GENETIC DIVERSITY AMONG SOYBEAN GENOTYPES CULTIVATED UNDER TROPICAL CONDITIONS

https://doi.org/10.56238/sevened2024.029-018

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ABSTRACT

Abstract–The edaphic and climatic conditions of the tropical regions of the world constitute a limiting factor for soybean growing, especially through aspects related to the specific photoperiod of the plants. Thus, the aim of this study was to estimate the genetic diversity among 16 Brazilian soybean cultivars [*Glycine max* (L.) Merrill and 76 plant introductions-PIs based on variables related to production and yield components. The multivariate analyses of Mean Euclidean Distance, Principal Component Analysis, and the UPGMA method summarized the traits evaluated in a dataset with smaller dimensions to facilitate identification of superior genotypes. The 16 Brazilian cultivars and 76 PIs were structured in six diversity panels that were consistent and without duplicates. The Brazilian soybean cultivars Sambaíba and 203404 and the PIs 165524, 407744, 205912, 381660, 203400, and 281911 show potential for providing genes related to tolerance to stress from temperatures greater than 30ºC and latitudes below 10ºS.

Keywords: *Glycine max*. Exotic germplasm. Multivariate analyses.

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INTRODUCTION

Soybean, *Glycine max* (L.) Merrill, has high potential and importance through versatility of uses and applications in nutritional and industrial fields. Its grain may be used as food for humans directly or through its by-products (oil and protein), in animal consumption, in formulation of soybean meal-based feeds, and even in production of biofuels, however, extreme climate variations can impact drastically impact production of this legume (GOMES et al., 2014; PANGENI et al., 2017, Pham et al., 2023).

A large part of the surplus in the economic balance of Brazilian agribusiness arises from exports that involve the soybean complex, a situation recurring over decades in Brazil (FIESP, 2020). In the 2023/2024 harvest, Brazil contributed to the production of 147.38 million tons of soybeans from a planted area of 79.82 thousand hectares, an increase of 1.6% or 1.27 million hectares over 2022/2023 (CONAB, 2024). Even though it is the second largest crop to be harvested in the historical series, the average productivity of the crops showed a reduction of 8.2%, going from 4,072 kilos per hectare in the last season to 3,739 kilos per hectare in the current cycle.

Soybean is the main product of the Brazilian grain harvest and the product with the greatest export volume. However, production is affected by the hot and dry climate in various regions of Brazil. In the Northeast region of low latitude and predominantly low altitudes, heat concentration in the air and capacity for retaining heat radiated from the land are greater, and consequently, temperature is higher by the nearness of heated surfaces through predominance of coastal plains, tablelands, and lowland backcountry (STEINKE, 2012).

Advancement of the soybean crop in the Cerrado (Brazilian tropical savanna) and low latitude regions of Brazil is due to incorporation of genes that delay flowering, even under conditions of a photoperiod that induces flowering, thus conferring a long juvenile period trait to soybean cultivars released after the 1990s (SPEHAR, 1994).However, the older cultivars only expressed satisfactory yield performance when grown under temperatures oscillating between 20 and 30ºC (FARIAS; NEPOMUCENO; NEUMAIER, 2007). This approach within soybean breeding programs made it possible to develop cultivars with high stability and adaptability for desirable agronomic traits and especially cultivars with tolerance to abiotic stresses, resistance to herbicides, and high grain yield (PRIOLLI et al., 2004).

Nevertheless, the yield levels of Brazilian soybean cultivars may decline in the long term, because they have a narrow genetic base (WYSMIERSKI; VELLO,2013). The incorporation of exotic germplasm may be a viable alternative to broaden the genetic base of the modern cultivars that are at risk of genetic erosion. Studies of this nature have already occurred for maize and papaya crops (OLIVEIRA et al., 2015, DAMASCENO JUNIOR et al., 2015).

Evaluation of genetic diversity is important in breeding programs through allowing identification of parents suitable for generating a segregating population with genetic variability and possibilities of giving rise to transgressive segregant populations (CRUZ; REGAZZI; CARNEIRO, 2012). Thus, the agromorphological traits can be subjected to multivariate biometric techniques that consider the correlations that exist among numerous variables simultaneously and allow the importance of each trait to be determined (Al-HAD et al., 2017; PERREIRA et al.,2017).

Considering the importance of soybean and the perspective of incorporation of new genotypes in plant breeding programs, Principal Component Analysis was applied, seeking to filter the information considered relevant contained in the original set of variables into datasets of smaller dimensions. Thus, the aim of this study was to estimate the genetic diversity among 16 Brazilian cultivars of soybean [*Glycine max* (L.) Merrill]and 76plant introductions (PIs)through variables related to production and yield components.

MATERIAL AND METHODS

SOYBEAN GENOTYPES AND GROWTH CONDITIONS

The experiment was conducted from February to May 2014 in the experimental area of the Colégio Técnico de Teresina at the Universidade Federal do Piauí – UFPI (lat 05º02’39.95” S;long 42º47’03.70” W, alt 72 masl).A total of 93 genotypes were used, including Brazilian cultivars and 76 PIs coming from the Soybean Breeding Program of the Genetics Department of the Escola Superior de Agricultura "Luiz de Queiroz" - USP/ESALQ (Table 1).

Table 1. Name/registration number and location of origin of the 76 PIs[1] and 16 Brazilian cultivars[2] of soybean [*Glycine max* (L.) Merrill] evaluated under conditions of low latitude and high temperatures. Teresina, PI, Brazil, 2014

GENOTYPE	ORIGIN	GENOTYPE	ORIGIN	GENOTYPE	ORIGIN
212606[1]	Afghanistan	407744[1]	China-Center	341264[1]	Liberia
148260[1]	South Africa	407764[1]	China–South	281898[1]	Malaysia
159097[1]	South Africa	265497[1]	Colombia	284816[1]	Malaysia
170889[1]	South Africa	84910[1]	North Korea	281907[1]	Malaysia
322695[1]	Angola	438301[1]	North Korea	200832[1]	Myanmar
222550[1]	Argentina	90251[1]	South Korea	210352[1]	Mozambique
222546[1]	Argentina	398493[1]	South Korea	166141[1]	Nepal
IAC100[2]	Brazil	153681[1]	El Salvador	209839[1]	Nepal
Paranagoiana[2]	Brazil	315701[1]	USA	259540[1]	Nigeria
A7002[2]	Brazil	Dowling[1]	USA	222397[1]	Pakistan
CD215[2]	Brazil	Bignam[1]	USA	159927[1]	Peru
Conquista[2]	Brazil	417581[1]	USA – S	265491[1]	Peru
Pintado[2]	Brazil	417582[1]	USA – S	159922[1]	Peru
Sambaíba[2]	Brazil	240665[1]	The Philippines	297550[1]	Russia
VMáx[2]	Brazil	281911[1]	The Philippines	341254[1]	Sudan
Potência[2]	Brazil	203400[1]	France	204333[1]	Suriname
Jab00-056/763d[2]	Brazil	164885[1]	Guatemala	204340[1]	Suriname
Jab00-02-2/2j3d[2]	Brazil	189402[1]	Guatemala	205912[1]	Thailand
LQ 1050[2]	Brazil	165524[1]	India	239237[1]	Thailand
LQ 1505[2]	Brazil	133226[1]	Indonesia	210178[1]	Taiwan
LQ 1421[2]	Brazil	148259[1]	Indonesia	283327[1]	Taiwan
LQ 1413[2]	Brazil	Orba(PI471904) [1]	Indonesia	306702[1]	Tanzania
203404[2]	Brazil	215692[1]	Israel	306712[1]	Tanzania
36906[1]	China	229358[1]	Japan	172902[1]	Turkey
79861[1]	China	274454-A[1]	Japan	381660[1]	Uganda
171437[1]	China	274454-B[1]	Japan	381680[1]	Uganda
253664[1]	China	360851[1]	Japan	285095[1]	Venezuela
274507[1]	China	416828[1]	Japan	331793[1]	Vietnam
377573[1]	China	Kinoshita(PI200487) [1]	Japan	331795[1]	Vietnam
90577[1]	China – NE	227687[1]	Japan	417563[1]	Vietnam
427276[1]	China – S	171451[1]	Japan	145079[1]	Zimbabwe

The soil used for conducting the experiment was classified as an *Argissolo Vermelho-Amarelo distrófico*,on flat topography. The seeds were inoculated with bacteria of the *Bradyrhizobium japonicum* species for the purpose of promoting N_2fixation, and they were treated with fungicide (MAXIM XL, 100 ml/100 kg of seed). Base fertilization was performed with NPK (nitrogen, phosphorus, potassium) withthe formulation 5-30-15, according to recommendation from soil analysis for the crop. A fixed sprinkler irrigation system was used, with a 12 × 12 m spacing between sprinkler heads and application rate of 5mm/h. Other management practices followed the conventional growing approach for the soybean crop.

HEAT TOLERANCE SCREENING

Mean annual rainfall where the experiment was conducted was 1.377mm, with more intense rain in March and April, which corresponded to the R1 to R6 development stages. The region has mean annual potential evapotranspiration of 2.973mm, mean annual relative humidity of 69.9%, total annual insolation of 2.625 horas, mean annual temperature of 28ºC, temperature amplitude of 11.5ºC, mean annual photoperiod of 12 hours and 19 min/day, with a minimum of 11 hours and 46 min/dayand maximum of 12 hours and 29 min/day (MEDEIROS, 2006).

During the period in which the experiment was conducted, the mean temperature was 26.09ºC (min–29ºC andmax - 34.3ºC). Mean relative humidity was 83.9%. Daily rainfall amounts ranged from 0 to 77.2 mm (mean accumulated total of 832.5 mm). Insolation ranged from 116 to 2218.5 hours (Total = 728.3 hours, mean 184.58 hour/month) (INMET, 2014).

STATISTICAL ANALYSIS OF THE DATA

An incomplete block experimental design was used, with three replications. Each plot consisted of one 5.0-m length row; between-row distance was 0.50 m.

Twelve (12) descriptors were used for agromorphological characterization: number of days to flowering (NDF),number of days to maturity (NDM),plant height at maturity (PHM),first pod height (FPH),seed-fill period (SFP),pod length (PL), number of pods per plant (NPP),pod weight (PW) in grams,100-seed weight (100SW) in grams,lodging (LG),agronomic value (AV),and grain yield (GY), according to recommendations made in instructions for carrying out trials for distinction, homogeneity, and stability of soybean cultivars from the Brazilian Ministry of Agriculture (Ministério da Agricultura e Agropecuária - MAPA, 2015).The agronomic value and lodging traits were transformed to $\sqrt{x+1}$

Principal component analysis was performed on the data, based on the original matrix of the means of the 93 genotypes evaluated for the twelve quantitative descriptors. For selection of the components that most contributed to variability, the criterion proposed by Kaiser (1960) was adopted, and the relative importance of the traits for genetic divergence was determined according to the method proposed by Singh (1981). Statistical-genetic analyses were performed using the Genes program (CRUZ, 2013).

RESULTS AND DISCUSSION

Principal component analysis allowed genetic diversity among the 93 soybean genotypes to be studied from69.34% of the total variance accumulated by the first three eigenvalues (Table 2). Considering absence of redundance between the contribution of the traits of greatest discriminatory power for structuring the orthogonal axes of the principal components (PC1, PC2 and PC3) and variance values greater than 1, the other principal components were not considered (Table 2).

Table 2. Principal Component Analysis based on twelve traits related to production and yield components evaluated in 76 PIs and 16 Brazilian soybean cultivars [*Glycine max* (L.) Merrill]. Teresina, PI, Brazil, 2014, UFPI

	Eigenvalues		
Parameters	**λ1**	**λ2**	**λ3**
Variance	5.31	1.9	1.11
Eigenvalues (%)	44.25	15.84	9.25
Accumulated	44.25	60.09	69.34
Traits	**Eigenvectors Principal Components**		
	PC1	**PC2**	**PC3**
Number of days to flowering - NDF	0.33	-0.02	0.37
First pod height - FPH	0.22	0.15	0.21
Number of pods per plant - NPP	0.30	-0.08	-0.31
Seed-fill period - SFP	0.38	-0.09	0.28
Number of days to maturity - NDM	0.31	0.07	0.43
Plant height at maturity - PHM	0.37	0.12	0.03
Agronomic value - AV	0.32	0.25	-0.45
Lodging - LG	0.34	-0.12	-0.02
100-seed weight - 100SW	-0.06	0.57	0.21
Grain yield - GY	0.32	0.21	-0.46
Pod length - PL	-0.23	0.37	0.07
Pod weight - PW	-0.04	0.60	0.01

Using at least 80% of the total variation from the first principal components, the genetic diversity among a group of genotypes can be satisfactorily studied (CRUZ; REGAZZI; CARNEIRO, 2012). Nevertheless, considering what the criterion proposed by Kaiser (1960) advocates, even with values of total accumulated variation below 80%, estimates of genetic diversity have been efficient. Al-Hadi et al. (2017) clearly and concisely estimated the genetic diversity among 80 soybean genotypes evaluated under middle latitudes (24°5' Nand 90°16' E) with a total accumulated variation of 75.6%of principal components resulting from morpho agronomic information.

The need for specific photoperiods is a factor that contributed to narrowing the genetic base of soybean, because most cultivars released in Brazil and in the world have a genealogy formed by parents in common or related parents (FERREIRA JÚNIOR et al., 2015). Thus, the criteria for studies on genetic diversity of a dataset with lower genetic dissimilarity can be flexibilized and adapted since there is lower gene complexity or lower variability of alleles than in the general pattern of agricultural crops (Table 2).

According to Agarwal et al. (2013), breeding studies have been conducted on the soybean crop for more than six decades and have led to yield increases in the order of 60% from approximately 4000 cultivars released throughout the world. However, even with the different approaches and the support of areas related to plant breeding that have led to advances and will yet make new advances for the soybean crop possible, such as genetic mapping, QTL analysis, genome sequencing, and development of transgenic plants, the genetic base in the soybean crop has gradually narrowed (RODRIGUES et al.,2010; LIN et al., 2016; HACISALIHOGLU et al., 2017).

The grain production and yield components of the 77 PIs and 16 Brazilian soybean cultivars established direct correlation among the traits of greatest discriminatory effect for the principal components PC1, PC2, andPC3. Selection of genotypes near the axes of these components increases the possibilities for selection of genes whose expression allows expansion of tolerance to abiotic factors. This results in maximization of yields for the soybean crop under high temperature and low latitude conditions (Table 2). Anderson et al. (2016) studied the genetic base of the *ex situ* collection of *Glycine soja* of the USDA with 32.416 SNPs, aiming to identify the population structure and test associations with bioclimatic variables to identify loci with associations with the variations of abiotic factors. Nevertheless, even with identification of genes for tolerance to abiotic factors, it is necessary to know the underlying molecular and physiological mechanisms that are still little known, for example, the role of plasto globules related to drought stress (ANDERSON et al.,2016) and especially the effect that high temperatures may have on plant physiological mechanisms (BITA; GERATS, 2013).

The first principal component, PC1, was established mainly through means of the contribution associated with the eigenvectors of the seed-fill period (0.38), plant height at maturity (0.37), lodging (0.34), and number of days to flowering (0.33) traits. Structuring of principal component 2, PC2, was based on eigenvectors estimated by the means of the traits related to the fruit [pod length (0.37) and pod weight (0.60)] and the seed [100 seed weight (0.57)]. The consistency of the third principal component, PC3, was mainly from the means of the number of days to pod maturation (0.43), number of days to flowering (0.37), and seed-fill period (0.28) traits.

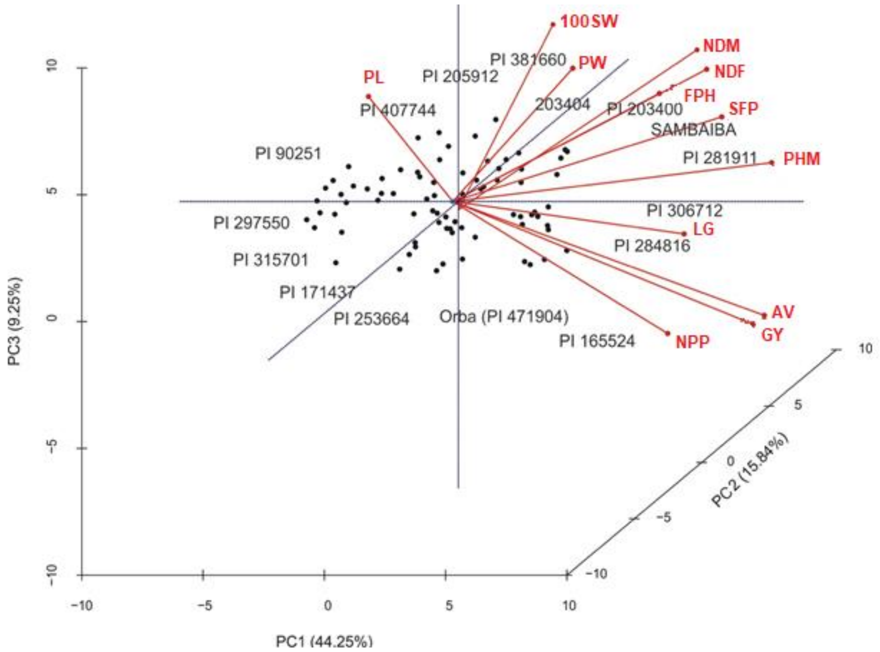
Thus, the axes of the first three principal components (PC1, PC2, andPC3) were established with traits of greater discriminatory power with direct associations among them, that is, greater mean values for one trait also imply greater mean values for the others with the same signal (Table 2).

Although it is recommended that the inferences regarding estimates for heritability necessarily be applied to the same set of genotypes, because the environmental component directly affects the values of the estimates, this recommendation can be made more flexible when dealing with traits with high magnitude of heritability. The traits that have expression regulated by a small number of genes are not greatly affected by the environment. In light of this information, directing strategies for selection of genotypes becomes more efficient (BALDISSERA et al., 2014).

The values in the literature for heritability of the variables of greatest discriminatory power among the three principal components (PC1, PC2, and PC3) were 93.23% (TEIXEIRA et al., 2017) for days to flowering of the PC1 and PC2, and 85.45% for 100 seed weight (TEIXEIRA et al.,2017) in PC2. Thus, it is possible to make inferences under the perspective of achieving genetic progress from selection of the soybean genotypes evaluated in this study, since we found values of high magnitude, classified as having high heritability. This makes the possibility of gains even more concrete since evidence in the literature shows that values greater than one in the CVg/CVe ratio for the traits mentioned indicates that genetic variation is the parameter of greatest importance in variation of the traits of greatest discriminatory power of PC1, PC2, and PC3.

The main associations among the traits and the soybean genotypes evaluated were analyzed in a three-dimensional plane in a biplot, considering the first principal components PC1 (35.29%), PC2(15.84%), andPC3 (9.25%) (Table2, Figure 1).

Figure 1. Three-dimensional scatter plot of 76 PIsand 16 Brazilian cultivars of soybean [*Glycine max* (L.) Merrill] and projections of the vectors of 12 traits related to production and yield components. Teresina, PI, Brazil, 2014, UFPI.

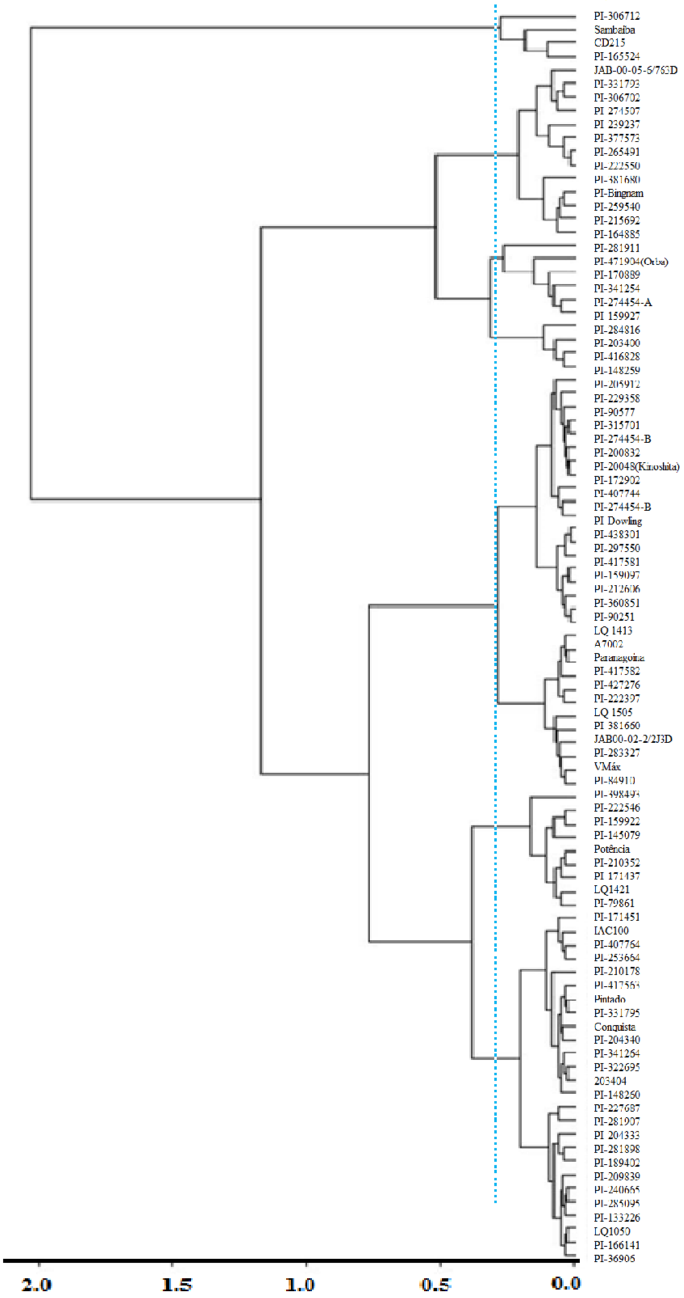


Among the genotypes plotted on the three principal components selected for estimating genetic diversity in the three-dimensional plane and taking the allocation of the Brazilian soybean cultivars Sambaíba and 203404 as a reference, the genotypes with best performance for the traits of greatest discriminatory power are the PIs 165524, 407744, 205912, 381660, 203400, and 281911(Figure 1). The genotypes also exhibit greater variability for the number of days to flowering, plant height at maturity, seed-fill period, number of days to maturity, pod weight, pod length, and 100-seed weight traits.

The Brazilian cultivars are already adapted to the edaphic and climatic conditions for low latitudes. They are therefore the best reference of adjustment for selection of new soybean genotypes to be included in the genealogy of future crosses that resulted in new varieties to be released in Brazil.

From Euclidean distance by the UPGMA method, a dendrogram was generated that was able to allocate the 16 Brazilian cultivars and 76 PIs in six diversity panels with consistent structuring and without the presence of duplicates, allowing high adjustment of the matrices and two-dimensional representation by the cophenetic correlation coefficient of 0.79 and mean similarity of 0.4 between the groups of genotypes studied (Figure 2).

Figure 2. Dendrogram of UPGMA hierarchical cluster analysis using mean Euclidean distance for the twelve traits related to the production and yield components among 76 PIs and 20 Brazilian cultivars of soybean [*Glycine max* (L.) Merrill]. Teresina, PI, Brazil, 2014.



Allocation of the genotypes among the diversity panels occurred in the following manner: Group I formed of two Brazilian genotypes, one from India and another from South Africa; Group II, formed of 46.2% of the genotypes belonging to the American continent (four from South America and the other two from Central America and North America), 38.5% belonging to the Asian continent, and 15.4% belonging to the African continent; Group III, 60% Asian, 20% African, 10% American, and 10% European; Group IV, with the greatest concentration of Brazilian cultivars, six in all, and composed in general by 38.71% belonging to the American continent (58.33% from South America, 28.57% from North America, and 2.96% from Central America), 51.61% to the Asian continent, 6.46% to the African continent, and 3.22% to the European continent; Group V was formed of nine accessions, among which four are South American, and the others Asian and African; and Group VI, 53.45% Asian, 34.62% South American, and 11.93% African (with most of the genotypes coming from the southern part of the continent) (Table 1 and Figure 2).

The hierarchical clustering with little gradation in the dendrogram and the allocation in different groups for genotypes of the same origin, such as Brazilian soybean cultivars allocated in Groups I, IV, and V, corroborate the narrow genetic base that these materials have. However, in spite of the low performance of the mean and not very productive genotypes, the genotypes identified as African PIs generally appeared distributed in defined groups, forming small subgroups, showing the variation in the gene pools of these materials for the morphoagronomic traits evaluated (Table 1 and Figure 2).

Expressive subgroups from Asian genotypes were structured in four of the diversity panels; geographic position, local trade, and distribution of soybean genotypes are a probable explanation for such fragmented allocations (Table 1 and Figure 2). It is noteworthy that the Chinese genotypes also had similar allocation and appeared in five of the six groups formed. A similar result was observed by Marconato et al. (2017), who attributed structuring as a result of the center of origin of soybean being China.

In Groups IV, V, and VI, the association between the improved Brazilian genotypes and the Chinese genotypes was observed, as was already found in other evaluations with the same genotypes (MARCONATO et al., 2017). In addition to the center of origin, the morphological similarity is evident among the soybean genotypes and, therefore, confirms the joint allocation.

In an overall manner within all the genetic diversity panels, there was structuring of subgroups among the soybean genotypes originating from China, Taiwan, the Philippines, Thailand, and Indonesia, which are coastal and island countries or regions. These same conformations can be found in studies of Oliveira et al. (2010) and Marconato et al. (2017), showing the consistency of the group formations established in this study. Another important fact was the prevalence of the joint allocation among South American genotypes, the only exception being observed in Group I, in which the Brazilian genotypes were associated with Asian and African genotypes (Figure 2).

The induction of flowering in soybean occurs in a critical and specific period for each genotype, constituting one of the limiting factors for broad cultivation of soybean in low latitude regions, since soybeans are plants adapted to short days (ZHANG; WANG; HESKETH, 2001). In a certain way, this physiological requirement selected a large group of soybean genotypes with similar traits, especially for the traits that are expressed between the phenological phases of emergence and the beginning of flowering, which are strongly affected by photoperiod and temperature (CÂMARA et al., 1997; DESTRO et al., 2001).

CONCLUSION

The genetic diversity studied through production and yield components of the soybean genotypes is estimated in a satisfactory manner through the following traits: number of days to flowering, seed-fill period, number of days to maturity; plant height at maturity, 100-seed weight, agronomic value, and lodging.

The 16 Brazilian cultivars and 76 PIs were structured in six diversity panels that were consistent and without duplicates.

The PIs 165524, 407744, 205912, 381660, 203400, and 281911 and the Brazilian cultivars Sambaíba and 203404 show potential for providing genes related to tolerance to stress from temperatures higher than 30ºC and latitudes below 10ºS.

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