

Grain yield, adaptability and stability of soybean genotypes in different Cerrado environments of Piauí, Brazil

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Abstract

The objective of the present study was to evaluate the grain yield and the phenotypic adaptability and stability of soybean genotypes in different Cerrado environments of Piauí, Brazil, to provide indications for cultivation in the region. Therefore, we evaluated 23 soybean genotypes and three checks in three different site (Bom Jesus-PI, Monte Alegre-PI and Currais-PI) and environments (crop year 2010/11, 2011/12 and 2012/13). Experiments were carried out in a randomized complete block design with four replications. The behavior for the average grain yield of genotypes within and among environments was verified using the Scott Knott's method of clustering of means ($P < 0.05$). For the study of adaptability and stability, the methods of analysis of Eberhart and Russell and AMMI were used. Genotypes had the best performance of genetic potential in 2010/11 crop year. The best group in Bom Jesus-PI consisted of 16 genotypes and had an average grain yield higher than 3181.61 kg ha⁻¹, what is well above the global average grain yield (2108.26 kg ha⁻¹). G5 and G9 genotypes were the ones with greater adaptability and stability in the three environments with high average grain yield (2362.5 kg ha⁻¹). Therefore, the identification of genotypes presenting such behavior is important for recommending cultivation in the studied environments or in similar areas. It was possible to identify genotypes that have high grain yield and that are stable and adapted for cultivation in the Cerrado at Piauí state.

Keywords: AMMI, Eberhart & Russell, Genotype x environment interaction, *Glycine max (L.) Merrill*, Productive performance

Introduction

Cerrado area in Piauí, which is inserted in the new agricultural frontier known as MATOPIBA and concentrated in the southwestern region of the state of Piauí, stands out in Brazil as a major grain producing region, and soybeans is the crop with the most relevant culture in this region. In crop year 2015/16, the area planted with soybeans in the Cerrado of Piauí was 565,000 hectares, with an average grain yield of 1143.00 kg ha⁻¹, representing a decrease of 58.0% of productivity compared to the crop year 2014/15, which was 2722.00 kg ha⁻¹ (Conab, 2016). This reduction in grain yield is due to long dry spells that coincided with the reproductive stage of plants in many

cultivated areas, besides the low volume of accumulated rainfall during the crop cycle.

Soybean genetic breeding programs seek to develop cultivars with high grain yield, stability of production and wide adaptability to various environments where the crop is grown (Vasconcelos et al., 2015; Lemos et al., 2011). Thus, the selection or recommendation of cultivars gathering these characteristics is one of the main problems faced by soybean breeding programs in Brazil, because according to Polizel et al. (2013), the expression of the productive potential is a function of genetic and environmental components and the interaction between them.

This challenge is posed by the interaction

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between genotype and environment (G x E), which makes the selection or recommendation of genotypes for cultivation in different environments difficult (Batista et al., 2015; Marques et al., 2011). Therefore, to enhance the ability to identify superior genotypes and study the G x E interaction, it is necessary to evaluate genotypes in different environments to minimize the effect of environment on the expression of the phenotype (Sousa et al., 2015; Malosetti et al., 2013; Meotti et al., 2012).

One of the alternatives to mitigate the influence of the G x E interaction is the recommendation of genotypes with wide adaptability and good stability (Barros et al., 2010). In this context, various methods can be used to evaluate the performance of soybean genotypes and their interaction with the environment aiming at direct selection of the most productive, adapted and stable genotypes for the cultivation in regions (Batista et al., 2015).

Given the difficulty of recommending genotypes for a region, studies on agronomic performance in various cultivation environments

are needed in order to detect the presence of genotypes x environments interaction. This way, genotypes with high grain yield, wide adaptation and stable behavior could be identified. The objective of the present study was to evaluate the grain yield and the phenotypic adaptability and stability of soybean genotypes in different Cerrado environments of Piauí, Brazil to provide indications for cultivation in the region.

Materials and Methods

Twenty-six early maturing soybean genotypes, of which, 23 were lineages in final regional assessment from the Soybean Genetic Improvement Program of the Federal University of Uberlândia, and three were checks: M-Soy 8001, UFUS Guarani and UFUS Riqueza. They were evaluated in three different site (Bom Jesus, Monte Alegre and Currais in the Cerrado region of southwestern Piauí) and environments (crop year 2010/11, 2011/12 e 2012/13) (Table 1).

The Figure 1 shows the pluviometric behavior in the different crop years (environments).

Table 1. Geographic coordinates of the environments where the tests were conducted

Site	Crop year	Latitude	Longitude	Altitude
Bom Jesus-PI	2010/11	09°04'28''S	44°21'31''W	277 m
Monte Alegre-PI	2011/12	09°45'14''S	45°18'14''W	453 m
Currais-PI	2012/13	09°00'25''S	44°21'26,16''O	320 m

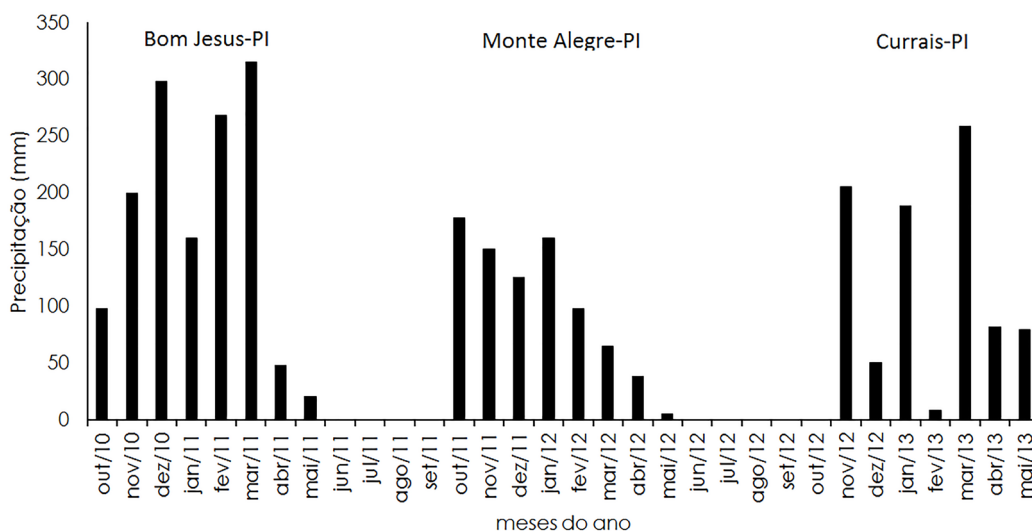


Figure 1. Cumulative monthly averages of precipitation occurred in Bom Jesus (2010/11), Monte Alegre (2011/12) and Currais (2012/13) during the period of conducting the trials.

Fertilization at sowing was performed according to the requirements of the crop after the soil analysis. For sowing, seeds were inoculated

with Bradyrhizobium japonicum strains at a dose of 150 g of inoculant per 100 kg of seeds. The control of pests, diseases and weeds was carried

out as necessary.

Genotypes were evaluated in the experimental design of randomized complete blocks with four replications. Each plot was represented by four rows of 5.0 m long, 0.5 m distant from each other. At harvest, 0.5 m of the end of each central row were discarded. The floor area of the plot was represented by the two central rows, which sums 4.0 m². In the R8 stage of development, plants of the two central rows were harvested and the grain produced were weighed and their specific humidity determined. Then, weight was adjusted to 13% moisture to estimate grain yield in kg ha⁻¹.

Grain yield data of genotypes in each environment were subjected to individual analysis of variance, followed by overall analysis of variance, using the computer program in Genetics and Statistics - Genes for processing these analyses (Cruz, 2013). Subsequently, the performance of genotypes was studied with the Scott-Knott test of cluster of means at 5% of probability for each environment, and the analytical methods of Eberhart & Russell (1966) and AMMI (Zobel et al., 1988) were used to compare the adaptability and stability under interaction between genotype and environment (G x E).

The analytical approach by the method of Eberhart & Russell (1966) is based on a simple linear regression in which the coefficient of the angular regression close ($\beta_{1i} \approx 1$) to one gives information on adaptability, and the variance of deviations close to zero ($\sigma^2 d_i \approx 0$) indicates high stability. Phenotypic adaptability and stability are characterized by three parameters: average grain yield, regression coefficient and variance of the regression deviations. This analytical method aids to collect information on performance of each genotype in relation to environmental means and can be used to help in the selection of genotypes with higher average grain yield β_{0i} , wider adaptability ($\beta_{1i} \approx 1$) and higher stability ($\sigma^2 d_i \approx 0$) (Batista et al., 2015). The regression model applied was:

$$Y_{ij} = \beta_{0i} + \beta_{1i} \cdot I_j + \delta_{ij} + \bar{\epsilon}_{ij}$$

The analysis using the AMMI method considers additive models for the main effects, that is, genotypes (g)_i and environments (e)

j and multiplicative models for effects of the interaction (ge)_{ij} (Malosetti et al., 2013). The AMMI model provides a graphic called "biplot" where the coordinates of genotypes and environments are represented on the main axes of interaction (IPAC's - Incremental Principal Component Analysis) which allow us to describe the adaptability and stability of genotypes in relation to the tested environments, as shown in Oliveira et al. (2016) and Sousa et al. (2015). In the AMMI method, the G x E interaction was decomposed by a Main Component Analysis, obtaining the IPCA1 and the IPCA2. For the Biplot AMMI analysis, the model is specified according to the equation:

$$Y_{ij} = \mu + g_i + a_j + \sum_{c=1}^n \sqrt{\lambda_c} \alpha_{ic} + \gamma_{jc} + \delta_{ij} + \bar{\epsilon}_{ij}$$

where Y_{ij} is the mean response of the i-th genotype ($i = 1, 2, \dots, G$ genotypes) at j-th environment ($j = 1, 2, \dots, E$ environments); μ is the overall mean of the trials; g_i is the effect of the genotype i, $i = 1, 2, \dots, g$; a_j is the effect of the environment j, $j = 1, \dots, a$; λ_c is the c-th singular value (scalar) of the original interaction matrix (denoted by GE); α_{ic} is the element corresponding to the i-th environment at c-th singular line vector of the GE matrix; γ_{jc} is the element corresponding to the i-th genotype in the c-th singular column vector of the GE matrix; δ_{ij} is the noise associated with the term (GE)_{ij} of the classical interaction of genotype i with j environment interaction; $\bar{\epsilon}_{ij}$ is the mean experimental error.

Results and Discussion

Considering the results of the individual analysis of variance of each environment, there was a relationship between the largest and smallest mean square of the residual 4.68. Besides this important parameter, homogeneity of residual variances was also observed and, thus, the analysis of variance could be carried out without problems. The overall analysis of variance for grain yield showed significant effects ($P < 0.05$) for the three sources of variation, namely, genotype, environment and genotypes x environments interaction (Table 2). Therefore, it is difficult to recommend genotypes for a specific environment because of this variation of grain yield according to environment. This indicates

that the relative behavior of genotypes was influenced by environments (crop year), and

this justified the application of the analysis of adaptability and stability.

Table 2. Summary analysis of variance for grain yield (kg ha^{-1}) of 26 soybean genotypes evaluated in three environments

Sources of variation	DF	Mean squares
Blocks/environment	6	378631
Genotypes (G)	25	514081.67*
Environments (E)	2	91336369.52*
G x E	50	532059.66*
Residue	150	324894.58
Overall average (kg ha^{-1})	-	2.108,26
CV%	-	27,03

* Significant at 5% ($P < 0.05$) of probability according to F test.

The coefficient of variation (CV%) obtained in this study was 27.03% (Table 2). This value is considered acceptable because of the genetic control of grain yield, and indicates precise control of the causes of environmental variation. In such case, a high coefficient of variation can be explained by the fact of multi-gene control and heavy influence of the environment (Barros et al., 2008; Costa et al., 2008). Batista et al. (2015), Leite et al. (2016) and Peluzio et al. (2008) reported a coefficient of variation of 25.49%, 30,79% and 22.77%, respectively, as acceptable for grain yield, because this is a quantitative characteristic.

The overall average grain yield was $2108.26 \text{ kg ha}^{-1}$, below the average of the crop year 2010/11 in Bom Jesus ($3340.55 \text{ kg ha}^{-1}$) and above the average of the crop year 2011/12 in Monte Alegre ($1671.22 \text{ kg ha}^{-1}$) and the crop year 2012/13 in Currais ($1313.01 \text{ kg ha}^{-1}$). However, in despite of the low average grain yield in the last two environments, genotypes specific for these sites could be identified and classified, with good productivity. The average grain yield of genotypes in 2010/11 crop year was higher than the national average of $2870.00 \text{ kg ha}^{-1}$ (Conab, 2016), as this is the most favorable environment for carrying out the selection and recommendation of genotypes.

All genotypes in Bom Jesus had the crop year 2010/11 average productivity superior to that obtained in the crop years 2011/12 and 2012/13, in Monte Alegre and Currais, respectively, according to the Scott Knott test ($P < 0.05$) (Table 3). Thus, the crop year 2010/11 was the environment in which genotypes had better performance of their genetic potential. The crop years 2011/12

and 2012/13 were the environments in which genotypes had lower performance, with no difference between these two environments on the performance of genotypes, except for the G3 and G14 genotypes.

In crop year 2010/11, in Bom Jesus, there were two groups of genotypes for grain yield. The group with the best performance was composed of 16 genotypes; those with the highest average grain yield, above $3181.61 \text{ kg ha}^{-1}$, well above the global average productivity ($2108.26 \text{ kg ha}^{-1}$) and the national average ($2870.00 \text{ kg ha}^{-1}$) (Conab, 2016). Within this environment, the cultivar UFUS Riqueza had the higher average grain yield ($4507.31 \text{ kg ha}^{-1}$) obtained in this study. The assessment of productivity of seven soybean cultivar grains in Uberlândia carried out by Marques et al. (2011) showed that the cultivar UFUS Riqueza showed high average grain yield in the first seeding time ($2864.52 \text{ kg ha}^{-1}$), but this value is lower than the obtained in the present study.

All genotypes showed similar results, with average or low values of grain yield in the crop years 2011/12 in Monte Alegre and 2012/13 in Currais. However, it is clear that the genotypes G5, G7, G9, G11, G19 and UFUS Riqueza, which were superior for grain yield in Bom Jesus, also had slightly higher grain yield in Monte Alegre and Currais. In Monte Alegre, the G24 genotype had the highest average grain yield ($2550.0 \text{ kg ha}^{-1}$), and higher than the overall average ($2108.26 \text{ kg ha}^{-1}$). In turn, in Currais, the G11 genotype showed the highest average grain yield ($1981.13 \text{ kg ha}^{-1}$), but this was lower than the overall average ($2108.26 \text{ kg ha}^{-1}$).

Table 3. Average grain yield (kg ha⁻¹) of 26 soybean genotypes evaluated in three environments

Genotypes	Environments			Mean
	2010/11	2011/12	2012/13	
G1	3053.33 Ab	1807.40 Ba	1587.16 Ba	2149.27
G2	3976.11 Aa	1550.00Ba	1250.83 Ba	2258.98
G3	3157.03 Aa	2063.88 Ba	928.75 Ca	2049.88
G4	3539.53 Aa	1345.37 Ba	999.32 Ba	1961.40
G5	3384.90 Aa	2100.00 Ba	1602.60 Ba	2362.50
G6	3204.91 Aa	1724.07 Ba	854.27 Ba	1927.75
G7	3535.46 Aa	1636.11 Ba	1673.28 Ba	2281.61
G8	2867.80 Ab	1296.29 Ba	1120.81 Ba	1761.63
G9	3558.42 Aa	2314.81 Ba	1777.52 Ba	2550.25
G10	3195.27 Aa	1770.37 Ba	1191.50Ba	2052.38
G11	3435.83 Aa	2159.26 Ba	1981.13 Ba	2525.40
G12	3138.61 Aa	1550.00 Ba	1368.85 Ba	2019.15
G13	2656.76 Ab	1992.59 Aa	1223.14 Ba	1957.49
G14	3709.44 Aa	2362.96 Ba	1040.91 Ca	2371.10
G15	2434.91 Ab	1418.51 Ba	1004.24 Ba	1619.22
G16	3324.35 Aa	1117.59 Ba	1438.34 Ba	1960.09
G17	2157.68 Ab	1669.44 Aa	1609.75 Aa	1812.29
G18	2972.13 Ab	1815.74 Ba	1430.2 Ba	2072.69
G19	3320.74 Aa	1661.11 Ba	1560.84 Ba	2180.89
G20	3850.74 Aa	1555.55 Ba	1089.83 Ba	2165.37
G21	3798.70 Aa	1084.26 Ba	1408.19 Ba	2097.05
G22	3871.39 Aa	1132.40 Ba	966.33 Ba	1990.04
M-soy 8001	3535.09 Aa	1263.89 Ba	808.83 Ba	1869.27
G24	3027.31 Ab	2550.00 Aa	972.14 Ba	2183.15
UFUS Guarani	3640.64 Aa	1069.44 Ba	1462.54 Ba	2057.54
UFUS Riqueza	4507.31 Aa	1440.74 Ba	1787.20 Ba	2578.40
Mean	3340.55	1671.22	1313.01	2108.26

Means followed by the same capital letters in horizontal represent a statistically homogeneous group. Means followed by the same lowercase letters in vertical represent a statistically homogeneous group. 2010/11 crop year in Bom Jesus-PI; 2011/12 crop year in Monte Alegre - PI; 2012/13 crop year in Currais-PI.

Therefore, it is difficult to recommend genotypes for a specific environment because of this variation of grain yield according to environment. The G x E significant interaction indicated that genotypes showed different performance under different conditions in the three environments/crop year, and, therefore, studies on genotype performance with use of methods to assess adaptability and stability are necessary. According Polizel et al. (2013), studies with application of such methods in final stages of soybean breeding programs are important to recommend productive genotypes, with high stability and wide adaptability to different growing regions. Oliveira et al. (2012) also stated that such studies may contribute to the identification and selection of genotypes with predictable behavior of that are responsive to environmental enhancement.

Adaptability refers to the ability that a given genotype has that makes it advantageous depending on environmental variation, while

stability is the ability of a given genotype present predictable behavior even with environmental variation (Cruz & Carneiro, 2003). According to the method of Eberhart & Russell (1966), an ideal genotype is one that has high average grain yield, with regression coefficient equal to 1.0 and regression deviation as low as possible. Estimates of the average of genotypes, of regression coefficients, regression deviations and coefficient of determination of genotypes are shown in Table 4.

Regression coefficients were not significant in any genotype, except for G17, G22 and UFUS Riqueza genotypes. This indicates that most of the genotypes had proportional performance related to improvement in the environment, as stated by Polizel et al. (2013).

The G5, G9 and G11 genotypes showed average yield higher than 2362.50 kg ha⁻¹, regression coefficient statistically equal to one ($\beta_{1i} = 1$) and non-significant regression deviation ($\delta di^2=0$). This indicates that these genotypes can

Table 4. Average grain yield (kg ha⁻¹) and estimates of adaptability and stability parameters by the method of Eberhart & Russell (1966) in 26 soybean genotypes

Genotypes	Mean	Eberhart & Russell		
		$\beta_{ij} \approx 1$	$\sigma^2 d_i \approx 0$	R^2 (%)
G1	2149.30	0.7304 ^{ns}	-107418 ^{ns}	99.9
G2	2258.98	1.3782 ^{ns}	-88852 ^{ns}	99.5
G3	2049.89	0.9606 ^{ns}	213376.7 ^{ns}	87.0
G4	1961.41	1.272 ^{ns}	-102123 ^{ns}	99.8
G5	2362.50	0.845 ^{ns}	-88807 ^{ns}	98.8
G6	1927.75	1.0745 ^{ns}	12575.9 ^{ns}	95.7
G7	2281.61	0.9868 ^{ns}	-29848.8 ^{ns}	96.6
G8	1761.63	0.8865 ^{ns}	-97924 ^{ns}	99.4
G9	2550.25	0.8368 ^{ns}	-79288.5 ^{ns}	98.2
G10	2052.38	0.9463 ^{ns}	-78712.7 ^{ns}	98.6
G11	2525.40	0.7322 ^{ns}	-104658 ^{ns}	99.7
G12	2019.15	0.8974 ^{ns}	-98178.5 ^{ns}	99.4
G13	1957.49	0.6107 ^{ns}	47595.6 ^{ns}	84.8
G14	2371.10	1.1574 ^{ns}	315039.6*	88.1
G15	1619.22	0.6755 ^{ns}	-93034.2 ^{ns}	98.5
G16	1960.09	1.0522 ^{ns}	141925.8 ^{ns}	91.1
G17	1812.29	0.2772**	-107493 ^{ns}	99.5
G18	2072.69	0.7394 ^{ns}	-100810 ^{ns}	99.4
G19	2180.89	0.9073 ^{ns}	-82334.3 ^{ns}	98.6
G20	2165.37	1.3658 ^{ns}	-108014 ^{ns}	99.9
G21	2097.05	1.3183 ^{ns}	217550.4 ^{ns}	92.5
G22	1990.04	1.4976*	-37779.6 ^{ns}	98.6
M-Soy 8001	1869.27	1.3496 ^{ns}	-107885 ^{ns}	99.9
G24	2183.15	0.7869 ^{ns}	0,5391 **	62.6
UFUS Guarani	2057.54	1.2194 ^{ns}	245767.8 ^{ns}	90.7
UFUS Riqueza	2578.42	1.4959*	291896.4 ^{ns}	92.9

^{ns}Non significant. *, ** Significant at the 0.05 and 0.01 probability levels, respectively.

$\beta_{ij} \approx 1$: regression coefficients; $\sigma^2 d_i \approx 0$: variance of the regression deviation; R^2 : coefficient of determination (%).

be classified for recommending for cultivation in the three environments, as they presented greater adaptability and stability. These are genotypes whose use requires no restriction for growing in environments with similar characteristics of the study, as they revealed greater adaptation and more stable or predictable behavior. It was also noted that the G5, G9 and G11 genotypes obtained R^2 above 98.0%, satisfactorily explaining their behavior in function of the environment according to Polizel et al. (2013).

The G17 genotype showed high grain yield and significant regression coefficient, which is statistically different and below then value of one ($\beta_{ij} < 1$). Thus, this genotype stands as the most adapted to harsh environments. Therefore, this is a rustic genotype, able to maintain its grain yield under adverse environmental conditions, what is indicated by the fact that the coefficient of determination was 99.5%, confirming the behavior observed. According Peluzio et al. (2010), genotypes with such behavior do not

respond satisfactorily to improvement of the environment. When maximizing returns is the purpose, these genotypes would not interesting for systems involving the use of high technology.

G22 and UFUS Riqueza genotypes showed significant regression coefficients, but with values that were statistically higher than one ($\beta_{ij} > 1$). Thus, these genotypes may be classified as the best adapted to favorable environments. A coefficient of determination superior to 92.9% was also observed, satisfactorily explaining the behavior observed for these genotypes. According to Oliveira et al (2012) genotypes with this behavior are indicated for environments where the technology content is high, and they should not be recommended for cultivation in low-tech environments, due to the high risk of reduced grain yield.

The G14 and G24 genotypes showed the significant regression deviation, that is, different from zero ($\sigma^2 d_i \neq 0$) and are, therefore, characterized as having low stability or

predictability.

An analysis using the AMMI method was carried out to study the adaptability and stability of soybean genotypes, in order to compare the results with the previous method, and then verify the existence or not of agreement. In this analysis, as used by Oliveira et al. (2016) and Yokomizo et al. (2013), the first two principal components must explain 70% or more of total accumulated and explained variance of all components.

In the present study, the first two principal components (CP1 and CP2), useful

in AMMI2 analysis, represented and explained 83.84% of the total accumulated and explained variance (Table 5). It also observed that these two principal components were significant. Yokomizo et al. (2013) found similar results for grain yield in soybean lineages selected for resistance to soybean rust. However, a study on adaptability and stability of soybean cultivars in five municipalities of Mato Grosso developed by Polizel et al. (2013) showed that all principal components were significant.

Table 5. Proportion of the sum of squares of the G x E interaction for each principal component of AMMI analysis for grain yield of 26 soybean genotypes in three environments

Principal component	Variance Explained (%)	Cumulative Variance Explained (%)
CP1**	49.63	49.63
CP2**	34.21	83.84
CP3 ^{ns}	16.15	100

^{ns} Nonsignificant. ** Significant at the 0.01 of probability according to F test.

Thus, the two-dimensional plane (Biplot) resulting from the two main components in the AMMI analysis was used to interpret the results (Figure 2). The abscissa represents the main effects (averages of genotypes and environments), and

the ordinate, the first interaction axis (IPCA1). Similar studies using this method for phenotypic adaptability and stability of soybean genotypes were performed by (Oliveira et al., 2016; Polizel et al., 2013; Yokomizo et al., 2013).

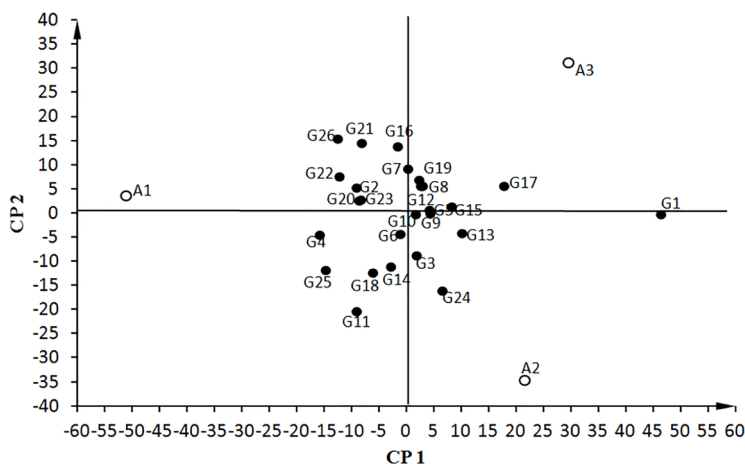


Figure 2. Biplot the first two principal components (CP1 and CP2) regarding the environmental stratification, according to AMMI2 model for grain yield of 26 early maturing soybean genotypes: G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20, G21, G22, G23 (M-Soy 8001), G24, G25 (UFUS Guarani) and G26 (UFUS Riqueza), in three environments: A1 (2010/11), A2 (2011/12) and A3 (2012/13).

For stability, the distance between the points representing the genotypes and environments and zero score (origin) was considered, according to Oliveira et al. (2016) and, therefore, genotypes with greater stability in the environments are those whose points are situated close to zero (center). As for adaptability

of genotypes in each environment, scores for genotypes and environment were considered. Thus, genotypes and environments whose points are located closer to each other, and have the same direction, interact in a positive way.

The G5, G6, G8, G9, G10, G12, G15 and G19 genotypes presented higher stability. Thus, it is

important to identify genotypes with this behavior for recommendation in the studied environments or in similar areas. In turn, the genotypes G1, G4, G11, G16, G18, G21, G22, G24, G25 (UFUS Guarani) and G26 (UFUS Riqueza) showed low stability and were considered the main contributors to the interaction G x E. Generally, genotypes that have high stability are those who contribute least to the G x E interaction, according to Oliveira et al. (2016).

The seven most stable genotypes showed an average grain yield of 2059.20 kg ha⁻¹, which is below the average of the eleven least stable genotypes (2157.50 kg ha⁻¹). Amira et al. (2013) and Oliveira et al. (2016) found similar results using AMMI analysis, where soybean cultivars with low stability exhibited highest average grain yield in relation to those with high stability.

As the objective is to select genotypes that have high yield and are stable and/or adapted to southern Piauí, it was possible to identify genotypes with varied and satisfying productive behavior. For the group of genotypes that showed high stability, the highest grain yield averages were presented by G5 (2362.50 kg ha⁻¹) and G9 (2550.50 kg ha⁻¹), respectively, higher than the overall average (2108.26 kg ha⁻¹). In the case of the group of genotypes that showed low stability, the G11 and UFUS Riqueza had the highest averages of grain yield, 2525.40 and 2578.40 kg ha⁻¹, respectively higher than the overall average (considering all experiments).

The AMMI methodology is an important statistical tool for studies on phenotypic adaptability and stability of genotypes, as it allows the classification of predictable and/or responsive behaviors in function of variation in environment, as well as the description of environments that may be more or less favorable to the performance of their genetic potential.

Conclusions

Based on the analysis of cluster of means, the crop year 2010/11 was the environment where all genotypes were superior in grain yield compared to other environments, and a specific group of genotypes (G2, G3, G4, G5, G6, G7, G9, G10, G11, G12, G14, G16, G19, G20, G21 and G22) showed an excellent performance in

this environment. The highest adaptabilities and stabilities in the three environments with high grain yield were found in the G5 and G9 genotypes, with a reasonable degree of agreement between the methods of analysis of Eberhart and Russell and AMMI that applied in the study. It was possible to identify genotypes that have high yield, and are adapted and stable and these will be recommended for cultivation in the Cerrado region of southwestern Piauí, as these are also important to be indicated for the studied environments or similar areas.

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References

- Amira, J.O., Ojo, D.K., Ariyo, O.J., Oduwaye, O.A., Ayo-Vaughan, M.A. 2013. Relative discriminating powers of GGE and AMMI models in the selection of tropical soybean genotypes. *African Crop Science Journal* 21: 67-73.
- Barros, H.B., Sedyama, T., Teixeira, R.C., Cruz, C.D. 2008. Análises paramétricas e não-paramétricas para determinação da adaptabilidade e estabilidade de genótipos de soja. *Scientia Agraria* 9: 299-309.
- Barros, H.B., Sedyama, T., Cruz, C.D., Teixeira, R.C., Reis, M.S. 2010. Análise de adaptabilidade e estabilidade em soja (*Glycine max* L.) em Mato Grosso. *Ambiência* 6: 75-88.
- Batista, R.O., Hamawaki, R.L., Sousa, L.B., Nogueira, A.P.O., Hamawaki, O.T. 2015. Adaptability and stability of soybean genotypes in off-season cultivation. *Genetics and Molecular Research* 14: 9633-9645.
- Conab. Companhia Nacional de Abastecimento. Acompanhamento da safra brasileira de grãos. 12º Levantamento Grãos Safra 2015/16 - Setembro 2016. http://www.conab.gov.br/OlalaCMS/uploads/arquivos/16_09_06_09_03_20_boletim_12_setembro.pdf <Acesso em 25 Set. 2016>.
- Costa, M.M., Mauro, A.O., Unêda-Trevisoli, S.H., Arriel, N.H.C., Bárbaro, I.M., Silveira, G.D., Muniz, F.R.S. 2008. Heritability estimation in early generations of two-way crosses in soybean. *Bragantia* 67: 101- 108.
- Cruz, C.D. 2013. GENES - a software package for analysis in experimental statistics and quantitative

- genetics. *Acta Scientiarum* 35: 271-276.
- Cruz, C.D., Carneiro, P.C.S. 2003. *Modelos biométricos aplicados ao melhoramento genético*. UFV, Viçosa, Brasil. 585 p.
- Eberhart, S.T., Russell, W.A. 1966. Stability parameters for comparing varieties. *Crop science* 6: 36-40.
- Leite, W.S., Pavan, B.E., Matos Filho, C.H.A., Alcântara Neto, F., Oliveira, C.B., Feitosa, F.S. 2016. Estimativas de parâmetros genéticos, correlações e índices de seleção para seis caracteres agrônômicos em linhagens F8 de soja. *Comunicata Scientiae* 7: 302-310.
- Lemos, L.B., Farinelli, R., Cavariani, C., Zapparoli, R.A. 2011. Desempenho agrônômico e produtivo de cultivares de soja em diferentes safras. *Científica* 39: 44-51.
- Malosetti, M., Ribaut, J.M., Van Eeuwijk, F.A.V. 2013. The statistical analysis of multi-environment data: modeling genotype-by-environment interaction and its genetic basis. *Frontiers in Physiology* 4: 1-17.
- Marques, M.C., Hamawaki, O.T., Sedyama, T., Bueno, M.R., Reis, M.S., Cruz, C.D., Nogueira, A.P.O. 2011. Adaptabilidade e estabilidade de genótipos de soja em diferentes épocas de semeadura. *Bioscience Journal* 27: 59-69.
- Meotti, G.V., Benin, G., Silva, R.R., Beche, E. 2012. Épocas de semeadura e desempenho agrônômico de cultivares de soja. *Pesquisa Agropecuária Brasileira* 47: 14-21.
- Pelúzio, J.M., Fidelis, R.R., Giongo, P., Silva, J.C. 2008. Adaptabilidade e estabilidade de cultivares de soja em quatro épocas de semeadura no sul do Estado do Tocantins. *Revista Ceres* 55: 34-40.
- Peluzio, J.M., Afféri, F.S., Monteiro, F.J.F., Melo, A.V., Pimenta, R.S. 2010. Adaptabilidade e estabilidade de cultivares de soja em várzea irrigada no Tocantins. *Revista Ciência Agronômica* 41: 427-434.
- Polizel, A.C., Juliatti, F.C., Hamawaki, O.T., Hamawaki, R.L., Guimarães, S.L. 2013. Adaptabilidade e estabilidade fenotípica de genótipos de soja no estado do Mato Grosso. *Bioscience Journal* 29: 910-920.
- Oliveira, L.G., Hamawaki, O.T., Simon, G.A., Sousa, L.B., Nogueira, A.P.O., Rezende, D.F., Hamawaki, C.D.L. 2012. Adaptabilidade e estabilidade da produtividade de soja em duas regiões sojícolas. *Bioscience Journal* 28: 852-861.
- Oliveira, V.M., Hamawaki, O.T., Nogueira, A.O., Sousa, L.B., Santos, F.M., Hamawaki, R.L. 2016. Selection for wide adaptability and high phenotypic stability of Brazilian soybean genotypes. *Genetics and molecular Research* 15: 1-13.
- Sousa, L.B., Hamawaki, O.T., Nogueira, A.P.O., Batista, R.O., Oliveira, V.M., Hamawaki, R.L. 2015. Evaluation of soybean lines and environmental stratification using the AMMI, GGE biplot, and factor analysis methods. *Genetics and molecular Research* 14: 12660-12674.
- Vasconcelos, E.S., Reis, M.S., Sedyama, T., Cruz, C.D. 2015. Produtividade de grãos, adaptabilidade e estabilidade de genótipos de soja de ciclos precoce e médio. *Semina: Ciências Agrárias* 36: 1203-1214.
- Yokomizo, G.K., Duarte, J.B., Vello, N.A., Unfried, J.R. 2013. Análise AMMI da produtividade de grãos em linhagens de soja selecionadas para resistência à ferrugem asiática. *Pesquisa Agropecuária Brasileira* 48: 1376-1384.
- Zobel, R.W., Wright, M.J., Gauch, H.G. 1988. Statistical analysis of a yield trial. *Agronomy Journal* 80: 388-393.