP), number of pods per plant (NPP), “a” and “b” chlorophyll content (TCab), weight of one hundred seeds (WHS), and grain yield as g plant⁻¹ (GY), relative to ten soybean parents in the municipality of Rio Verde, Goiás

Treatment	DTF	PHF	DTM	PHM	NNP	NPP	TCab	WHS	GY
Group I									
NA 5909 RG	1.4	2.4	-0.4	-1.4	-0.9	3.0	0.1	0.1	-1.1
NS 4823 RR	-1.7	-2.6	-4.0	-5.1	-0.4	-4.4	1.3	0.2	0.2
SYN 1163 RR	1.4	1.7	1.7	12.9	-0.1	1.6	-0.3	0.4	2.9
PRE 6336 RR	1.0	0.9	1.0	-4.4	0.2	-4.0	0.1	-0.2	-0.2
CG 7262 RR	-2.0	-2.4	1.7	-2.0	1.2	3.8	-1.2	-0.4	-1.8
Group II									
BMX Desafio RR	-0.3	-2.5	3.5	-2.0	0.7	2.5	-1.1	0.5	-1.0
FMT Anta 82 RR	-0.5	-2.6	-0.4	-0.2	0.5	2.7	0.4	-0.6	-0.5
TMG 7262 RR	-0.1	-0.8	-0.1	-3.5	-0.7	-5.1	-0.3	0.8	-0.7
BRSO 6959 RR	0.9	4.3	-2.7	1.1	-1.6	-1.7	0.1	-0.7	-2.6
CG 7370RR	-0.1	1.6	-0.3	4.6	1.2	1.6	0.9	0.1	4.8

Plant height is a characteristic that determines the adaptation or non-adaptation of the genotype to a particular environment. Therefore, selection of early parents based on positive combining ability estimates is recommended, that is, parents that transfer alleles that express less sensitivity at sowing time to their offspring, which can cause reduction in size and consequently in grain yield. Thus, the parents that contributed to increasing the height of plants during flowering and maturity were SYN 1163 RR (PHF: 1.7 and PHM: 12.9), BRSGO 6959 RR (PHF: 4.3 and PHM: 1.1), and CG 7370 RR (PHF: 1.6 and PHM: 4.6) (Table 3).

According to GCA estimates, the cultivars that tend to contribute to an increase in the number of nodes per plant are CG 7262 RR (1.2), BMX Desafio RR (0.7), FMT Anta 82 RR (0.5), and CG 7370 RR (1.2) (Table 3). The parents that presented positive GCA estimates for number of pods

per plant were NA 5909 RG (3.0), SYN 1163 RR (1.6), CG 7262 RR (3.8), BMX Desafio RR (2.5), FMT Anta 82 RR (2.7), and CG 7370 RR (1.6) (Table 3). This is relevant information for soybean improvement, because the number of pods per plant is the variable that contributes the most to the increase in grain yield (Mahbud *et al.*, 2015; Bisinotto *et al.*, 2017). Considering the variables APF, APM, NN and NVP simultaneously, as well as the heritability of a character with an additive gene effect (Ramalho *et al.*, 2012), the parent CG 7370 RR showed to be promising to be included in new crossing blocks.

The variable “a” and “b” chlorophyll content, among the parents of group-I had positive and high GCA (1.3) effects for the cultivar NS 4823 RR (1.3). Group II showed no significant effect for GCA, and among the parents, CG 7370 RR had the highest estimate (0.9) (Table 3).

The variable weight of one hundred seeds had no significant effect for GCA in group-I. For the parents in group-II, the cultivars BMX Desafio RR and TMG 7262 RR contributed the most to increasing the weight of one hundred seeds in their offspring, with values of 0.5 and 0.8, respectively (Table 3).

Among the parents that contributed the most to grain yield, the cultivars SYN 1163 RR and CG 7370 RR stood out with positive GCA estimates of 2.9 and 4.8, respectively (Table 3). Grain yield is a characteristic strongly influenced by the environmental effect as it is a quantitative trait, thus, parents that contribute with allelic frequency to simultaneously increase several traits should be used in breeding programs aiming at higher yields. In this aspect, the parent CG 7370 RR stood out for presenting estimates that contribute to all variables, even with the lowest-magnitude estimates for days to flowering and maturity and weight of one hundred seeds.

Estimates of specific combining ability are shown in Table 4. The crosses that showed the lowest SCA estimates for days to flowering were NA 5909 RG x CG 7370 RR (-1.2), SYN 1163 RR x BMX Desafio RR (-1.6), SYN 1163 RR x TMG 7262 RR (-1.0), PRE 6336 RR x BMX Desafio RR (-1.2), PRE 6336 RR x FMT Anta 82 RR (-1.4), CG 7262 RR x BRSGO 6959 RR (-2.5) and CG 7262 RR x CG 7370 RR (-1.9).

The combinations with the highest positive SCA estimates for plant height at flowering were NA 5909 RG x BRSGO 6959 RR (5.1); NA 5909 RG x CG 7370 RR (3.0); NS 4823 RR x TMG 7262 RR (1.7); NS 4823 RR x BRSGO 6959 RR (1.3); NS 4823 RR x CG 7370 RR (1.5); SYN 1163 RR x FMT Anta 82 RR (3.0) and CG 7262 RR x BMX Desafio RR (2.2) (Table 4). The combination NA 5909 RG x BRSGO 6959 RR involves the two parents with the highest GCA estimates, and the other combinations except for CG 7262 RR x BMX Desafio RR have at least one parent with a good GCA estimate in their genealogy. These SCC estimates are relevant to breeding, because they showed complementarity between parents, enabling new gains in the selection of new genotypes.

In relation to days to maturity, the combinations NA 5909 RG x TMG 7262 RR (-2.3), NA 5909 RG x BRSGO 6959 RR (-2.1), NS 4823 RR x BRSGO 6959 RR (-4.0), SYN 1163 RR x FMT Anta 82 RR (-3.2), SYN 1163 RR x TMG 7262 RR (-3.3), PRE 6336 RR x CG 7370 RR (-4.3), and CG 7262 RR x BRSGO 6959 RR (-1.0) (Table 4) showed SCA estimates tending to cycle reduction.

In addition to a proper estimation of GCA of the parents, gene complementation was found between them, as shown by the SCA estimate of the combinations NA 5909 RG x BRSGO 6959 RR (11.3), NS 4823 RR x BRSGO 6959 RR (28.7), PRE 6336 RR x FMT Anta 82 RR (7.9), CG 7262 RR x BMX Desafio RR (9.3), CG 7262 RR x FMT Anta 82 RR (9.4) and CG 7262 RR x TMG 7262 RR (5.2). Among the parents involved in these combinations, only BRSGO 6959 RR had a good GCA estimate, which is an indication of gene complementarity between the parents due to non-additive gene effects, and the presence of larger genes with a dominance effect providing greater heterotic effect for populations.

The combinations that presented the highest positive SCA estimates for the variable number of nodes per plant were NS 4823 RR x TMG 7262 RR (1.7), NS 4823 RR x BRSGO 6959 RR (1.6), SYN 1163 RR x BMX Desafio RR (1.9), SYN 1163 RR x CG 7370 RR (1.4), PRE 6336 RR x FMT Anta 82 RR (2.1), PRE 6336 RR x BRSGO 6959 RR (1.6), CG 7262 RR x TMG 7262 RR (1.1), and CG 7262 RR x BRSGO 6959 RR (0.9) (Table 4).

The crosses with the highest SCA for number of pods per plant were NA 5909 RG x TMG 7262 RR (6.7), NA 5909 RG x BRSGO 6959 RR (14.8), NS 4823 RR x BMX Desafio RR (14.7), NS 4823 RR x CG 7370 RR (6.4), SYN 1163 RR x TMG 7262 RR (8.7), SYN 1163 x CG 7370 RR (6.2), PRE 6336 RR x BMX Desafio RR (7.3), PRE 6336 RR x FMT Anta 82 RR (11.8), PRE 6336 RR x BRSGO 6959 RR (15.3), CG 7262 RR x BMX Desafio RR (8.0), CG 7262 RR x TMG 7262 RR (4.9), and CG 7262 RR x BRSGO 6959 RR (6.2) (Table 4).

Later in this section, we discuss that the variable number of pods per plant makes a considerable contribution to the genetic divergence found in this study, which infers the existence of genetic variability for this attribute, providing greater selection gains. According to Bagateli *et al.* (2020), positive estimates of SCA reveal the existence of a large amount of heterozygous loci with greater potential for genetic variability, in addition to being associated with high means.

Except for PRE 6336 RR x BRSGO 6959 RR, all the other crosses have at least one parent with a good GCA estimate in their genealogy. In cases where the parents do not present a good GCA, the population potential can be predicted based only on the SCA, indicating superiority of parents based only on their GCA, which infers the existence of gene complementation between the parents.

Table 4: Estimates of specific combining ability for: days to flowering (DTF), plant height at flowering (PHF), days to maturity (DTM), plant height at maturity (PHM), number of nodes per plant (NNP), number of pods per plant (NPP), “a” and “b” chlorophyll content (TCab), weight of one hundred seeds (WHS), and grain yield in g plant⁻¹ (GY), relative to twenty-five F₁ soybean populations in the municipality of Rio Verde, Goiás

Treatment	DTF	PHF	DTM	PHM	NNP	NPP	TCab	WHS	GY
NA 5909 RG x BMX Desafio RR	1.3	-1.4	1.0	-2.5	0.6	-5.8	-1.8	1.5	2.2
NA 5909 RG x FMT Anta 82 RR	0.9	-1.2	-0.7	-5.6	0.4	0.5	2.6	-0.3	-4.7
NA 5909 RG x TMG 7262 RR	-0.3	-0.3	-2.3	0.9	-0.4	6.7	1.3	-0.8	-2.6
NA 5909 RG x BRSGO 6959 RR	-0.6	5.1	-2.1	11.3	0.1	14.8	-0.1	-0.1	3.0
NA 5909 RG x CG 7370 RR	-1.2	3.0	0.8	-1.0	-0.8	0.1	-2.3	0.9	-7.2
NS 4823 RR x BMX Desafio RR	0.7	0.2	4.3	2.8	0.7	14.7	-0.1	1.7	0.3
NS 4823 RR x FMT Anta 82 RR	-0.1	-1.4	-0.4	-7.3	-0.7	1.4	-0.3	-0.1	-6.6
NS 4823 RR x TMG 7262 RR	0.3	1.7	1.7	3.8	1.7	-0.6	-0.4	0.4	2.4
NS 4823 RR x BRSGO 6959 RR	0.9	1.3	-4.0	28.7	1.6	-1.9	5.0	0.3	12.7
NS 4823 RR x CG 7370 RR	0.9	1.5	3.3	-1.7	0.5	6.4	0.1	0.9	16.1
SYN 1163 RR x BMX Desafio RR	-1.6	-2.3	-0.6	-0.1	1.9	-0.2	-1.1	-0.7	7.7
SYN 1163 RR x FMT Anta 82 RR	-0.2	3.0	-3.2	2.2	-1.5	-0.5	1.3	-1.0	-4.7
SYN 1163 RR x TMG 7262 RR	-1.0	1.4	-3.3	-1.1	0.7	8.7	0.3	1.1	-4.0
SYN 1163 RR x BRSGO 6959 RR	0.4	-4.9	5.6	3.5	-0.2	-23.7	-3.9	1.3	2.8
SYN 1163 RR x CG 7370 RR	0.9	1.1	0.2	1.3	1.4	6.2	2.1	0.6	16.2
PRE 6336 RR x BMX Desafio RR	-1.2	-3.2	-0.5	-4.8	-0.7	7.3	1.0	-0.3	-2.0
PRE 6336 RR x FMT Anta 82 RR	-1.4	2.4	1.7	7.9	2.1	11.8	2.3	0.3	15.9
PRE 6336 RR x TMG 7262 RR	0.1	0.1	-0.7	2.7	0.1	-13.7	0.7	-0.2	8.5
PRE 6336 RR x BRSGO 6959 RR	1.0	-1.6	1.5	2.5	1.6	15.3	-1.3	1.3	-1.1
PRE 6336 RR x CG 7370 RR	0.4	1.9	-4.3	-1.2	-0.3	-11.9	1.3	-1.1	-7.2
CG 7262 RR x BMX Desafio RR	3.1	2.2	1.0	9.3	-0.6	8.0	-2.0	0.1	-0.5
CG 7262 RR x FMT Anta 82 RR	2.2	-0.5	1.3	9.4	0.8	-11.6	-0.6	2.3	7.5
CG 7262 RR x TMG 7262 RR	0.9	0.5	3.1	5.2	1.1	4.9	1.2	1.6	8.0
CG 7262 RR x BRSGO 6959 RR	-2.5	-3.7	-1.0	-6.0	0.9	6.2	1.0	1.3	-6.8
CG 7262 RR x CG 7370 RR	-1.9	-2.9	0.5	-5.4	0.1	-11.1	2.2	1.9	0.1

The combinations that presented the highest SCA estimates for the variable “a and “b” chlorophyll content were NA 5909 RG x FMT Anta 82 RR (2.6), NS 4823 RR x BRSGO 6959 RR (5.0), PRE 6336 RR x FMT Anta 82 RR (2.3), and CG 7262 RR x CG 7370 RR (2.2) (Table 4). It was observed that, except for CG 7262 RR, all the other parents involved in these crossings had positive GCA estimates. The SCA estimate showed that the parents complemented each other, even those not differing in

allelic concentration with additive effect, which suggest the occurrence of non-additive gene effects also controlling the expression of the characteristic “a and “b” chlorophyll content in soybeans.

The variable weight of one hundred seeds had the highest positive SCA estimates for the hybrid combinations NA 5909 RG x BMX Desafio RR (1.5), NS 4823 RR x BMX Desafio RR (1.7), SYN 1163 RR x TMG 7262 RR (1.1), SYN 1163 RR x BRSGO 6959 RR (1.3), PRE 6336 RR x

BRSO 6959 RR (1.3), CG 7262 RR x FMT Anta 82 RR (2.3), and CG 7262 RR x TMG 7262 RR (1.6) (Table 4).

The highest SCA estimates of the variable grain yield were found in the crosses NS 4823 RR x BRSO 6959 RR (12.7), NS 4823 RR x CG 7370 RR (16.1), SYN 1163 RR x CG 7370 RR (16.2), and PRE 6336 RR x FMT Anta 82 RR (15.9) (Table 4). Except for PRE 6336 RR x FMT Anta 82 RR, all the other crosses had at least one parent with good GCA, particularly SYN 1163 RR x CG 7370 RR, which has the two parents with the highest GCA estimates.

In this study, in the same way as Rocha *et al.* (2018), we found genetic complementarity in the cross PRE 6336 RR x FMT Anta 82 RR, indicating it is superior to the parents. In addition, crosses with the highest SCA estimates can release greater variability after self-fertilization generations, essential for plant breeding (Abreu *et al.*, 2004).

Figure 1 shows the dendrogram of the dissimilarity between the genotypes by the hierarchical average linkage clustering (UPGMA). The cophenetic correlation coefficient (CCC) estimated was 0.74. The cophenetic correlation coefficient indicates the efficiency of the dendrogram in

representing the genetic distances obtained in the distance matrix. It indicates the goodness of fit of the dendrogram and the original matrix, which must be greater than 0.70, according to Cruz *et al.* (2020).

The measures of genetic distances among the genotypes analyzed were high (4.41 to 122.91), indicating wide genetic variability. Analysis of the dendrogram simultaneously with the effects of GCA and SCA shows that the results contrast for the variables days to flowering, plant height at flowering, days to maturity, and plant height at maturity, demonstrating that the genotypes are little divergent for those characters.

However, the cluster analysis for the variables number of nodes per plant, number of pods per plant, “a” and “b” chlorophyll content, weight of one hundred seeds, and grain yield confirmed a great variability between the genotypes tested. It showed that the greatest distance was recorded between NS 4823 RR and SYN 1163 RR x CG 7370 RR (122.91), confirming the GCA values of their parents, as well as the SCA value of the hybrid combination for grain yield.

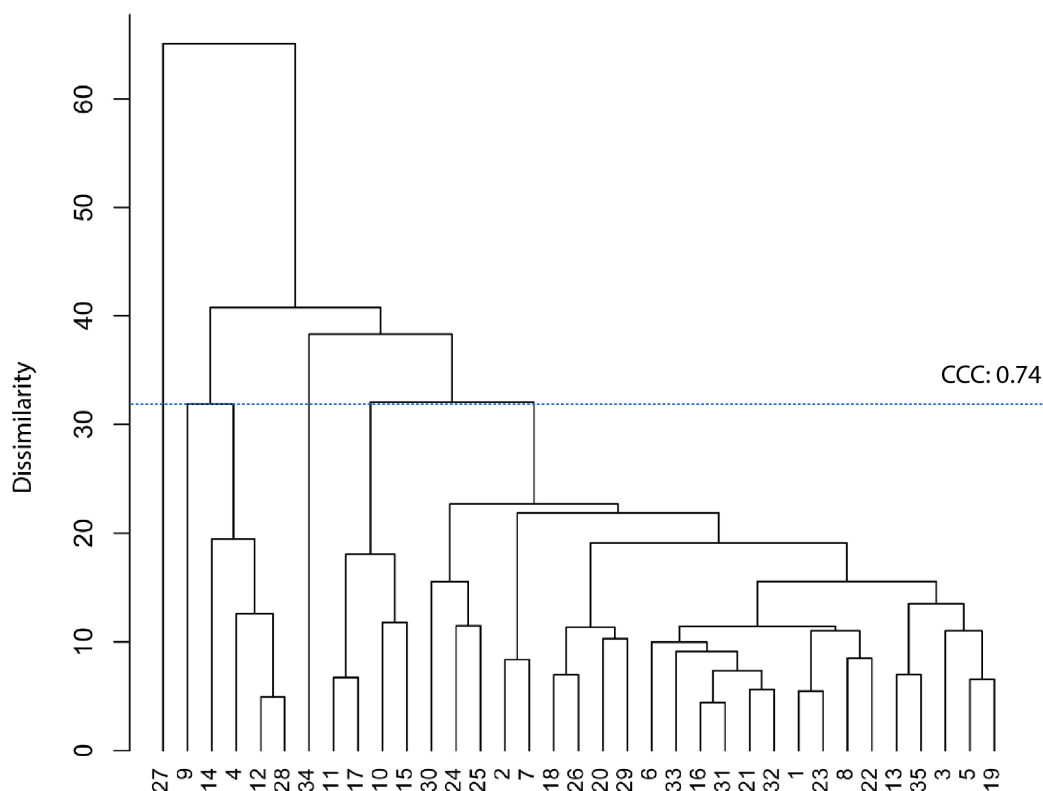


Figure 1: Dendrogram of the genetic dissimilarity among 35 soybean genotypes (10 parents and 25 F_1 combinations) using the UPGMA method, based on the Mahalanobis generalized distance matrix (D_2). Legend of treatments (Table 1).

In relation to the importance of the variables for genetic diversity, this study found that the weight of one hundred seeds had the greatest contribution (13.3%), followed by number of nodes per plant (11.2%), and number of pods per plant (11.0%) (Figure 2).

This result has great relevance to the genetic improvement of the crop, because the genetic diversity estimates can be used to guide new crossings and obtain new gains with selection within populations using a greater genetic variability.

Sousa *et al.* (2015) evaluated the genetic diversity among soybean crosses and found that the most contributing variables to genetic diversity among the crosses studied

were plant height at maturity, number of pods with one seed, and grain yield, with a relative importance of 31.0, 19.5, and 13.2%, respectively. Torres *et al.* (2015), in a similar study, found that number of pods per plant was the trait that contributed the most to genetic diversity.

Moreover, the variables that contributed the least to genetic diversity were grain yield, days to maturity, and “a” and “b” chlorophyll content, with values of 8.9%, 8.8%, and 7.4%, respectively. The finding that the variable grain yield did not contribute much to genetic diversity of soybean in this study corroborates the results obtained by Oliveira *et al.* (2017) in a study of genetic divergence between 24 soybean genotypes using multivariate clustering methods.

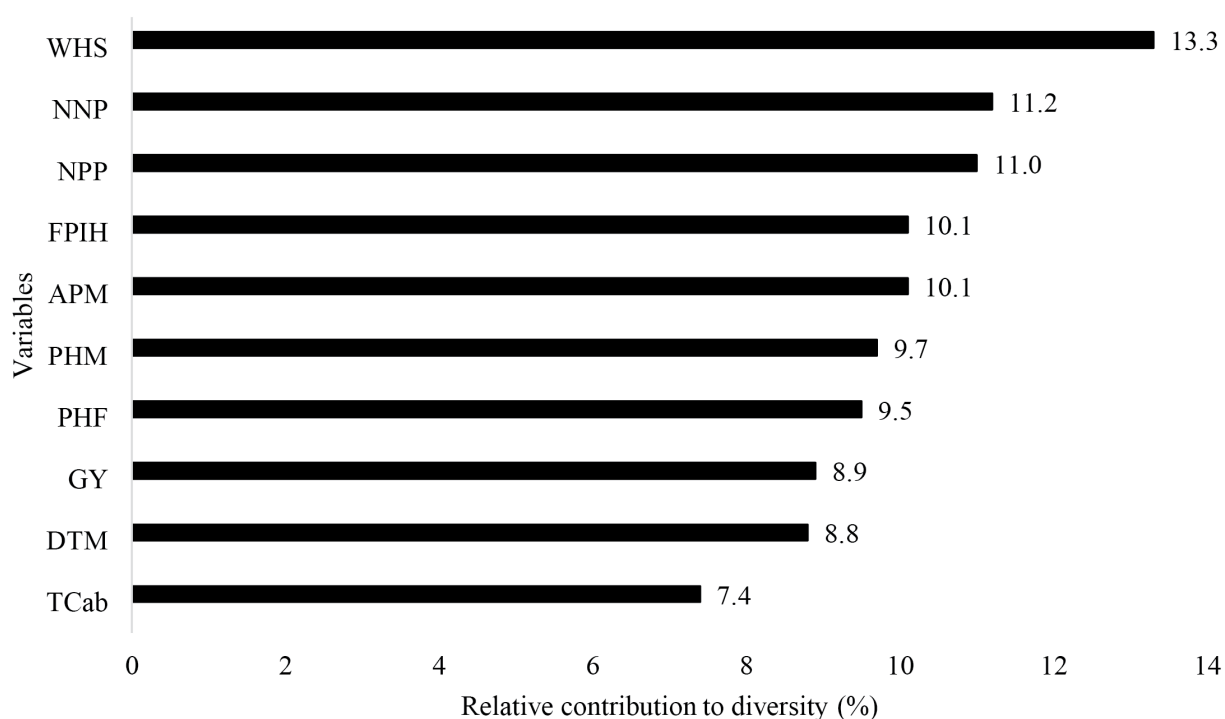


Figure 2: Relative contribution of 10 characteristics to quantify genetic diversity among 35 soybean genotypes: weight of one hundred seeds (WHS), number of nodes per plant (NNP), number of pods per plant (NPP), first pod insertion height (FPIH), plant height at maturity (PHM), days to flowering (DTF), plant height at flowering (PHF), grain yield in g plant⁻¹ (GY), days to maturity (DTM) and “a and b” chlorophyll content (TCab).

CONCLUSIONS

The additive gene effects were the most important for the expression of the variables analyzed.

Overall, the parent CG 7370 RR is the most promising to be used in new crossing blocks, as it simultaneously contributed to enhancement of the variables analyzed.

Six groups of genotypes were formed based on the UP-

GMA cluster analysis, and the variables that presented the greatest relative contribution to genetic diversity were the weight of one hundred seeds, number of nodes per plant, and number of pods per plant.

The generalized Mahalanobis distance matrix was used to confirm the occurrence of genetic diversity of great magnitude among the treatments analyzed.

CONFLICT OF INTEREST

Authors do not have any conflict of interest to declare.

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