



Genetic diversity and responses of soybean genotypes to water deficit induced by PEG 6000¹

Isabella de Castro Silveira² , Polianna Alves Silva Dias^{2,3*} , Osvaldo Toshiyuki Hamawaki² , Luiza Amaral Medeiros² , Sílvia Barbosa Ferreira² , Ana Paula Oliveira Nogueira²

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ABSTRACT

Water stress is one of the limiting factors for obtaining maximum yield in soybean, which makes the identification of tolerant genotypes an important approach in breeding programs. The objectives of this work were evaluate soybean genotypes in conditions of water deficit, determine traits that allow the identification of genotypes tolerant to water deficit, and suggest promising crosses. Sixteen soybean genotypes were submitted to two osmotic potentials (0.0 MPa and -0.2 MPa) induced by PEG 6000 and the traits of germination and growing were evaluated. Genetic dissimilarity analysis was performed. There was genetic variability among genotypes for all traits, and significant interaction for root length, shoot and total fresh matter and dry root matter. Based on root length, it was possible to discriminate genotypes tolerant to water deficit. The cultivars BRS 7270 IPRO, TMG 2158 IPRO, UFUS Tikuna and UFU_P32 showed higher root length and stood out for dry root, fresh shoot and total fresh matter under water stress conditions and are indicated as promising parents in crosses.

Keywords: *Glycine max*; multivariate analysis; polyethylene glycol; water stress.

INTRODUCTION

Soybean (*Glycine max* L. Merrill) is one of the most important crops in the world, being a source of edible oil and protein in human and animal nutrition. In Brazil it is one of the main agricultural species, occupying a great extension of cultivation and expressive importance in Brazilian exports. In 2023 Brazilian harvest there was a record production of over 154 million tons of the grain, making Brazil the largest soybean producer in the world (Conab, 2023).

One of the major challenges to grain production has been the losses resulting from the water deficit. Especially for soybeans, whose agricultural factor of greatest impact is

drought stress, which severely affects its quality and grain yield (Morando *et al.*, 2014; Wang *et al.*, 2022). On the other hand, the demand for food in the face of population growth has intensified, bringing to breeders challenges to obtain increasingly productive plants in conditions of water restriction (Cavatte *et al.*, 2011). Several studies have been conducted to evaluate the morphophysiological behavior of soybean plants in relation to water deficit as a strategy for selecting genotypes that are more resistant to stress (Vieira *et al.*, 2013; Fenta *et al.*, 2014; Basal *et al.*, 2020). In addition to these strategies, the use of polyethylene glycol (PEG) in the study and identification of water stress tolerant

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² Universidade Federal de Uberlândia, Uberlândia, MG, Brazil. isabellacs10@hotmail.com; polianna.dias@ifgoiano.edu.br; osvaldohamawaki@yahoo.com.br; luizaamaral.m@gmail.com; ferreirasb@hotmail.com; ana.paula@ufu.br

³ Instituto Federal de Educação, Ciência e Tecnologia Goiano, Campus Urutai, Urutai, GO, Brazil. polianna.dias@ifgoiano.edu.br

*Corresponding author: polianna.dias@ifgoiano.edu.br

genotypes is an important tool in the selection of promising genotypes in the early stages of plant development and in a short evaluation period (Basal *et al.*, 2020; Esan *et al.*, 2023). According to Dantas *et al.* (2017), in the soybean culture, conducting a germination test with a PEG 6000 solution at -0.2 MPa is the most efficient way to identify the genetic variability between genotypes.

Following the selection of tolerant genotypes, it is necessary to identify divergent parents with agronomic traits of interest to obtain superior hybrids in segregating populations. To that end, genetic diversity studies have been widely used by breeders (Vieira *et al.*, 2013; Cantelli *et al.*, 2016; Dantas *et al.*, 2017). Among the techniques, multivariate analyses, such as principal components, cluster analyses and canonical variables, can be applied in diversity studies, turning easier with the advantage of being able to unify multiple information from a set of variables of interest, which facilitates the process of selecting parents (Cruz *et al.*, 2014).

In this sense, the objectives of this work were to evaluate the responses of soybean genotypes in conditions of water deficit induced by PEG 6000; determine traits that allow the identification of soybean genotypes that are tolerant to water deficit; identify soybean genotypes tolerant of water deficit; and selecting promising parents for crosses to obtain water deficit tolerant soybean populations.

MATERIAL AND METHODS

The experiment was carried out at the Seed Analysis Laboratory of the Federal University of Uberlândia (UFU), in Uberlândia-MG. Ten soybean cultivars (TMG 801, TMG 2158 IPRO, BRS 7270 IPRO, NA 5909 RG, NS 6909 IPRO, UFUS Tikuna, UFUS 7415, UFUS 7401, BMX Desafio RR, BRSMG 68) and six elite lines of UFU's Soybean Breeding Program (UFU_P18, UFU_P39, UFU_P34, UFU_P2, UFU_P32, UFU_P10) were evaluated. The 16 soybean genotypes, potential parents in breeding programs for presenting favorable agronomic traits, were submitted to two water availability conditions (0 MPa and -0.2 MPa) in which the osmotic potentials were obtained with the addition of polyethylene glycol 6000 (PEG) in the solutions. The experiment consisted of a 2x16 factorial, the first factor corresponding to the two osmotic potentials and the second factor to the 16 soybean genotypes, evaluated in a complete randomized block experimental design with four replications.

The amount of PEG 6000 solubilized in deionized water to obtain water tensions was determined according

to Teixeira *et al.* (2008) based on the following equation:

$$\Psi_{os} = -(1.18 \times 10^{-2}) C - (1.18 \times 10^{-4}) C^2 + (2.67 \times 10^{-4}) CT + (8.39 \times 10^{-7}) C^2$$

in which: Ψ_{os} : osmotic potential (bar); C: osmotic agent concentration (grams of PEG 6000 L⁻¹ of water); T: temperature (°C).

After preparing the solutions with PEG 6000, the *Germitest* sheets were soaked in their respective solutions. The plots consisted of rolls formed by three sheets of *Germitest* paper, two of which were overlapped and served as a support and the third was used to cover the seeds, preventing them from falling. The experiment was divided into two stages, being a seed germination test and a seedling growth test. For the germination test, 50 seeds were distributed evenly throughout the length of the *Germitest* leaves, while in the seedling growth test, 20 seeds were distributed in the central portion of the leaves, with the micropyles facing downwards. The treatments were placed in plastic bags so that a microenvironment was formed, preserving only the water potential to be tested in that plot.

Five days after at a constant temperature of 25 °C, the following traits were evaluated, according to the Regras para Análise de Sementes (RAS) (Mapa, 2009). Based on the germination test (GERM, %) they were counted the normal (seedlings with root, shoot and cotyledons fully developed and healthy) and abnormal seedlings (unable to continue their development). The following traits were evaluated only in normal seedlings and excluding the cotyledons. Seedlings total length (TL), root length (RL) and shoot length (SL) were measured (cm) with a millimeter rule. After measuring the length, all normal seedlings were divided into shoot and root parts and the matter of the fresh shoot (MFS), fresh root (MFR) and total fresh seedling (MFT) were determined (g). After that, the matter of dry shoot (MDS), dry root (MDR) and total dry matter of the seedlings (MDT) were determined (g) after drying in a forced air circulation oven for a period of 24 hours at 80 °C.

After verifying the normality of the data and homogeneity of the variances, the data were submitted to analysis of variance, and when the F test was significant ($p \leq 0.05$), the averages were grouped by the Scott-Knott test. Multivariate analyses were performed to characterize genetic divergence using the Unweighted Pair Group Method with Arithmetic Mean (UPGMA) and the Tocher method, based on the standardized average Euclidean distance; principal component analysis was also performed. The data was

standardized for Principal Components Analysis (PCA) to ensure that traits with different units contributed equally to the analysis. All analyses were performed based on $\alpha = 5\%$.

RESULTS AND DISCUSSION

There was variability between the genotypes for all the evaluated traits, indicating the possibility of selecting the best genotypes to be used as parents in crossings aiming at resistance to water deficit. It was observed significant genotype by osmotic potentials interaction (OP x G) for the traits root length (RL), matter of the fresh shoot (MFS), the total fresh seedling (MFT) and the dry root (MDR), showing that the behavior of the genotypes depends on the applied osmotic potential. The presence of OP x G interaction is reported for several morpho-agronomic traits in soybean under water stress induced by PEG (Dantas *et al.*, 2017; Vieira *et al.*, 2013). The other traits evaluated were influenced by the factors isolated.

There was a reduction in RL, MDR, MFS and MFT under water deficit (-0.2 MPa) when compared to control condition (0.0 MPa) (Table 1). During the initial stages of seedling development there is dependence on the

occurrence of hydrolytic proteins to degrade and use carbohydrates, proteins and lipids reserves. The reduced water supply and the change in protein composition during seed germination under water stress directly influence the biochemical processes related to germination, causing reductions in seedling growth and fresh mass (Swigonska & Weidner, 2013).

It was observed the formation of two groups for RL in the potential 0.0 MPa, with ten genotypes in the first group ranging from 8.09 cm (UFUS Tikuna) to 9.20 cm (BRSMG 68) (Table 1). For the potential -0.2 MPa three groups were formed, with the group with the highest RL under water restriction averaging from 5.14 cm (UFUS 7401) to 6.71 cm (BRS 7270 IPRO). Five genotypes showed the highest MDR in the potential 0.0 MPa, with averages ranging from 0.07 g (NS 6909 IPRO) to 0.09 g (NS 5909 RG, BRSMG 68 and BRS 7270 IPRO). At an osmotic potential of -0.2 MPa, the seven genotypes with the highest MDR ranged from 0.06 g (TMG 801) to 0.08 g (NS 6909 IPRO, BRS 7270 IPRO, TMG 2158 IPRO and NS 5909 RG).

The reduction in soybean RL and MDR due to water restriction has been extensively reported in soybean (Fenta

Table 1: Root length (RL, cm), matter of dry root (MDR, g), matter of fresh shoot (MFS, g) and total fresh matter (MFT, g) of seedlings of sixteen soybean genotypes submitted to two osmotic potentials induced by PEG 6000

Genotypes	RL (cm)		MDR (g)		MFS (g)		MFT (g)	
	Osmotic potentials (MPa)							
	0.0	-0.2	0.0	-0.2	0.0	-0.2	0.0	-0.2
BRSMG 68	9.20Aa	5.37Ba	0.09Aa	0.05Bb	2.77Ab	0.38Ba	3.88Ab	0.95Ba
NA 5909 RG	8.96Aa	4.89Ba	0.09Aa	0.08Aa	2.52Ac	0.27Ba	3.54Ab	0.79Ba
UFU_P39	8.79Aa	4.22Bb	0.05Bb	0.07Aa	2.02Ac	0.26Ba	2.67Ac	0.65Ba
UFUS 7415	8.76Aa	4.28Bb	0.08Aa	0.05Bb	2.51Ac	0.30Ba	3.48Ab	0.61Ba
UFU_P32	8.69Aa	5.98Ba	0.06Ab	0.06Ab	2.82Ab	0.32Ba	3.57Ab	0.99Ba
NS 6909 IPRO	8.58Aa	5.40Ba	0.07Aa	0.08Aa	2.27Ac	0.48Ba	3.09Ac	1.06Ba
BRS 7270 IPRO	8.49Aa	6.71Ba	0.09Aa	0.08Aa	3.72Aa	0.57Ba	4.71Aa	1.16Ba
UFUS 7401	8.23Aa	5.14Ba	0.06Ab	0.07Aa	1.98Ac	0.31Ba	2.73Ac	0.87Ba
TMG 2158 IPRO	8.13Aa	4.81Ba	0.07Ab	0.08Aa	3.46Aa	0.26Ba	4.43Aa	0.72Ba
UFUS Tikuna	8.09Aa	5.86Ba	0.05Ab	0.06Ab	1.99Ac	0.41Ba	2.62Ac	0.74Ba
UFU_P2	7.80Ab	5.53Ba	0.07Ab	0.05Ab	2.26Ac	0.44Ba	2.90Ac	0.83Ba
TMG 801	7.59Ab	4.12Bb	0.06Ab	0.06Aa	2.90Ab	0.23Ba	3.81Ab	0.63Ba
UFU_P10	7.58Ab	4.58Bb	0.05Ab	0.05Ab	1.86Ac	0.15Ba	2.50Ac	0.53Ba
BMX Desafio RR	7.39Ab	3.17Bc	0.06Ab	0.05Ab	2.07Ac	0.26Ba	2.67Ac	0.47Ba
UFU_P34	7.14Ab	4.15Bb	0.05Ab	0.04Ab	1.86Ac	0.34Ba	2.43Ac	0.66Ba
UFU_P18	6.72Ab	2.65Bc	0.06Ab	0.04Ab	2.45Ac	0.25Ba	3.06Ac	0.54Ba
Average	8.13	4.80	0.07	0.06	2.47	0.33	3.26	0.76

Average followed by the same letters, lower case in the columns and upper case in the rows, belong to the same group by the Scott Knott test ($p < 0.05$).

et al., 2014; Dantas *et al.*, 2017; Basal *et al.*, 2020; Esan *et al.*, 2023). The reduction in RL and, consequently, in MDR, occurs due to several processes related to growth, cell elongation and wall synthesis are extremely sensitive to water deficit and the interference in these processes causes a decrease in cell expansion, which affects the seedling growth process (Shaheen *et al.*, 2016).

Several studies have considered root length to be the most sensitive trait for differentiating the physiological quality of seeds, because drought-tolerant genotypes emit roots even in adverse conditions, allowing their separation from sensitive genotypes, which only emit roots under ideal growing conditions (Echer *et al.*, 2010). Recently, Esan *et al.* (2023) observed that the drought stress simulated by PEG 6000 reduced the average root diameters and the number of lateral roots of all 20 accessions evaluated. They also affirmed that developing longer roots is a mechanism to resist water deficit by reaching water in the deep.

Regarding MFS and MFT under potential 0.0 MPa three groups were formed, with emphasis on the cultivars TMG 2158 IPRO and BRS 7170 IPRO in both traits, whose averages were 3.46 and 3.72 g of MFS and 4.43 and 4.71 g for MFT, respectively (Table 1). Similar results of reduction in matter of fresh seedling under water restriction are reported for soybeans (Vieira *et al.*, 2013).

The low availability of water reduces the speed of physiological processes, leading the seedlings to have less development, which results in shorter length and less accumulation of fresh and dry biomass, however, seedlings that have tolerance to water deficit have an increase in these variables, such as the UFU_P39 line that showed an increase in MDR (Table 1). The genotypes NA 5909 RG, NS 6909 IPRO, BRS 7270 IPRO, UFUS 7401, TMG 2158 IPRO and TMG 801 also showed higher MDR under water deficit and showed the same behavior without stress, indicating the lower sensitivity of these genotypes to water stress.

They were observed reductions under water deficit (-0.2 MPa) for the percentage of germination (GERM), shoot (SL) and total (TL) length, matter of fresh root (MFR), of dry shoot (MDS) and of total dry soybean seedling (MDT) (Table 2). The ranking of genotypes in the groups were similar for all traits, showing similar morphological responses of the cultivars, with the exception of MDS, in which there was the formation of a single group. The cultivars BRS 7270 IPRO, NS 6909 IPRO and TMG 2158 IPRO stood out for presenting greater GERM, SL, TL, MFR and MDT,

regardless of the applied osmotic potential. In contrast, the lines UFU_P18, UFU_P34 and UFU_P10 showed the worst performance for the evaluated traits.

Germination is a crucial stage in the development of soybean and is strongly affected by water supply, the greater the water restriction, the lower the germination percentage (Basal *et al.*, 2020). Under water stress, changes in metabolism occur and the activity of enzymes involved in germination decreases, which reduces the percentage of seed germination (Muscolo *et al.*, 2014).

Following germination, seedling growth occurs due to cell differentiation, divisions and growth, which are also negatively affected by the water deficit. Under water deficit conditions, there is a reduction in turgor pressure, which causes a reduction in the rate of cell elongation (Shaheen *et al.*, 2016), as well as the modification of the protein profile (Swigonska & Weidner, 2013), also reduces photosynthesis, changes the cell wall structure and alters the biosynthesis and signal transduction of plant hormones (Wang *et al.*, 2022).

The characterization of soybean cultivars regarding phenotypic responses to abiotic stresses, such as water deficit, is essential to provide information on the potential of each genotype for breeding purposes. The use of multivariate analyses, including genetic divergence studies, is useful in parent selection phase. Soybean is a crop with narrow genetic base (Rodrigues *et al.*, 2017), therefore, the analysis of divergence by reliable methods is considered even more important, in order to obtain the formation of really contrasting clusters and efficient selection of parents in crosses. The genetic distance between soybean genotypes ranged from 0.08 to 7.09 for the potential 0.0 MPa (above the diagonal), indicating the presence of good genetic variability (Table 3).

The longest distance was observed between the line UFU_P34 and the cultivar BRS 7270 IPRO, while the shortest distance was observed for lines UFU_P10 and UFU_P34 (Table 3). For the -0.02 MPa potential, the genetic distance ranged from 0.13 to 0.80, lower than that observed under normal conditions, suggesting less dissimilarity between the genotypes under water restriction. The greatest distance found was between the line UFU_P18 and the cultivar BRS 7270 IPRO, and the shortest between cultivars TMG 2158 IPRO and NA 5909 RG under water deficit.

After obtaining the dissimilarity matrix, clusters were analyzed using the UPGMA method for the nine traits eval-

Table 2: Seed germination percentage (GERM, %), shoot length (SL, cm), total length (TL, cm), fresh root matter (MFR, g), dry shoot matter (MDS, g), total dry matter (MDT, g) of seedlings of sixteen soybean genotypes submitted to the osmotic potential induced by PEG 6000

Genotypes	GERM (%)	SL (cm)	TL (cm)	MFR (g)	MDS (g)	MDT (g)
BRS 7270 IPRO	93.75a	3.87a	11.47a	0.79a	0.15a	0.24a
NA 5909 RG	88.67a	3.04b	9.96a	0.77a	0.12a	0.21a
UFU_P32	83.33a	3.22b	10.55a	0.71a	0.12a	0.18b
TMG 2158 IPRO	82.33a	3.57a	10.04a	0.71a	0.14a	0.21a
NS 6909 IPRO	81.75a	3.51a	10.50a	0.70a	0.15a	0.23a
UFU_P39	81.17a	3.15b	9.66a	0.52b	0.09a	0.15b
UFUS 7401	79.92a	2.60b	9.28b	0.66a	0.09a	0.15b
BRSMG 68	78.50a	3.02b	10.31a	0.84a	0.14a	0.21a
BMX Desafio RR	77.00a	2.82b	8.10b	0.40b	0.11a	0.17b
UFUS Tikuna	71.83b	3.74a	10.72a	0.48b	0.10a	0.15b
UFU_P2	71.50b	3.51a	10.17a	0.52b	0.10a	0.16b
UFU_P10	66.75b	2.71b	8.79b	0.51b	0.08a	0.13b
UFU_P18	62.75b	2.73b	7.42b	0.45b	0.10a	0.16b
UFUS 7415	61.75b	2.71b	9.23b	0.64a	0.12a	0.19a
UFU_P34	58.00b	2.85b	8.49b	0.45b	0.09a	0.13b
TMG 801	58.00b	2.84b	8.70b	0.65a	0.15a	0.22a
Potentials (MPa)						
0	84.32A	4.83A	12.96A	0.79A	0.17A	0.23A
-0.2	65.30B	1.41B	6.21B	0.44B	0.07B	0.13B

Means followed by the same letters, lower case between genotypes and upper case letters between potentials, belong to the same group by the Scott Knott test ($p < 0.05$).

Table 3: Genetic dissimilarity matrix based on the standardized average Euclidean distance for 16 soybean genotypes in two osmotic potentials

Genotype	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
UFU_P18		1.84	0.70	0.75	0.95	1.82	3.53	1.67	4.66	2.76	0.26	2.54	1.01	1.72	1.47	0.63
UFU_P39	0.31		1.07	0.57	2.05	1.10	3.18	0.87	4.61	3.04	0.82	2.21	0.60	1.63	0.13	0.68
UFU_P34	0.23	0.28		1.00	2.36	2.61	5.27	2.38	7.09	4.68	0.30	3.80	0.50	2.73	0.86	0.08
UFU_P2	0.47	0.34	0.27		1.04	0.51	2.27	0.58	3.10	1.98	0.38	1.34	0.67	0.94	0.35	0.68
TMG 801	0.44	0.33	0.38	0.48		0.85	1.17	0.63	1.90	0.62	1.17	1.08	1.77	0.66	1.92	1.81
NS 6909 IPRO	0.73	0.52	0.58	0.45	0.43		0.80	0.28	1.67	1.07	1.34	0.46	1.56	0.43	1.07	1.89
BRSMG 68	0.45	0.31	0.29	0.25	0.38	0.41		1.08	0.97	0.83	3.37	0.28	3.30	0.52	3.42	4.16
UFU_P32	0.54	0.34	0.40	0.30	0.47	0.44	0.15		1.63	0.72	1.23	0.86	1.49	0.62	0.94	1.72
BRS 7270 IPRO	0.80	0.56	0.63	0.43	0.57	0.21	0.41	0.40		0.50	4.83	1.49	5.38	1.96	4.44	6.06
TMG 2158 IPRO	0.49	0.20	0.39	0.32	0.34	0.38	0.32	0.32	0.42		2.89	1.25	3.59	1.25	2.92	3.85
BMX Desafio RR	0.19	0.28	0.24	0.45	0.30	0.63	0.44	0.53	0.72	0.41		2.34	0.49	1.54	0.62	0.16
NA 5909 RG	0.50	0.22	0.41	0.38	0.28	0.35	0.29	0.30	0.40	0.13	0.41		2.01	0.13	2.40	2.88
UFUS 7401	0.44	0.23	0.34	0.34	0.31	0.40	0.16	0.19	0.43	0.25	0.40	0.17		1.26	0.73	0.24
UFUS 7415	0.26	0.24	0.18	0.36	0.24	0.54	0.31	0.41	0.60	0.36	0.15	0.33	0.28		1.83	1.95
UFUS Tikuna	0.55	0.37	0.36	0.14	0.50	0.45	0.35	0.38	0.43	0.30	0.50	0.39	0.40	0.43		0.60
UFU_P10	0.24	0.24	0.23	0.39	0.43	0.68	0.36	0.40	0.71	0.40	0.29	0.41	0.34	0.25	0.45	

Values above the diagonal refer to the potential 0.0 MPa, and values below the diagonal refer to the potential -0.2 MPa. Euclidean distance obtained from the average of nine characters of seedlings from 16 soybean genotypes submitted to two osmotic potential.

uated under 0.0 MPa potential (Figure 1A) and -0.2 MPa (Figure 1B). For the 0.0 MPa potential, five distinct groups were formed, in which the cultivar TMG 801 remained in an isolated group, being considered distinct from the others (Figure 1A). Under water deficit (-0.2 MPa), the formation of six distinct groups was observed (Figure 1B). The cultivar TMG 801 remained in an isolated group, reinforcing its genetic dissimilarity from the others. The lines UFU_P34, UFU_P18 and UFU_P10 and the cultivar BMX Desafio RR remained in the same groups under conditions of control and stress, such as the UFU_P2 line and UFUS Tikuna cultivar, which shows the genetic proximity between these genotypes and similar behavior under normal and water stress conditions. Vale *et al.* (2012) used a similar methodology for the evaluation and classification of bean genotypes in tolerant and sensitive to water deficit for use in crossing blocks. The use of the Mahalanobis distance and the UPGMA method made it possible to form clusters and discriminate genotypes, facilitating the identification of the most tolerant to water deficit.

In addition to the hierarchical clustering methods, optimization methods are also used, such as the Tocher

method. It was observed that the genotypes were separated into seven groups by the Tocher method for both osmotic potentials and the results were similar to the UPGMA method. In both osmotic potentials, the cultivar TMG 801 again remained in an isolated group, while UFU_P2 and UFUS Tikuna (Group III at 0.0 MPa potential and Group II at -0.2 MPa potential) and UFU_P34 and BMX Desafio RR (Group I at 0.0 MPa potential and Group IV at -0.2 MPa potential) were placed in the same groups in both methods, confirming the genetic proximity between these genotypes and similar behavior in both water conditions. However, there were exceptions such as the cultivar UFUS 7415, which varied between groups in both potentials and methods.

In general, the Tocher and UPGMA methods were in agreement, since there was a relative coincidence in the classification of both methods. Similar results between cluster using Tocher and UPGMA methods have been observed for soybeans (Cantelli *et al.*, 2016; Oliveira *et al.*, 2017). The similar clustering between the methods provides a good interpretation of the information regarding the genotypes and the safe selection of parents to form

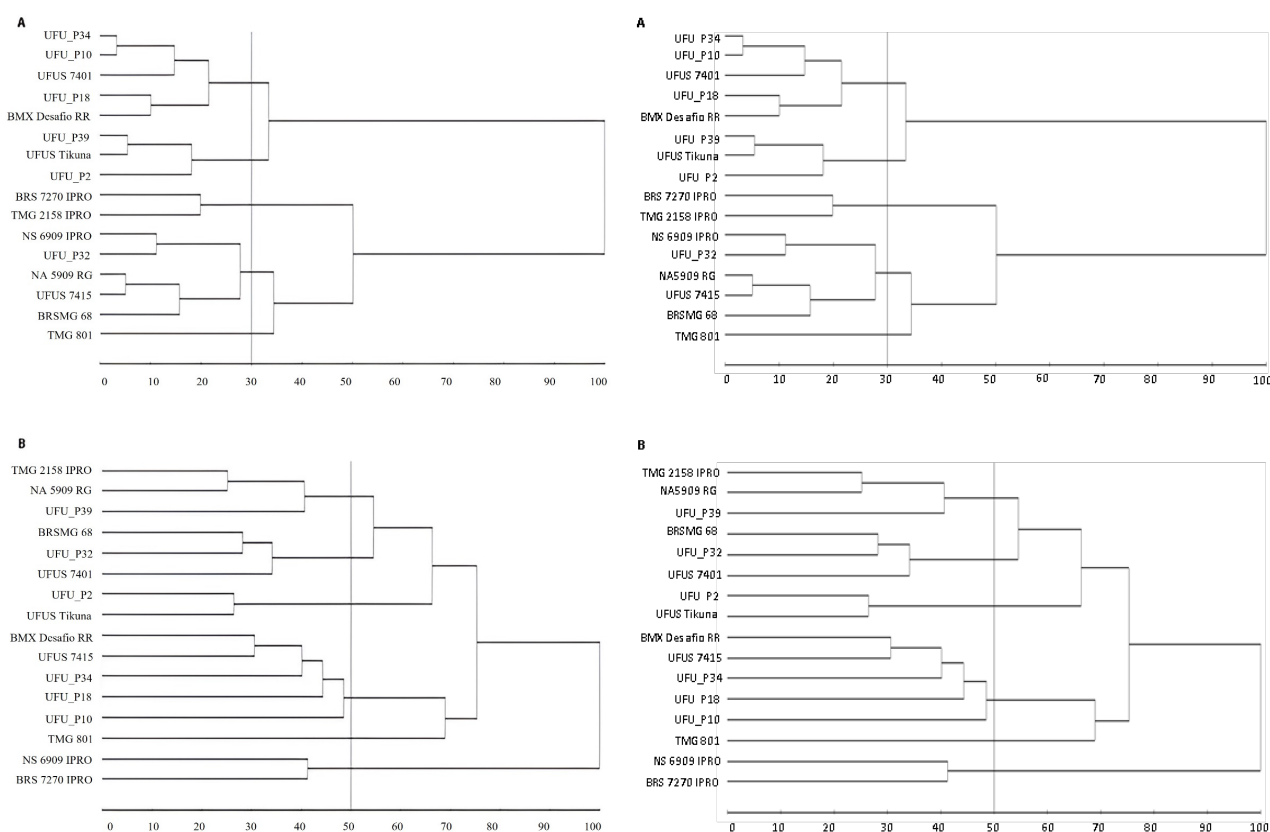


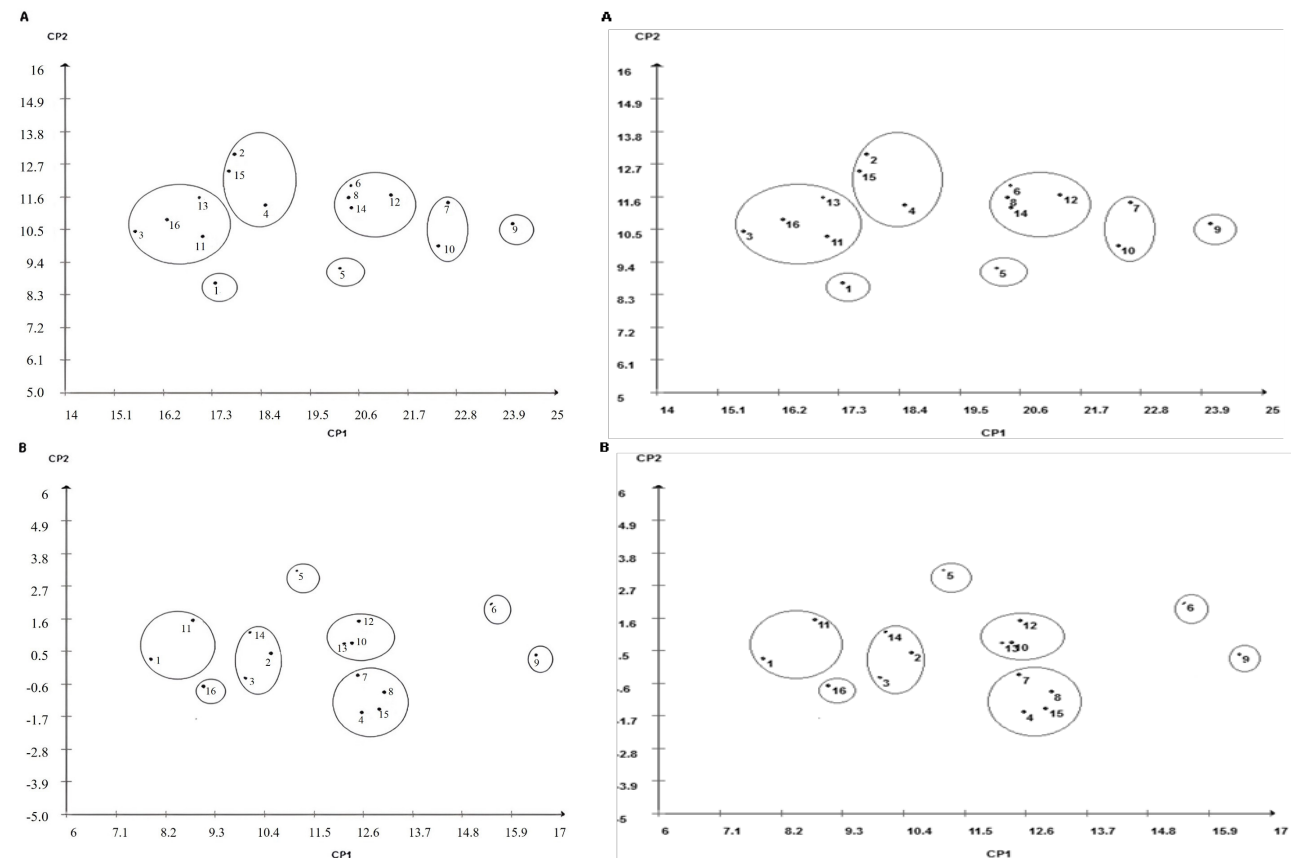
Figure 1: Dendrogram of the analysis of 16 soybean genotypes using the UPGMA (Unweighted Pair Group Method with Arithmetic Mean) obtained from the standardized average Euclidean distance for nine seedling traits under 0.0 Mpa (A) and -0.2 MPa (B) osmotic potential.

crossing blocks.

The cluster techniques are efficient in establishing similarity groups, however, principal components analysis allows visualizing the relative distance between genotypes. The PCA analysis was performed by combining the original variables SL, RL, TL, MFS, FRM, TFM, MDS, MDR and MDT. The first two components of PCA explained 84.00% and 77.61% of the total variation for the potentials of 0.0 MPa and -0.2 MPa, respectively. The formation of seven groups was observed when the genotypes were submitted to the potential 0.0 MPa (Figure 2A). The genotypes UFU_P18, BRS 7270 IPRO and TMG 801 constituted isolated groups. The behavior of the other groups followed similarly to that observed in the UPGMA and Tocher cluster methods, confirming the genetic similarity between these genotypes. The cultivars BRS 7270 IPRO, TMG 2158 IPRO and BRSMG 68 showed greater distance from the group with the lines UFU_P34, UFU_P10, UFUS 7401 and BMX Desafio RR, suggesting a greater genetic dissimilarity between these genotypes. The dissimilarity between them, combined with other traits of interest, allows these genotypes to be considered potential divergent parents in crosses.

For the potential of -0.2 MPa, the formation of eight distinct clusters was observed, which allowed the differentiation of the genotypes, in which TMG 801, UFU_P10, BRS 7270 IPRO and NS 6909 IPRO constituted isolated clusters (Figure 2B), following the pattern observed in 0.0 Mpa potential. The greatest distance was between the cultivar BRS 7270 IPRO and the clusters with the UFU_P18, BMX Desafio RR and UFU_P10 genotypes, reinforcing the genetic dissimilarity between them. In general, the formation of clusters followed a pattern similar to that found for the potential 0.0 MPa, emphasizing the genetic proximity between the genotypes belonging to the same cluster, and the dissimilarity between the different clusters.

The PCA analysis has been used successfully in the study of water stress, as in the characterization of genetic



CP1: Principal component 1; CP2: Principal component 2. Genotypes 1: UFU_P18; 2: UFU_P39; 3: UFU_P34; 4: UFU_P2 5: TMG 801 6: NS 6909 IPRO; 7: BRSMG 68; 8: UFU_P32; 9: BRS 7270 IPRO; 10: TMG 2158 IPRO; 11: BMX Desafio RR; 12: NA 5909 RG; 13:UFUS 7401; 14:UFUS 7415; 15:UFUS Tikuna; 16: UFU_P10.

Figure 2: Graphic dispersion of 16 soybean genotypes using the first two main components obtained with nine seedlings under 0.0 Mpa (A) and -0.2 Mpa (B) osmotic potential.

diversity to identify genotypes with tolerance to water deficit, as well as in determining the best combinations for crosses. Partheeban *et al.* (2017) used this technique to investigate the effects of water stress caused by different concentrations of PEG in emergency traits and growth of corn genotypes, allowing the identification of two water deficit-tolerant genotypes, with the potential to be used in future crosses. This approach has also been used in the study and identification of traits that most contribute to the stability of genotypes under water stress (Giordani *et al.*, 2019) and in the study of the relationship between physiological, biochemical and agronomic variables under stress (Ergo *et al.*, 2018).

Although water restriction affects soybean genotypes differently, it is evident that water deficit causes more or less degree of genetic morphophysiological manifestations. TL and RL were the most important traits in the differentiation of tolerance to water deficit for the cluster of soybean genotypes, contributing respectively with 39.90% and 18.79% in potential 0.0 MPa and 56.00% and 37.81% in potential -0.2 MPa. Teixeira *et al.* (2008), also using PEG to characterize soybean cultivars in terms of water stress, observed that one of the traits that provided greater variability between genotypes was the reduction in the primary root length of the seedlings. It is known that there is a positive relationship between traits related to the root system and tolerance to water deficit, which can be used as an indicative of tolerance in the selection of genotypes (Manavalan *et al.*, 2009; Shaheen *et al.*, 2016).

Genotypic determination coefficients (H^2) above 70% express the proportion of phenotypic variability that is due to genetic variations. The H^2 ranged from 67.9% (matter of dry shoot, MDS) to 85.0% (RL), which indicates a greater influence of the genetic component in these traits, and less environmental interference, providing greater security in the selection of the parents.

CONCLUSIONS

The cultivars BRS 7270 IPRO, TMG 2158 IPRO, UFUS Tikuna, NS 6909 IPRO, NS 5909 RG, BRSMG 68, UFUS 7401 and the lines UFU_P32 and UFU_P2 present superior performance in the traits of shoot, root and total length, under conditions of water deficit induced by PEG 6000.

The root length allowed the differentiation of soybean genotypes under conditions of water deficit induced by

PEG 6000 at -0.2 MPa.

The clusters generated by the different methods demonstrated consistency and allowed the characterization of genetic variability and the identification of parents for crosses.

Based on the analyzes it was possible to indicate the following crosses aiming at tolerance to the water deficit: BRS 7270 IPRO x TMG 2158 IPRO; BRS 7270 IPRO x UFUS Tikuna; BRS 7270 IPRO x UFU_P32; TMG 2158 IPRO x UFUS Tikuna, TMG 2158 IPRO x UFU_P3, TMG 801 x UFU_P32, TMG 801 x UFUS Tikuna, TMG 801 x UFU_P2 and TMG 801 x BRSMG 68.

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