Selection of soybean (*Glycine max* (L.) Merril) genotypes for cultivation in the Brazilian Brejo Paraibano

Selección de genotipos de soya (*Glycine max* (L.) Merril) para su cultivo en el Brejo Paraibano brasileño

Guilherme Chaves de Holanda[1]*, Lais Tomaz Ferreira[1], Felipe da Silva Lopes[2], and Naysa Flávia Ferreira do Nascimento[1]

ABSTRACT

Soybeans have great commercial value and there are still regions with no indications of promising genotypes, such as Brejo Paraibano region. The objective of this study was to analyze the adaptability of 20 soybean genotypes selected with a relative maturity degree above 9. The genotypes used were: M8867RR, M8766RR, M9144RR, SYN1059 RR, M-SOY 9350, ST 920 RR, TMG1175RR, M8372IPRO, M8527RR, M8644IPRO, TOPAZIO RR, UFV - 16 (Capinópolis) and UFVS: Berilo RR, 2013, 2012, 2010, 2005, QUARTZO, 2001, and 2008. A completely randomized experimental design was used with five replicates. The data were subjected to analysis of variance and Tukey test to compare the means. From the Mahalanobis generalized distance, it was possible to apply the Tocher and UPGMA tests. In addition, using the Singh method and canonical correlation, the quantification of the characteristics that contributed most to genetic divergence was evaluated. Only ten genotypes reached the physiological maturity, and the following variables were evaluated: hypocotyl length, leaf width and length, plant height, flower diameter, and seed width and length. The characteristics leaf width, flower diameter, and seed width were significant (*P*<0.05) and obtained values above 1 for the ratio between genotypic variation and environmental variation (CV_G/CV_E). The higher means for the significant characteristics were observed in the genotypes SYN1059 RR, UFVS: Berilo and 2013. The genotypes SYN1059 RR, M8766RR, M8867RR, UFVS: Berilo, 2012 and 2013 were selected as the most suitable parental material to use in breeding programs.

Key words: characterization, genetic diversity, genetic breeding, adaptability, superior genotypes.

RESUMEN

La soya tiene un gran valor comercial y todavía hay regiones sin indicaciones de genotipos tolerantes, como la región del Brejo Paraibano. El objetivo de este estudio fue analizar la adaptabilidad de 20 genotipos de soya seleccionados con grado de maduración relativo superior a 9. Los genótipos utilizados fueron: M8867RR, M8766RR, M9144RR, SYN1059 RR, M-SOY 9350, ST 920 RR, TMG1175RR, M8372IPRO, M8527RR, M8644IPRO, TOPAZIO RR, UFV-16 (Capinópolis), UFVS: Berilo RR, 2013, 2012, 2010, 2005, QUARTZO, 2001 y 2008. El experimento fue conducido bajo diseño completamente al azar con cinco repeticiones. Los datos fueron sometidos a análisis de varianza y test de Tukey para comparación de medias. Por medio de la distancia generalizada de Mahalanobis fue posible aplicar las pruebas de Tocher y UPGMA. Además, con el método Singh y la correlación canónica evaluamos la cuantificación de las características que más contribuyeron a la divergencia genética. Sólo diez genotipos alcanzaron la madurez fisiológica de los cuales se evaluaron las siguientes características: longitud del hipocótilo, longitud y ancho de la hoja, altura de planta, diámetro de la flor, y longitud y ancho de la semilla. Las características del ancho de la hoja, diámetro de la flor y ancho de la semilla fueron significativas (*P*<0.05) y obtuvieron entre sí valores superiores a 1 para la relación entre el coeficiente de variación genética y el coeficiente de variación ambiental (CV_G/CV_A). Los promedios más altos de las características significativas se observaron en los genotipos SYN1059 RR, UFVS: Berilo RR y 2013. Los genotipos SYN1059RR, M8766RR, M8867RR, UFVS: Berilo RR, 2012 y 2013 fueron seleccionados como los materiales parentales más apropiados para usar en programas de mejoramiento.

Palabras clave: caracterización, diversidad genética, mejoramiento genético, adaptabilidad, genotipos superiores.

Introduction

Soybean (*Glycine max* (L.) Merril) is one of the main oleaginous crops in the world (Cruz *et al*., 2016). This quality relates to its productive potential, chemical composition, and nutritive value, which allows it to have multiple uses, for both human and animal feeding. This crop is also of socio-economic importance since it is a raw material that

is indispensable to boost several agro-industrial complexes (Mauad *et al.*, 2010).

Brazil is the second-largest producer of soybeans; in the 2017/2018 harvest, it produced 116,996 million t, being only behind the United States, which produced 119,518 million t of this grain (EMBRAPA, 2018). After the 1970s, soybean production became of high relevance to agribusiness. Currently the Brazilian territory has the availability of natural resources that can be favorable for the maintenance and expansion of its production (Silva *et al.*, 2011). However, some regions with production potential do not have recommended and tested genotypes, such as the Brejo da Paraiba region.

Plant breeding programs can overcome some limitations, given that soybean cultivars have a broad genetic diversity related to adaptation, especially for photoperiod sensitivity and temperature, which are indispensable factors for crop expansion (Viana *et al.*, 2009). It is necessary to access the genetic variability available for future uses in breeding programs since this will make possible the selection of parent plants that will form the population with the highest proportion of desirable recombinants (Vasconcelos *et al.*, 2015).

In addition to an adequate genotype selection, the success of soybean cultivation depends on several factors. The most important one is the use of high-quality seeds, resulting in high vigor plants that will perform better in the field. The use of high-quality seed allows access to genetic advances, quality assurance, and adaptation technologies in different regions, ensuring higher yields (França-Neto *et al.*, 2016).

Soybean is considered a short-day plant; for this reason, most of the world's cultivated area is located at latitudes greater than 30. The adaptation of soybean to the latitude conditions of the Brazilian Midwest, North, and Northeast regions was one of the major challenges faced by soybean breeding programs (Almeida *et al.*, 2011). In the Northeast region, there is a great demand for soybean for animal feeding in farms of almost all states. As a highly valued crop, it has great potential for gains for producers in the region, meeting regional and global market demands (Campos *et al.*, 2016).

The precipitation of the Brejo da Paraiba region allows the cultivation of many vegetable crops of short and perennial cycle, including some species that require high amounts of water (Costa *et al.*, 2015). However, there is a lack of practical and scientific information in the literature regarding the recommendation of genotypes for this region.

The objective of this study was to analyze the genetic diversity of soybean genotypes provided by the germplasm bank of the Universidade Federal Viçosa through uni and multivariate techniques and recommend the superior genotypes for the analyzed characteristics.

Materials and methods

The experiment was conducted at the Departamento de Ciências Biológicas (DCB), Centro de Ciências Agrárias (CCA) of the Universidade Federal da Paraíba (UFPB), campus II, located in the municipality of Areia, in the Brejo Paraibano Microregion at an altitude of 623 m a.s.l. and with coordinates 06°57'48" S and 35°41'30" W. The annual average temperature was 24.0°C with a relative average humidity of approximately 80% and annual average precipitation of 1,400 mm (Costa *et al.*, 2015). The climate, according to Köppen (1936), is classified as As, a tropical climate, semi-humid, with rains during the autumn-winter season.

The seeds were donated by the plant breeding program of the Universidade Federal de Viçosa. The following genotypes with a relative maturity degree above 9 were pre-selected: M8867RR, M8766RR, M9144RR, SYN1059 RR, M-SOY 9350, ST 920 RR, TMG1175RR, M8372IPRO, M8527RR, M8644IPRO, TOPAZIO RR, UFV - 16 (Capinópolis) and UFVS: Berilo RR, 2013, 2012, 2010, 2005, QUARTZO, 2001, and 2008. The seeds were sown in a commercial substrate (Basaplant®) and arranged to place three seeds of the genotypes per cell. Fifteen days after germinated, plants were transferred to 5 L plastic pots maintained under greenhouse conditions.

The harvest was performed continuously; when the pods reached the point of physiological maturity and presented predominance of a brown color, they were harvested to avoid future losses, considering that soybean has a dehiscent characteristic. The experiment was located in a region with a high level of humidity (close to 80%) with regular rainfall during short periods of drought. For this reason, the seeds were harvested because they presented a decrease in humidity.

A ruler and pachymeter were used for quantitative evaluations such as hypocotyl length, leaf width and length, flower diameter, plant height, seed length and width. To

perform the germination index analysis, we divided the number of germinated seeds by the total number of seeds and multiplied by 100 to obtain the result as a percentage.

A completely randomized design with five replicates was used. Data were previously subjected to analysis of variance, with a subsequent Tukey test ($P \leq 0.05$) to compare the means. For the multivariate analysis, a residual covariance matrix was obtained and as a measure of dissimilarity, the generalized distance of Mahalanobis (D^2) was estimated; based on this, it was possible to apply the Tocher and UPGMA grouping method. The cut-off point of the dendrograms generated by the hierarchical methods, as well as the number of groups were estimated based on the method of Mojena (1977) based on the relative size of the levels of fusions (distances) in the dendrogram. The Singh criterion was also applied to quantify the relative contribution of these characteristics to the genetic divergence. Finally, the canonical correlation was also used. The analyses were performed using the Genes computational program (Cruz, 2013).

Results

From the 20 genotypes used, only 10 reached physiological maturity. The germination index of the seeds is shown in Table. 1. The genotypes that had the highest germination percentage were M8867RR, M8766RR, SYN1059 RR, TMG1175RR, UFVS: 2012 and 2005. The genotypes M8527RR and M8644IPRO had the lowest percentage of germination (6%).

According to the analysis of variance by the F test at 5% probability, a significant difference was observed for leaf

TABLE 1. Seed size and germination index of 20 soybean genotypes.

Genotypes	Seed size	% germination
UFVS Berilo RR	Big	26.60
UFVS 2013	Big	20.00
M8867RR	Big	33.30
UFVS 2012	Medium	33.30
UFVS 2010	Big	20.00
M8766RR	Medium	33.30
M9144RR	Big	20.00
UFVS 2005	Big	33.30
SYN1059 RR	Big	33.30
UFVS QUARTZO	Big	20.00
M-SOY 9350	Big	13.30
ST 920 RR	-	13.30
UFV - 16 (Capinópolis)	-	13.30
UFVS 2001	-	13.30
UFVS 2008	-	20.00
TMG1175RR	Medium	33.30
M8372IPRO	-	13.30
M8527RR	-	6.60
M8644IPRO	Medium	6.60
TOPAZIO RR	-	13.30

Fields filled with "-" did not reach the breeding stage and had no seeds to be quantified.

width, flower diameter, and seed width (Tab. 2). For hypocotyl length, leaf length, plant height, and seed length, no significant difference was observed.

The characters that had heritability values (h^2) above 60% were leaf width, flower diameter, and seed width, which indicates that phenotypic selection can be performed with

TABLE 2. Summary of the ANOVA for the seven traits evaluated in ten soybean genotypes.

SV	MQ							
	DF	HL	LW	LH	PH	FD	SL	SW
Treatments	9	2.82ns	1.41*	1.54ns	331.16ns	1.72*	0.67ns	0.74*
Residues	20	2.25	0.43	0.81	147.91	0.50	0.39	0.29
CV	-	17.25	25.94	28.06	26.04	13.65	9.06	12.33
CV_F	-	0.93	0.47	0.51	110.38	0.57	0.22	0.24
CV_E	-	0.75	0.14	0.27	49.30	0.16	0.12	0.09
CV_G	-	0.18	0.32	0.24	61.08	0.40	0.09	0.15
h^2	-	19.95	70.00	47.21	55.33	70.69	42.24	61.18
CVg (%)	-	4.97	22.70	15.32	16.73	12.24	4.47	8.93
CV_G/CV_E (%)	-	0.24	2.28	0.88	1.24	2.50	0.75	1.66

SV - source of variation; MQ - medium square; DF - degree of freedom; HL - hypocotyl length; LW - leaf width; LH - leaf length; PH - plant height; FD - flower diameter; SL - seed length; SW - seed width; CV - coefficient of variation; CV_F - phenotypic variation; CV_E - environmental variation; CV_G - genotypic variation; h^2 - heritability coefficient; CVg - genetic coefficient of variation; CV_G/CV_E - ratio between genotypic variation and environmental variation; ns - not significant and ** significant at 5% probability by the F test.

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higher accuracy in relation to the other analyzed variables. This can be confirmed by the values of CV_G/CV_E, above 1 for the same characters.

The means of the characteristics were analyzed by the Tukey test ($P \leq 0.05$) (Tab. 3). The highest averages in these characteristics were obtained by five genotypes, M8867RR, SYN1059 RR, UFVS: Berilo RR, 2013 and 2012. The values obtained for leaf width ranged from 1.83 to 3.63 cm. Based on this characteristic the most recommended genotype was SYN1059 RR. For flower diameter, the values ranged from 3.91 to 6.26 cm, and the superior genotypes were M8867RR, UFVS: Berilo RR and 2012. For seed width, the values ranged from 3.71 to 5.27 cm, and the genotype that obtained the highest value was UFVS 2013.

TABLE 3. Mean of three traits evaluated in ten soybean genotypes according to the Tukey test.

Genotypes	Traits		
	LW	FD	SW
UFVS Berilo RR	1.83b	6.26a	4.25ab
UFVS 2013	1.86b	4.74ab	5.27a
M8867RR	2.20ab	6.24a	4.76ab
UFVS 2012	2.60ab	5.74a	3.71b
UFVS 2010	3.50ab	5.14ab	4.22ab
M8766RR	1.93b	4.53ab	3.73b
M9144RR	2.00b	5.18ab	3.92ab
UFVS 2005	3.16ab	4.75ab	4.40ab
SYN1059 RR	3.63a	3.91b	4.77ab
UFVS QUARTZO	2.50ab	5.57ab	4.47ab

LW - leaf width; FD - flower diameter; SW - seed width. Means followed by the same letter in the column do not differ at 5% probability according to the Tukey test.

The Tocher's clustering method, from the generalized distance of Mahalanobis (1936), makes it possible to divide the genotypes into three genetically distinct groups (Tab. 4).

TABLE 4. Grouping of ten soybean genotypes evaluated for seven traits established by the Tocher method, using the generalized Mahalanobis distance as a measure of dissimilarity.

Groups	Genotypes
1	UFVS 2012; UFVS 2005; UFVS 2010; M9144RR; UFVS QUARTZO; M8867RR
2	UFVS Berilo RR; UFVS 2013; M8766RR
3	SYN1059 RR

In group 1, six genotypes that show genetic similarity (60% of the total) were included. Group 2 was composed of three genotypes with genetic similarity (30% of the total). Group 3 comprised only one genotype (10% of the total), indicating that it has genetic dissimilarity with the others.

A co-phenotype correlation coefficient of 0.76 was obtained using the Mahalanobis dissimilarity matrix to generate the dendrogram by the UPGMA method. This correlation confirms an adequate relation between the distance matrix and the generated dendrogram (Fig. 1). Using the Mojena method, it was possible to obtain two groups: one with the genotypes M8766RR, M9144RR, M8867RR, UFVS: Berilo RR, 2010, 2012, 2005, 2013 and QUARTZO; and another with only the SYN1059 RR genotype.

In both the Tocher and UPGMA methods, the SYN1059 RR genotype was isolated in a different group from the others, which indicates a significant genetic dissimilarity when compared to the other genotypes tested.
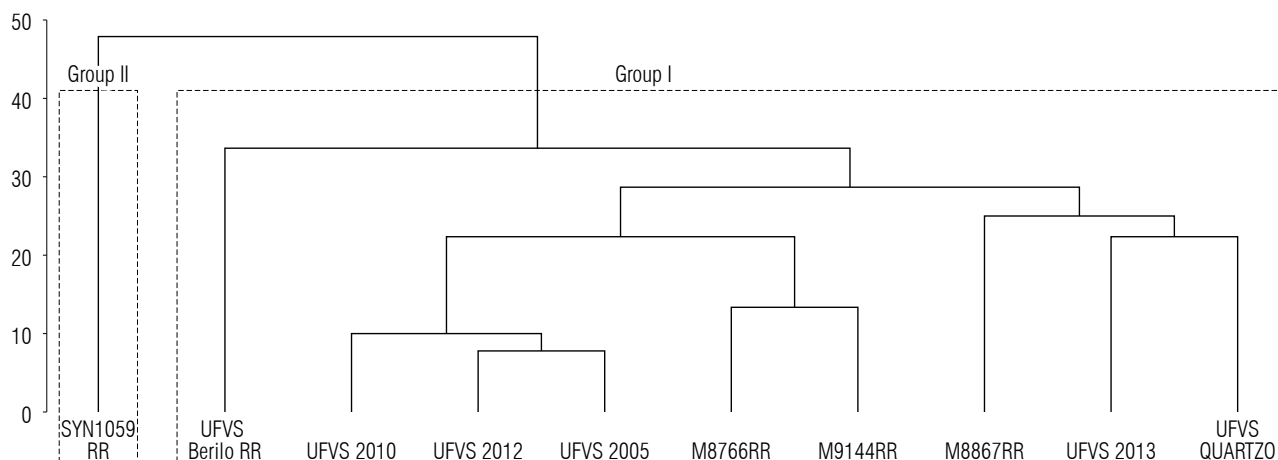
FIGURE 1. Dendrogram of the analysis of ten soybean genotypes by the UPGMA method obtained from the generalized distance of Mahalanobis, generated with seven characteristics. Coefficient of correlation (r) = 0.76.

From the Singh method (1981), which consists of the relative contribution of the characters to the diversity (value in %), based on the generalized distance of Mahalanobis, it was observed that the leaf width (35.45%) was the characteristic that contributed the most to the data variability, followed by the characteristics flower diameter (19.13%) and plant height (18.34%) (Tab. 5).

TABLE 5. Relative contribution of seven characteristics to the genetic dissimilarity of 10 soybean genotypes according to the method proposed by Singh (1981).

Traits	Value in %
HL	8.08
LW	35.45
LH	2.08
PH	18.34
FD	19.13
SL	8.51
SW	8.41

HL - hypocotyl length; LW - leaf width; LH - leaf length; PH - plant height; FD - flower diameter; SL - seed length; SW - seed width.

In order to analyze the canonical correlation, the first three canonical pairs had a genetic contribution of 90.14% (Tab. 6), thus permitting the presentation of the genotypes in a graphical dimension, where six groups were observed (Fig. 2), different from the cluster analyses mentioned above.

TABLE 6. Canonical correlation of the relative characteristics evaluated in the 10 soybean genotypes.

Traits	Eigenvalues %	Accumulated %
HL	48.02	48.02
LW	21.95	69.97
LH	20.17	90.14
PH	4.92	95.07
FD	2.92	98.02
SL	1.59	99.61
SW	0.38	100.00

HL - hypocotyl length; LW - leaf width; LH - leaf length; PH - plant height; FD - flower diameter; SL - seed length; SW - seed width.

Discussion

For the selection of promising soybean genotypes, those with significant values of leaf width, flower diameter, and seed size are of interest since they contribute to a higher photosynthetic surface, pod size, and physiological quality of the plant, which are associated with higher yields.
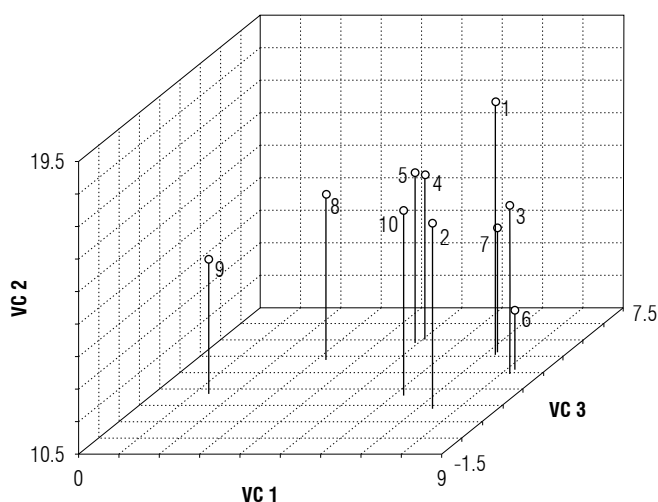
FIGURE 2. Analysis of the canonical correlation by the graphic dispersion. 1) UFVS Berilo RR; 2) UFVS 2013; 3) M8867RR; 4) UFVS 2012; 5) UFVS 2010; 6) M8766RR; 7) M9144RR; 8) UFVS 2005; 9) SYN1059 RR; 10) UFVS QUARTZO.

Given that the main commercial product of soybeans is the grain, it should be pointed out that the size of the seed affects its physiological quality, as mentioned by Pádua *et al.* (2010). Thus, the selection of larger seeds is indicated, because these will theoretically originate more vigorous plants. Therefore, the genotypes M8867RR, SYN1059 RR and UFVS 2005 are recommended based on the superiority of this characteristic (Tab. 1).

Another important attribute for selection is the existence of genetic variability. According to Martins *et al.* (2012), the characteristics that have significant differences according to the F test indicate the existence of genetic variability (Tab. 2). According to Domiciano *et al.* (2015), the values of the CV_G/CV_E ratio above 1 indicate that the plant breeding of the species through morphological characteristics is possible to be carried out through phenotypic selection of promising genotypes.

The multivariate analysis is a tool widely used in genetic divergence studies, as evidenced by Santos *et al.* (2011) and Almeida *et al.* (2011) in studies with soybean. This analysis offers the possibility of using various techniques, such as the Tocher grouping, or UPGMA dendogram the Singh method, and the canonical correlation. Viana *et al.* (2009) mentioned that the characters used in these analyzes allow the identification of genotypes with higher agronomic limits, identifying superior materials for breeding programs.

According to Martins *et al.* (2012), it is not viable to cross varieties contained in the same group as in the Tocher

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method since they present significant genetic similarity, which theoretically reduces the obtaining of superior materials. It would be recommended to cross genotypes that are in different groups, which increases the genetic dissimilarity and facilitates obtaining superior materials. However, besides the genetic divergence, it is necessary to observe mainly the values of heritability and variances.

For the Tocher grouping, the UPGMA method and the graphic dispersion, showed a difference in the formation and distribution of the genotypes within the groups. According to Azevedo *et al.* (2013), it is possible that this occurs since there is a difference between the accuracy and grouping criteria of the methods.

Based on the Singh test (Tab. 5), it is possible to notice the importance of the leaf width characteristic, since it contributes to genetic divergence and is closely related to the photosynthetic capacity of assimilatory tissues; thus, a higher leaf width may increase energy synthesis and finally improve the productive use (Petter *et al.*, 2016)

Conclusions

The genotypes M8766RR, M8867RR, SYN1059 RR, UFVS Berilo RR, and UFVS 2012 showed the best values for leaf width, plant height, and flower diameter, having great potential to be cultivated in the target region, and are indicated for the continuity of the soybean plant breeding program.

The crosses between these genotypes are indicated as promising to obtain hybrids, since they have genetic variability and higher averages in the characteristics that contributed the most to the genetic divergence, such as leaf width, flower diameter, and seed width.

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