

# GGE biplot projection in adaptability and stability inference of soybean in an agricultural center Paraná, Brazil<sup>1</sup>

## Projeção GGE biplot na inferência de adaptabilidade e estabilidade da soja em um centro agrícola do Paraná, Brasil

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**ABSTRACT** - The state of Paraná is among the main producers of soybeans not only in Brazil, but in the World. However, it presents considerable edaphoclimatic variation throughout its area. This is one of the main causes genotype-by-environment interactions, hindering the selective process as well as the recommendation of cultivars in the state. Therefore, the objective of this study was: (i) to identify the environment that make it possible to represent the conditions of the state of Paraná, in order to facilitate the selection and recommendation of cultivars in future breeding programs; (2) to identify soybean inbred lines stable and adapted to state of Paraná. For this, data from trials in the agricultural year of 2013/2014 conducted with 24 soybean inbred lines in 18 locations. Genotypic differences were observed with a level of accuracy of 0.93. Despite the environmental differences, it was possible to explain approximately 70% of the global variation of the data with the first three main components. Based on the biplots, it was verified that the locality of Record-PR was the most discriminant and representative, whereas Iporã-PR provided lower. In general, inbred lines 5, 9, 23 and 24 showed good adaptability and stability as well as high grain yield.

**Key words:** *Glycine max*. Multivariate analysis. Inbred lines selection. Recommendation of cultivars. G x E interaction.

**RESUMO** - O estado do Paraná está entre os principais produtores de soja não só do Brasil, mas do Mundo. Contudo, apresenta variação edafoclimática considerável ao longo de sua área. Isso é uma das principais causas da interação genótipos por ambientes, dificultando o processo seletivo bem como a recomendação de cultivares no estado. Diante disso, objetivou-se com esse estudo: (i) identificar ambiente(s) que possibilite(m) representar as condições edafoclimáticas do estado do Paraná, visando facilitar o processo de seleção e recomendação de cultivares em futuros programas de melhoramento e (ii) identificar linhagens de soja estáveis e adaptadas a essas condições. Para isso, foram usados dados de ensaios no ano agrícola de 2013/2014 conduzidos com 24 linhagens de soja em 18 localidades distintas. Observou-se diferenças genotípicas entre as linhagens com um nível de acurácia de 0,93. Apesar das diferenças ambientais, foi possível explicar aproximadamente 70% da variação global dos dados com os três primeiros componentes principais. Com base das dispersões gráficas (*biplots*), constatou-se que a localidade de Record-PR foi a mais discriminante e representativa, enquanto que Iporã-PR propiciou menores produtividades de grãos entre as linhagens avaliadas. No geral, as linhagens 5, 9, 23 e 24 apresentaram boa adaptabilidade e estabilidade bem como elevadas produtividade de grãos.

**Palavras-chave:** *Glycinemax*. Análises multivariadas. Seleção de linhagens. Recomendação de cultivares. Interação G x E.

DOI: 105935/1806-6690.20210009

Editor do artigo: Professor Salvador Barros Torres - sbtorres@ufersa.edu.br

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Received for publication 27/01/2020; approved on 17/09/2020

<sup>1</sup>Artigo extraído de Dissertação em Fitotecnia, Universidade Federal do Ceará/UFC e financiado pelo Centro Educacional Integrado

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## INTRODUCTION

The grain yield of soybean is among the economic activities that in the last decades presented more significant growths, being one of the greater importance of agribusiness (PASSOS *et al.*, 2019). This can be attributed to several factors, among which: annual increase in demand for cheaper oils and proteins (GASPARRI *et al.*, 2016; HARTMAN *et al.*, 2011) seeking to serve mainly the animal products market; development and structuring of a international market in soybean agroindustrial products (AREGA *et al.*, 2018); generation and supply of technologies (KANG *et al.*, 2017). These factors made it possible to expand soy cultivation to various regions of the world.

Brazil is one of the primary producers and exporters of soybeans, and the agribusiness of this legume moves millions of dollars every year, contributing considerably to the country's gross domestic product (GDP). Currently, the state of Paraná is considered the second largest producer of this commodity in the country (GRZEGOZEWSKI *et al.*, 2017). Despite this, throughout the state, there are marked edaphoclimatic variations, which results in genotype-by-environment (GE) interactions.

The GE interaction is defined by Sharifi *et al.* (2017), as the variation of performance of a genotype in different environments. The existence of GxA interaction, depending on its nature (simple or complex) directly impacts the actions of breeding programs, especially those related to the selection process of superior genotypes, as well as the recommendation of cultivars (CRUZ; CARNEIRO; REGAZZI, 2014).

Thus, various methodologies have been proposed for investigating GE interactions. However, are far too complex to be summarized using one or two stability parameters in univariate analyses. Multiplicative statistical approaches for assessing interactions, such as the GGE biplot method, are very useful for studying performance patterns in genotypes according to the environment and making predictions about the average performance of genotypes in specific environments (KARIMIZADEH *et al.*, 2013; SANTOS *et al.*, 2017).

There are several studies reported in the literature that sought to incorporate the GGE biplot methodology to make an inference of the adaptability and stability of soybean genotypes for the state of Paraná (MATEI *et al.*, 2017; FERREIRA *et al.*, 2018). However, the vast majority of them are limited to a few environments, not being representative. Based on this, the objective of this study was: (i) to identify environments(local) that make it possible to represent the edaphoclimatic conditions of the state of Paraná, in order to facilitate the selective process and recommendation of cultivars in future breeding programs and (ii) soybeans inbred lines stables and adapted to these conditions.

## MATERIAL AND METHODS

Twenty-four inbred soybean lines (Table 1) belonging to breeding program of Centro Educacional Integrado Campo Mourão (CEI) were evaluated as to grain yield in the crop year 2013/14. The trials were conducted under field conditions in 18 environments (Table 2), located in the states of Paraná and São Paulo.

**Table 1** - Mean grain yield, plant height, cycle and growth habit of 24 inbred soybean lines evaluated in 18 environments in the states of Paraná and São Paulo, crop year of 2013/14

Ord.	Inbredlines	Mean grain yield (kg ha <sup>-1</sup> )	Plantheight (cm)	Cycle	Growthhabit
1	INT 596	2844	109	Late	Undetermined
2	INT 609	2779	110	Late	Undetermined
3	INT 625	2642	107	Late	Undetermined
4	INT 4901	3094	108	Intermediary	Undetermined
5	INT 5175	3219	92	Early	Undetermined
6	INT 5177	2875	107	Intermediary	Undetermined
7	INT 5467	2631	96	Intermediary	Undetermined
8	INT 5648	2944	100	Tardio	Undetermined
9	INT 5678	3030	96	Intermediary	Undetermined
10	INT 5686	2892	106	Late	Undetermined
11	INT 5691	2836	95	Late	Undetermined
12	INT 5694	2634	95	Late	Undetermined
13	INT 5705	2129	124	Late	Undetermined

*Continuation table 1*

14	INT 5716	2877	95	Early	Undetermined
15	INT 5721	2782	104	Intermediary	Undetermined
16	INT 5745	2705	110	Late	Undetermined
17	INT 5765	3040	112	Intermediary	Undetermined
18	INT 6903	3208	113	Intermediary	Undetermined
19	INT 7020	2891	110	Late	Undetermined
20	INT 7415	2989	95	Early	Undetermined
21	INT 7422	2504	96	Late	Undetermined
22	INT 7585	2841	99	Early	Undetermined
23	INT 7650	3014	102	Early	Undetermined
24	INT 7651	3073	92	Early	Undetermined

**Table 2** - Characterization of the 18 environments used in the evaluation of the 24 soybean inbred lines in the crop year of 2013/14

Ord.	Environments	Altitude (m)	Latitude	Longitude
1	Arapongas-PR	816	23° 25' 08" S	51° 25' 26" W
2	Araruna-PR	610	23° 55' 55" S	52° 29' 45" W
3	Cascavel-PR	800	24° 57' 21" S	53° 27' 18" W
4	Catanduvas- PR	762	25° 12' 10" S	53° 09' 25" W
5	Engenheiro Beltrão-PR	520	23° 47' 49" S	52° 16' 08" W
6	Floresta-PR	392	23° 35' 56" S	52° 04' 51" W
7	Guarapuava-PR	1120	25° 23' 42" S	51° 27' 28" W
8	Iepê-SP	400	22° 39' 39" S	51° 04' 33" W
9	Integrado-PR	630	24° 02' 45" S	52° 22' 58" W
10	Iporã-PR	400	24° 00' 10" S	53° 42' 14" W
11	Kaloré-PR	520	23° 49' 01" S	51° 40' 04" W
12	Klabin-PR	851	24° 17' 09" S	52° 16' 33" W
13	Palotina-PR	335	24° 17' 02" S	53° 20' 24" W
14	Ponta Grossa-PR	975	25° 05' 42" S	50° 09' 43" W
15	Record-PR	751	24° 17' 09" S	52° 16' 33" W
16	Sítio Casa Branca I-PR	630	24° 02' 45" S	52° 22' 58" W
17	Sítio Casa Branca II-PR	630	24° 02' 45" S	52° 22' 58" W
18	Terra Boa-PR	635	23° 46' 04" S	52° 26' 38" W

The trials were installed in a randomized block design with three replications. The plots were formed by four rows of 5 m long plants, with a spacing of 0.50 m between rows and 0.05 m between plants. Collecting the two central rows as a useful area. All cultural practices were conducted according to the recommendations of soybean plantation for the region.

Initially, a variance analysis was performed for each environment to verify the homogeneity of the residual variance.

Subsequently, combined analysis of variance was performed, considering the effects of genotype and environments with the primary objective being to determine possible interactions of genotypes with environments evaluated. The selective accuracy (RESENDE; DUARTE, 2007) was estimated as  $SA = (1-1/F)^{1/2}$ , where F is the F-test value for genotypes.

The multivariate GGE biplot analysis was based on the average phenotypic information, considering the

following model:  $\bar{Y}_{ij} - \mu = G_i + E_j + GE_{ij}$ , where  $\bar{Y}_{ij}$  represents the phenotypic average of genotype  $i$  in environment  $j$ ;  $\mu$  is the overall constant;  $G_i$  is the effect of genotype  $i$ ;  $E_j$  is the effect of environment  $j$ ; and  $GE_{ij}$  is the effect of the interaction between genotype  $i$  and environment  $j$ .

The GGE biplot model does not separate the genotype effect ( $G$ ) from the effect of the genotype x environment ( $GE$ ) interaction, keeping them together in two multiplicative terms, represented in the following equation:  $Y_{ij} - \mu - \beta_j = g_{i1}e_{1j} + g_{i2}e_{2j} + \varepsilon_{ij}$ , where  $Y_{ij}$  is the performance expected of genotype  $i$  in environment  $j$ ;  $\mu$  is the overall constant from the observations;  $\beta_j$  is the main effect of environment  $j$ ;  $g_{i1}$  and  $e_{1j}$  are the main scores for the  $i$ th genotype in the  $j$ th environment, respectively;  $g_{i2}$  and  $e_{2j}$  are the secondary scores for the  $i$ th genotype in the  $j$ th environment, respectively; and  $\varepsilon_{ij}$  is the residual not explained by either of the effects (“noise”).

Thus, construction of the biplot in the GGE model is accomplished by the simple dispersion of  $g_{i1}$  and  $g_{i2}$  for genotypes and  $e_{1j}$  and  $e_{2j}$  for environments, via singular value decomposition (SVD), according to the following equation:  $Y_{ij} - \mu - \beta_j = \lambda_1 \xi_{i1} \eta_{1j} + \lambda_2 \xi_{i2} \eta_{2j} + \varepsilon_{ij}$ , where  $\lambda_1$  and  $\lambda_2$  are the largest eigenvalues of the first and second principal components,  $PCE_1$  and  $PCE_2$ , respectively;  $\xi_{i1}$  and  $\xi_{i2}$  are the eigenvalues of the  $i$ th genotype for  $PCE_1$  and  $PCE_2$ , respectively; and  $\eta_{1j}$  and  $\eta_{2j}$  are the eigenvalues of the  $j$ th environment for  $PCE_1$  and  $PCE_2$ , respectively. The GGE biplot analysis was performed with the aid of R software (R DEVELOPMENT CORE TEAM, 2014).

To assess the suitability of a biplot to display the patterns of a double-entry table, the information ratio (IR) — proposed by Yan and Tinker (2006) — was calculated. The IR can be calculated for each principal component using the proportion of the total variance explained by each principal component multiplied by  $k$ . If there is no correlation between the environments, all of the  $k$  PCs must be completely independent, and the proportion of the total variance explained by each PC must be precisely  $1/k$ .

When there is a correlation between the environments, the proportion of the variation explained by the first PCs must be higher than  $1/k$ , and the variation explained by other PCs must be less than or equal to  $1/k$ . A PC with an  $IR > 1$  contains patterns (associations between environments); a PC with an  $IR = 1$  does not include patterns but may contain some independent information; and a PC with an  $IR < 1$  does not provide any profile or information (YAN, 2011).

## RESULT AND DISCUSSION

There was a significant effect ( $P < 0.01$ ) for all of the sources of variation (Table 3). Similar results were observed by Tessele *et al.* (2016), in soybean cultivars in southern Brazil. The significant difference between the genotypes indicates the existence of genetic variability among the soybean inbred lines. The significant effect of the environment demonstrates that the locations were sufficiently contrasting to discriminate the performance of the inbred lines. The significant effects of the genotype x environment ( $G \times E$ ) shows that the mean grain yield is distinct and that the genotype classifications may have changed between the environments evaluated. Thus, the selection of genotypes that efficiently must be specific to the environment and must not be performed regarding the average performance.

The experimental precision was evaluated through the estimation of accuracy. This parameter reflects the quality of the information and the procedures used in the prediction of genetic values (PIMENTEL *et al.*, 2014). Thus, a suitable parameter for evaluating the quality of experiments can be summarized regarding a single statistic that includes the coefficient of experimental variation, the number of replications, and the coefficient of genotypic variation (RESENDE; DUARTE, 2007). In this context, there is a significant level of accuracy, which represents higher precision in the identification of superior inbred lines in the environments evaluated.

**Table 3** - Summary of the combined analysis of variance for the grain yield ( $\text{kg ha}^{-1}$ ) of 24 inbred soybean lines evaluated in 18 environments in the states of Paraná and São Paulo, crop year of 2013/14

Sources of variation	Degrees of freedom	Means squares	Pr > F
Genotypes (G)	23	292,135.04	0,000
Environment (E)	17	597,194.38	0,000
Genotype x Environment (G x E)	391	83,372.26	0,000
Error	864	33,206.23	
Accuracy	0.93		
Mean	2768		

Through the analysis of main components, it was observed that the first three components explained approximately 70% of the global variation (Table 4). For Sousa *et al.* (2015), although these main components have a value below the ideal limit (70%), is acceptable, since there may be a complex interaction between the environments, especially when the number of genotypes and environment is too much. Thus, the GGE biplot method explained a large proportion of the sum of squares of genotypes and the GE interaction, indicating that there is a high level of confidence in the results produced using the multivariate technique.

The first three main components have IR values greater than one unit (Table 4) does. This demonstrates that these PCs present more information, and that is why they are actually more important in explaining the variation in the data. Therefore, the biplot was considered appropriate for representing the patterns related to the interaction. As the dispersion pattern was similar between PC1 / PC2 and PC1 / PC3, we chose to detail the behavior pattern of the genotypes in the environments considering PC1 / PC2, since it retained a higher percentage of variation.

The graph was divided into five sectors, these consisting of a line extending perpendicular to each side of

the polygon (Figure 2A). Regarding these segments, they indicate the average productivity ratio of the genotypes in association with the evaluated environments. Two of these sectors were presented in small sections, where it is not possible to identify values. For Qin *et al.* (2015), small sections with no values should be excluded.

Concerning the productive performance, the genotypes allocated on the vertex of the polygon were farther from the origin than the other genotypes within the sector bounded by them, and they are classified as the most responsive to the stimuli of the environments. These may be the genotypes showing better or worse performance in some or all of the environments and, therefore, they can be used to identify possible mega-environments. In turn, the genotypes located within the polygon are the least responsive to the stimuli of the environments (CHEELO *et al.*, 2017; SANTOS *et al.*, 2017). Genotypes 7, 13 and 18 represent the vertices of the polygon in which the environments are contained. Thus, they were used to identify at least three environmental groups (Figure 2A), which corroborates the results obtained by Amira *et al.* (2013), with soybean genotypes in Africa, where the biplot delimited three environmental sectors (mega-environments). For Oliveira *et al.* (2017) the number of mega-environments is variable and depends

**Table 4** - Singular value, explained variation, cumulative proportion, and information ratio (IR) for the four principal components (PCs) of the GGE biplot analysis of 24 inbred soybean lines evaluated in 18 environments in the states of Paraná and São Paulo, crop year of 2013/14

PC	Singular value	% explained	% accumulated	IR
1	1,365,847.27	40.62	40.62	4.98
2	632,357.37	18.81	59.43	2.31
3	313,443.42	9.32	68.75	1.14
4	269,285.57	8.01	76.76	0.98
5	214,499.55	6.38	83.14	0.78
6	144,826.63	4.31	87.45	0.53
7	109,556.88	3.26	90.71	0.40
8	75,937.27	2.26	92.97	0.28
9	63,592.69	1.89	94.86	0.23
10	48,422.53	1.43	96.29	0.18
11	34,909.07	1.04	97.33	0.13
12	24,190.26	0.72	98.05	0.09
13	20,939.71	0.63	98.68	0.08
14	16,942.87	0.50	99.18	0.06
15	12,953.92	0.38	99.56	0.05
16	8,334.85	0.25	99.81	0.03
17	5,495.01	0.17	99.98	0.02
18	801.18	0.02	100.00	0.00



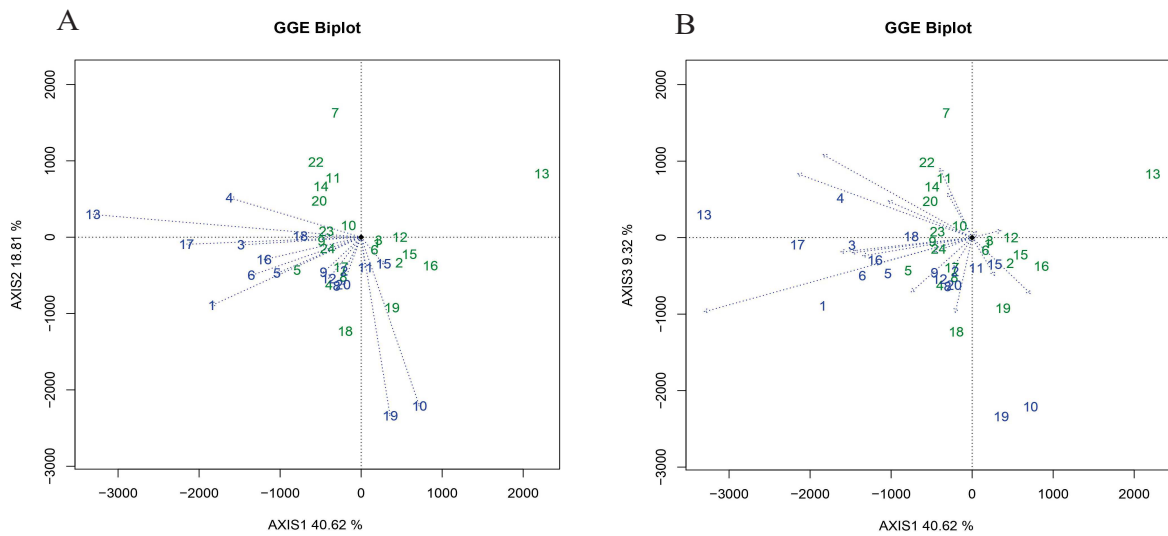
on the species, the characteristics of the genotypes and environments, as well as the character evaluated.

Group 1 is represented by environments 10, 15 and 19 (Integrado, Palotina e Sítio Casa Branca II), Group 2 formed by environment 4 (Catanduvas) and Group 3, where environments 1, 2, 3, 5, 6, 8, 9, 12, 13, 16, 17, 18 and 20 (Arapongas, Araruna, Cascavel, Catanduvas, Engenheiro Beltrão, Floresta, Guarapuava, Iepê-SP, Kaloré, Klabin, Ponta Grossa, Record, Sítio

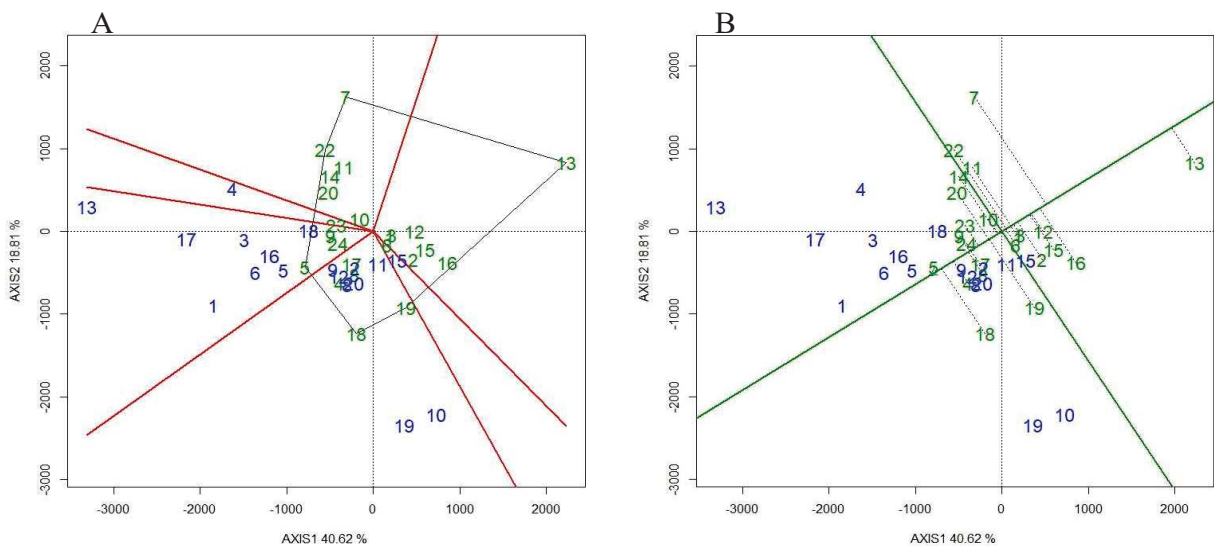
Casa Branca I e Terra Boa). The environment 11 (Iporã) is at the apex of a polygon, not falling into any of the classified groups, possibly because it gives the genotypes a low productivity, which is strongly unfavorable for cultivation.

Each sector of the polygons includes a set of environments correlated positively which can be considered by definition as mega-environments (YAN *et al.*, 2000; YAN, 2015). In group 1, the formation of

**Figure 1** - GGE biplot representing: (A) components 1 and 2 and (B) components 1 and 3, in 24 inbred soybean lines evaluated in 18 environments in the states of Paraná and São Paulo, crop year of 2013/14



**Figure 2** - GGE biplot representing: (A) the “which-won-where” graph and (B) means x stabilities, in 24 inbred soybean lines evaluated in 18 environments in the states of Paraná and São Paulo, crop year of 2013/14



mega-environments, classified genotypes 1, 2, 3, 6, 12, 13, 16 and 19 with the highest average of productivities for all environments of this group, these genotypes can be classified as stable to favorable environments. In addition, genotypes 7, 18 and 19 presented high stability, since there was less projection about axis 1. These, still had greater distance concerning axis 2, indicating high productivity (Figure 2B). The genotypes 1, 3, 6 and 10 stood out as unstable, and of lower productivity, in this case, immediate discarding is recommended in order to reduce expenses. In this way, those who have excelled should be emphasized.

The GGE biplot allows inferring about the specific adaptability of the genotypes with each environment. For example, genotype 5 showed a good productive relationship in environments 5, 6 and 16 (Engenheiro Beltrão, Floresta and Ponta Grossa). Genotypes 9, 8 and 17 were adapted to the environment 18 (Sitio Casa Branca I). Genotypes 1, 2, 3, 6, 12, 15 and 16 presented high productivity in environment 15 (Palotina). Thus, the results generated seem to be interesting for broad and specific recommendations of genotypes in the final phase of an improvement program.

The environments on the longer vector graph are considered the most discriminating (YAN; TINKER, 2006), indicating that genotypes tend to express good information about genotype differences. Therefore, environments are meant as favorable in preliminary trials of cultivars. The environments 2, 8, 9, 11, 12 and 20 (Araruna, Guarapuava, Iepê, Iporã, Kaloré and Terra Boa) presented the smallest vectors, so they were the least

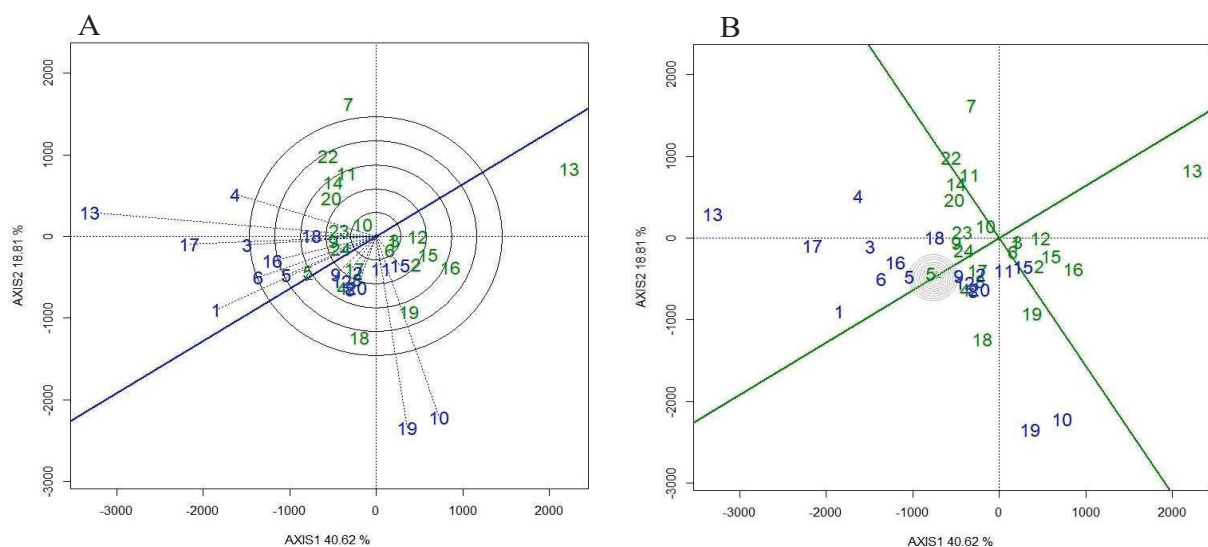
discriminating environments, so these environments are the least indicated for initial tests (Figure 3A).

The grain yield values and the stability of the genotypes were evaluated based on the average environment coordination (AEC) (Figure 3B). In this method, an ideal environment is defined based on the mean score of principal components 1, 2 and 3 for all of the environments, which is represented in the graph by a small circle. The line that passes through the origin of the biplot and the ideal environment is referred to as the axis of the ideal environment, which represents the AEC abscissa, whereas the small arrow points to the highest genotypic value with the main effect. The AEC ordinate is the axis that passes through the origin of the biplot — it is perpendicular to the AEC abscissa and indicates a more significant impact of the genotype x environment interaction and lower stability, and it separates the genotypes that are superior and inferior to the overall mean (YAN; TINKER, 2006; SANTOS *et al.*, 2017).

At least one of the environments [17 (Record)] presented a small angle about the AEC, indicated as a representative environment. This environment is classified as ideal for the selection of genotypes during the breeding process, since, it was discriminant and representative. However, environments 10 and 19 (Integrado and Sítio Casa Branca II) were discriminating but were not representative. It means that they were useful in identifying genotypes with specific adaptability to target environments.

Genotypes 5, 9, 23 and 24 showed high productivity and excellent adaptability and stability (Figure 3B). These genotypes were kept closer to the central circle, which are

**Figure 3** - GGE biplot is representing: (A) the discrimination and representativeness graph of the and (B) means x stabilities for grain yield (kg ha<sup>-1</sup>), in 24 inbred soybean lines evaluated in 18 environments in the states of Paraná and São Paulo, crop year of 2013/14



classified as ideal genotypes. Santos *et al.* (2016), report that an ideal genotype should have consistently high grain yield in all the environments in question. However, it is important that these genotypes are stable and responsive to environmental variations. Genotypes 7 and 13 were the least responsive, being unstable and with low grain yield.

## CONCLUSIONS

1. Genotypes 5, 9, 23 and 24 showed good adaptability and stability and high grain yield;
2. The Record-PR environment was the most discriminating and representative, in this way, it is highly indicated for the selection of genotypes and recommendation of the cultivars;
3. The Iporã-PR environment provided low grain yield of the studied inbred lines; this is unfavorable to cultivation;
4. GGE biplot analysis was effective in discriminating superior genotypes in specific cropping environments, as well as discriminating favorable environments.

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