

Original Article

Comparative analysis of adaptability and stability of soybean genotypes for cultivar registration and protection

Análise comparativa da adaptabilidade e estabilidade produtiva de genótipos de soja para registro e proteção de cultivares

A. P. L. Costa^a, A. C. R. Moitinho^a , A. P. Silva^a, L. O. Amaral^a , J. S. Souza^{a*}  and S. H. Unêda-Trevisoli^a 

^aUniversidade Estadual Paulista – Unesp, Faculdade de Ciências Agrárias e Veterinárias, Jaboticabal, SP, Brasil

Abstract

One of the challenges for genetic and plant breeding is the selection of genotypes that are increasingly adapted, productive, and stable to the cultivation environments, without losing the desired agronomic traits. These evaluations are important for determining the ideal genotypes for each environment. Without these evaluations, the behavior of cultivars or genotypes cannot be predicted, affecting performance, and causing losses for farmers. This work aimed to characterize, by different methodologies, the agronomic performance, adaptability, and stability of soybean genotypes in a preliminary trial, to select the superior genotypes, aiming at the Registration and Protection of Cultivars. The experiment was conducted in the field in a randomized block design with two replications, where 50 soybean genotypes were evaluated, including 3 checks, during two agricultural, two different environments. Agronomic traits were evaluated: number of days to maturity, number of days to flowering, plant height at maturity, the weight of a thousand grains, lodging, oil content, and grain yield. To determine the adaptability and productive stability of the genotypes, GGE biplot multivariate prediction methodologies and REML/BLUP mixed models were used and compared, using the main agronomic traits of production and oil content, which are of industrial importance in human and animal nutrition. The methods of the analysis showed differences regarding the ordering of adaptability and stability, however, they were unanimous in considering the genotypes as superior: 24; 29; 30; 32; 34, and 42 for yield and 4; 17; 37, and 44 for oil content. The predominant pedigree of the selected genotypes consists of bi-parental crosses, except genotype 24, which comes from a quadruple cross.

Keywords: *Glycine max*, GGE biplot, REML/BLUP.

Resumo

Um dos desafios do melhoramento genético e vegetal é a seleção de genótipos cada vez mais adaptados, produtivos e estáveis aos ambientes de cultivo, sem perder as características agrônômicas desejadas. Essas avaliações são importantes para determinar os genótipos ideais para cada ambiente. Sem essas avaliações, não é possível prever o comportamento de cultivares ou genótipos, afetando o desempenho e causando prejuízos aos agricultores. Este trabalho teve como objetivo caracterizar, por diferentes metodologias, o desempenho agrônômico, a adaptabilidade e a estabilidade de genótipos de soja em um ensaio preliminar, para selecionar os genótipos superiores, visando ao Registro e à Proteção de Cultivares. O experimento foi conduzido no campo em um delineamento em blocos casualizados com duas repetições, onde foram avaliados 50 genótipos de soja, incluindo 3 controles, durante duas safras agrícolas, ou seja, dois ambientes diferentes. Foram avaliadas as características agrônômicas: número de dias para a maturação, número de dias para a floração, altura da planta na maturação, peso de mil grãos, acamamento, teor de óleo e rendimento de grãos. Para determinar a adaptabilidade e a estabilidade produtiva dos genótipos, foram usadas e comparadas as metodologias de previsão multivariada GGE biplot e os modelos mistos REML/BLUP, usando as principais características agrônômicas de produção e teor de óleo, que são de importância industrial na nutrição humana e animal. Os métodos de análise mostraram diferenças quanto à ordenação da adaptabilidade e da estabilidade, mas foram unânimes em considerar os genótipos superiores: 24; 29; 30; 32; 34 e 42 para produção e 4; 17; 37 e 44 para teor de óleo. O pedigree predominante dos genótipos selecionados consiste em cruzamentos biparentais, exceto o genótipo 24, que vem de um cruzamento quádruplo.

Palavras-chave: *Glycine max*, GGE biplot, REML/BLUP.

*e-mail: jardel.souza@unesp.br

Received: May 21, 2024 – Accepted: January 22, 2025



This is an Open Access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

1. Introduction

Soybean is the main oilseed and protein crop of the world, used for the production of animal feed, numerous food components and non-food products. In 2023, global soybean production reached an all-time high of 401 million tons. While Brazil and the United States cultivated 163 and 112.8 million tons, respectively (USDA, 2023).

Soybeans have their main source of germplasm for breeding in China, where they originate, and have a history of cultivation of more than 5,000 years. In Brazil, the crop has a recent history of cultivation (around 70 years), and began with cultivation to improve soil fertility, however, currently numerous soybean varieties have been developed to meet the diverse needs of the crop. (Guo et al., 2022). As this crop is grown in different regions of Brazil, it shows variability in its production performance, which leads breeding programs to select productive genotypes with desired characteristics in different environments (Matei et al., 2018; Komariah et al., 2023).

Due to the performance fluctuation presented by the presence of the genotype (G) $\times$ environment (A) interaction (IGA), conducting experiments is based on different locations for selecting superior genotypes and indicating cultivars that show more expressive genetic gains (Alves et al., 2018). Among the methodologies used, the adaptability and stability analyses have relevance when used in characters of greater interest as production and oil content for the industry, thus aiming for a safer recommendation of cultivars (Bernardo, 2020).

Several methods are used to reliably estimate genotypic performance. We will highlight here the adaptability and stability evaluation methodologies, through the analysis of the main effects of the genotype and the interaction genotype $\times$ environment (GGE biplot) (Yan et al., 2000). Another very important methodology uses mixed models (REML/BLUP), which allows the estimation of variance components by restricted maximum likelihood (REML) and prediction of genetic values by the best linear non-biased prediction (BLUP), based on the harmonic mean method of the relative performance of predicted genetic values (MHPRVG) (Resende, 2007).

At present, the selection of superior conventional genotypes with high productivity is of great importance, as these genotypes can be used as progenitors for the introduction of new transgenic traits, expanding the potential for genetic improvement. Furthermore, they cater to a growing niche of consumers who prefer non-transgenic products, offering alternatives to the global agricultural market (Colombari Filho et al., 2013; Resende, 2007; Guo et al., 2022).

There is still disagreement about the ideal statistical model to evaluate performance and estimation of superior genetic gain. Because the difference in the use of existing methods is in the accuracy of the comparison of means. Thus, it is necessary to compare the methodologies, aiming to increase the accuracy in the selection process of soybean genotypes using adaptability and stability parameters (Colombari Filho et al., 2013).

The objective was to characterize the agronomic performance, adaptability, and stability conventional and

RR soybean genotypes in a preliminary trial, by different methodologies, and to select the superior genotypes to compose future trials of Value for Cultivation and Use, aiming at Registration and Protection of Cultivars.

2. Material and Methods

The experiments were conducted in the field in the agricultural years 2018/2019 and 2019/2020 in the no-till system at São Paulo State University - UNESP/FCAV Jaboticabal, Brazil, located, at 21°15' S and 48°18' W, at an altitude of approximately 575 m, on a very argillaceous eutrophic Red-Shaded Latosol, with gently undulating relief. The region's climate is of tropical type (Aw) with an average annual temperature of 22.2°C and an average rainfall of 1,400 mm (Gazotto et al., 2020).

For analysis and interpretation, each crop year was considered as an environment, being, 2018/2019 environment 1 and, 2019/2020 environment 2. In addition, the FCAV's Agroclimatology Station was used to monitor rainfall during the experiments, resulting in accumulated rainfall of 1,053 mm for Environment 1 and 1,038 mm for Environment 2.

We used 47 superior soybean genotypes, developed by the genetic improvement program of UNESP/FCAV Jaboticabal, obtained by artificial hybridization between cultivars, with 41 genotypes from crossings of different biparental genealogies, 3 from quadruple crossings, 3 from octuple crossings, and 3 commercial cultivars (M5947IPRO, AS3680IPRO and TMG 1175 RR) used as witnesses (Table 1).

The randomized block design was used, with two repetitions, and 12 to 15 plants were kept per linear meter. Each experimental plot was composed of four 5 m long rows spaced 0.5 m apart, considering the two central rows as the useful area and leaving aside 0.5 m at each end of the rows (totaling 4.0 m²). Fertilization, management, and phytosanitary control followed the recommendations for soybean cultivation (Embrapa, 2018).

Phenotypic characterization was performed by evaluating the following agronomic traits: number of days at maturity (NDM), between emergence and R8 stage; the number of days at flowering (NDF), from emergence to the R1-R2 stage; plant height at maturity (APM), arithmetic mean of the measurement in centimeters of five random plants in the useful area of the plots, measured from the base of the stem (at the soil surface) to the top of the canopy; lodging (AC) was evaluated using a visual scale of scores, 1 = fully erect plants, to 5 = lodged plants; thousand-grain weight (PC) obtained by the average of the weight of four samples with 1000 grains; oil content (OIL) determined in samples of whole soybeans by the Near Infrared Reflectance technique; yield grain (PG) obtained by the weight of grains harvested in the useful area of the plots extrapolated in kg.ha⁻¹, being corrected to 13% of grain humidity.

Aiming at the selection of the most adapted and stable genotypes to the environment, the environment was considered a random effect, while the genotypes were treated as fixed effects for modeling purposes. Although the evaluation was conducted over only two years, which

Table 1. Genealogy of soybean genotypes from the Soybean Genetic Improvement Program of FCAV/UNESP and commercial cultivars used in the experiments. Jaboticabal, SP.

Crossing	Derived Genotypes	Crossing	Derived Genotypes
BR-16 x Paraná	1	BR-16 x Ocepar-5	30
FT-Cometa x Bossier	2; 3; 4; 5; 6; 7; 29	JAB.00-05-1/5C3B x M 7211 RR	31
FT-Cometa x IAC-13	8	JAB.00-05-5/4A2D x M 7578 RR	32; 45
FT-Cometa x IAC-10	9	JAB.00-05-1/5C3B x M 7639 RR	33; 37; 38
FT-Cometa x Paraná	10; 11; 12; 13; 14; 15	JAB.00-05-5/4A2D x M 7908 RR	34; 35; 39
EMBRAPA 48 x Conquista	16; 17; 18	JAB.00-06-2/3I3D x M 8236 RR	36; 40
CAC 1 x BR-16	19	JAB.00-01-21/4M1D x M 8336 RR	41; 42
CAC 1 x BR-19	20	JAB.03-3/1H2D x M 8360 RR	43
IAC 17 x BR-16	21	JAB.04-1/5A4D x M 8230 RR	44
CD 204 X Liderança	22	JAB.03-3/1C3D x M 7211 RR	46
(BRS -137 x Hartwig) x (IAC-8-2 x Embrapa 48)	23	JAB.04-1/5A4D x M 7639 RR	47
(Hartwig x BRS-134) x (Coodetec-201 x BRS MS Bacuri)	24	M5947IPRO*	48
(Hartwig x BRS-134) x (Tainung-4 x Renascença)	25	AS3680IPRO*	49
[[Tainung-4 x Renascença] x (FT- Estrela x BRS-134)] x [(EMBRAPA-59 x CD-204) x (CAC-1 x BRS-137)]	26; 28	TMG 1175 RR*	50
[[(BR-16 x Tainung-3) x (CAC-1 x BRS- 137)] x [(Embrapa-59 x FT-2) x (Conquista x CD-204)]]	27		

could be considered a limited timeframe for defining the environment as a random effect, this choice was made to capture environmental variability and its impact on genotypic stability. The genotypes were considered fixed because they represent a specific set of interest within the regional breeding program of UNESP, rather than a random sample of a broader population. The evaluation of genetic variability between treatments (controls and genotypes) was based on the analysis of variance of the main effects and the interaction between variation sources, tested by the F test. The means were compared using the Scott-Knott test at 5% probability, with the lodging (AC) data transformed using $\sqrt{X}$.

After verifying the significance of the interaction genotypes x environments using the statistical computer program Genes, version 2020 (Cruz, 2013), the adaptability and stability analyses of the 50 soybean genotypes were performed by the GGE Biplot methodologies (Yan et al., 2000) using the software RStudio, and MHPRVG for mixed models using the software Selegen.

The GGE Biplot method considers the effect of genotype and its interaction with years. Thus, the effects of environments were considered fixed, while the effects of genotypes were considered as random. For only the main effect of genotype and IGA are important and interpreted simultaneously in two multiplicative terms, which can be seen in the following equation:

$$Y_{ijk} = m + g_i + l_k + glik + r_{j/k} + e_{ijk} \quad \text{Equation 1}$$

Where: Y_{ijk} = is the observed value at the i-th genotype, j-th repetition, at the k-th location; m = is the overall mean; g_i = is the effect of the i-th genotype; l_k = is the effect of the k-th location; $glik$ = is the effect of the interaction of the i-th genotype with the k-th location; $r_{j/k}$ = is the effect of the j-th repetition within the k-th location, e_{ijk} = error.

Performing this analysis assuming the genotypes as random, was assigned only to the variables of the greatest importance for selection in this study (PG and OIL), considering the year 2018/2019 as Environment 1 and the year 2019/2020 as Environment 2.

For the Restricted Maximum Likelihood/Best Linear Unbiased Predictor (REML/BLUP) analysis, the statistical model of genetic evaluation by the highest values of the harmonic mean of the genotypic values was used:

$$y = Xr + Zg + Wb + e \quad \text{Equation 2}$$

Where: y is the vector of data, r is the vector of repetition effects added to the overall mean, g is the vector of genotypic effects, b is the vector of block effects, and e is the vector of errors or residuals. The capital letters in the formula represent the incidence matrices for these effects.

This statistical model allows to obtain joint inferences of adaptability and stability by ranking obtained from the Mean Harmonic Relative Performance of Genotypic Values (MHPRVG), by the accumulated genetic gain (GA) with the selection generations:

$$GA = \text{new mean} + g - (u + g) \quad \text{Equation 3}$$

Where: GA is the cumulative genetic gain; new mean = overall mean of productivity; g is the additive genetic effect and (u + g) is the additive genetic value.

Thus, by simultaneously correcting the data for environmental effects, estimate the variance components and genetic parameters. If aims to maximize genetic gain and efficiency of breeding programs, it ensures the ability to evaluate many genitors, being promising in the intensity of selection in terms of gain (Resende, 2007).

3. Results and Discussion

The overall average soybean yield grain of the experiment for the two environments was 3326,59 kg.ha⁻¹. Table 2 presents the analysis of the variance of the main effects and the interaction between the sources of variation for each agronomic trait evaluated.

The analysis of variance showed significant genotype x environment interaction for most of the agronomic traits evaluated. There were exceptions for thousand-grain weight and oil content indicating that the years of cultivation should be considered as distinct environments for the significant traits.

The coefficients of variation obtained in the experiments evaluated were of low magnitude (CV ≤11,51%). This allowed us to consider that the experiments presented good accuracy and that there is no major interference from uncontrolled factors (Table 2). SOARES et al. (2017) confirm that the constancy in the performance of experiments that involve environments justifies the good precision of the data, and that results in low CV rates, which obtained rates around 8.45%. For the source of variation Genotypes (Treatments), all the evaluated traits were significant, indicating the variability present among them.

For the genotypes, there was a significant interaction for all at 1% probability, which indicates that despite the high number of genotypes they differed from each other. For the environment, the traits that did not obtain significant difference were TWG and PG. This leads us

to consider that the environment did not interfere with the plant performance, being for the improvement of a favorable condition in which it presents constancy and stability between environments. When analyzing the IGE, the PG trait presented significance at 1% probability, and for OIL and TWG the test was not significant.

Since the effect of genotypes was significant for all characters, to better illustrate the difference between them, comparisons of means of the genotypes by the Scott and Knott test were represented in scatter plots (Figures 1, 2, 3 and 4).

For the grouping of cycles in NDF (Figure 1) and NDM (Figure 2), genotypes 4, 17, 48, and 49 showed fewer days, indicating greater earliness in both environments. For flowering, these genotypes demonstrated shorter NDF values, while for maturity, they presented reduced NDM values as well. In contrast, genotypes 18, 36, 43, and 47, which displayed higher NDM values, behaved as the later ones when analyzed for maturity in both growing seasons. Storck and Ribeiro (2011) relate that phenotypic expression in NDM is associated with high heritability values, indicating great potential for the selection of soybean genotypes.

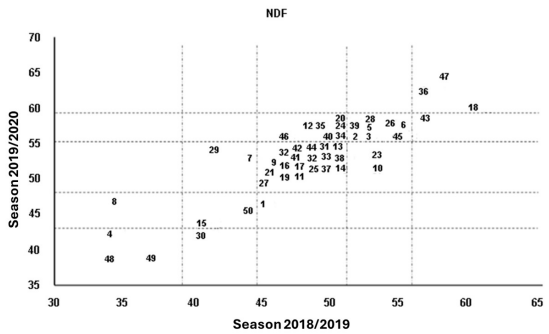


Figure 1. Projection of 50 soybean genotypes as a function of environments for the NDF trait. The dotted lines in the x and y axes represent the separation point of the different groups according to the Scott-Knott grouping test at 5% probability.

Table 2. Mean squares (QM) and their respective significances obtained in the analysis of variance for the traits: number of days to flowering (NDF), number of days to maturity (NDM), plant height at maturity (APM), lodging (AC), thousand-grain weight (PC), oil content (OIL) and grain yield (PG) of 50 soybean genotypes in the seasons 2018/2019 and 2019/2020. Jaboticabal, SP.

FV	GL	MQ						
		NDF	NDM	APM	AC ¹	PC	OIL	PG
Block	3	2.10	5.30	178.91	0.01	1.66	0.84	317555.20
Genotype	49	113.45**	80.43**	950.48**	0.12**	15.28*	3.78**	668965.20**
Environment	1	1176.12**	1095.12**	35154.91**	2.26**	16.84 ^{ns}	24.73*	139860.20 ^{ns}
IGA	49	8.38**	17.49**	126.96*	0.05**	1.12 ^{ns}	0.43 ^{ns}	260651.60**
Residue	98	4.77	6.25	76.40	0.02	0.77	0.51	47774.90
Total	199	-	-	-	-	-	-	-
Means		50.71	118	75.90	1.64	13.22	21.16	3326.50
CV(%)		4.31	2.12	11.51	9.56	6.64	3.40	6.57

¹ grades from 1 to 5. ** significant at 1% probability. *significant at 5% probability. ns not significant. CV(%) coefficient of variation in percent; Mean = overall average of the experiment.

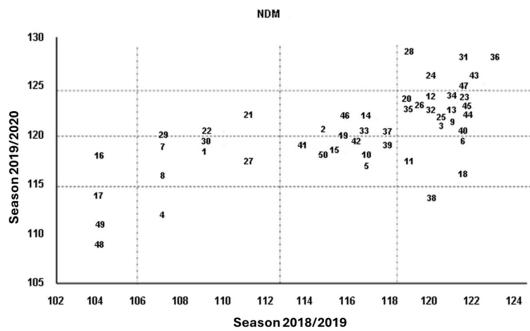


Figure 2. Projection of 50 soybean genotypes as a function of environments for the NDM trait. The dotted lines on the x and y axes, represent the separation point of the different groups according to the Scott-Knott grouping test at 5% probability.

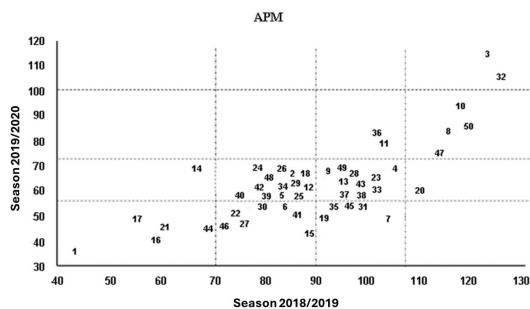


Figure 3. Projection of 50 soybean genotypes as a function of environments for the APM trait. The dotted lines on the x and y axes represent the separation point of the different groups according to the Scott-Knott grouping test at 5% probability.

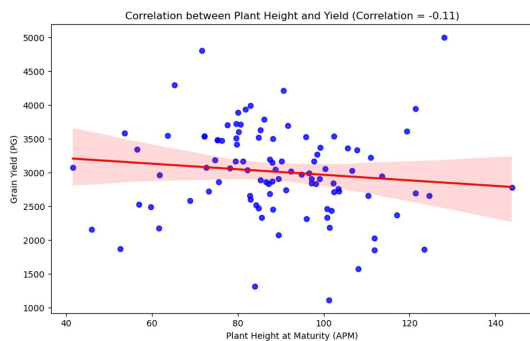


Figure 4. Correlation between plant height at maturity (APM) and grain yield (PG).

Soybean plants that reach height ≥ 100 cm are subject to lodging, making harvesting difficult and consequently causing grain losses, and the ideal height of a maturing soybean plant is considered to be around 80 cm (Peluzio et al., 2014). It was possible to observe that the genotypes 1; 16; 17; 21 and 44, present a lower height and are among the lowest lodging grades, indicating a more erect behavior, while genotype 32 presents a higher height and high lodging for both traits (Figure 3).

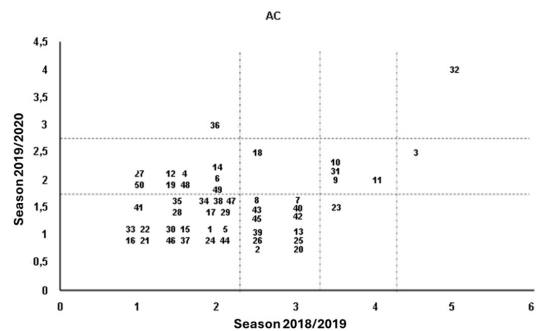


Figure 5. Projection of 50 soybean genotypes as a function of environments for the AC trait. The dotted lines in the x and y axes represent the separation point of the different groups according to the Scott-Knott grouping test at 5% probability.

Taller plants at maturity can result in higher productivity if they do not experience lodging, as this trait increases the usable area for the formation of productive nodes. While this principle, as described by Leite et al. (2016), is relevant, the data presented in Figure 5 do not provide direct evidence to confirm this relationship. Specifically, although Genotype 32's higher productivity could be consistent with this idea, the figure alone does not allow us to conclusively associate greater plant height with increased productivity. Although plant height can be considered a potentially beneficial characteristic in the selection of more productive genotypes when topping is avoided, the results of this study did not show a significant positive correlation between plant height and productivity, with a correlation of -11%. Therefore, based on the data analyzed, there is not enough evidence to support this relationship in this research (Figure 4).

The mixed model method using the MHPRVG estimates generates results that can be directly interpreted as genotypic values, already penalized or discounted by the stability and adaptability estimates. According to Melo (2009), the analysis of the Coefficient of Variation must be considered according to the crop studied. Generally, it is adopted as a criterion to consider in VCU experiments, experimental coefficients of variation (CvE) less than or equal to 20% as being ideal. The heritability coefficient (h^2) is the ratio of the genetic variance to the phenotypic variance. The selection precision is related to the values determined for a given trait, with the heritability coefficients classified as low < 0.2 , medium 0.2 to 0.5, and high > 0.5 , obtaining greater success in the selection of traits with higher coefficients (Ramalho et al., 2012).

The Coefficient of Genetic Variation (CVg) is an essential parameter for understanding the extent of genetic variability in a population for a specific trait. It quantifies the available genetic variation that can be harnessed through selection. According to Melo (2009), high CVg values are advantageous as they indicate a greater potential for genetic selection. In the study presented in Table 3, the CVg values varied significantly across traits and seasons. Specifically, Plant Height at Maturity (APM), it reached up to 17.92. Additionally, for the Number of

Table 3. REML analysis of the Mean Harmonic Genotypic Values (MHVG), by means of variance components and genetic parameters for the agronomic traits: number of days to flowering (NDF), number of days to maturity (NDM), plant height at maturity (APM), lodging (LD), thousand-grain weight (PC), grain yield (PG) and oil content (OIL).

Component	NDF (days)	NDM (days)	APM (cm)	AC ¹	PC (g)	PG (kg ha ⁻¹)	OIL (%)
Season 1							
σ^2_g	29.65	15.27	255.50	0.64	4.29	229018.78	0.75
σ^2_b	0.53	1.14	10.28	0.05	0.12	1623.27	0.09
σ^2_e	4.25	9.11	82.24	0.46	0.97	12986.29	0.77
σ^2_f	34.43	25.52	348.03	1.17	5.38	243628.26	1.63
h^2	0.86 ± 0.26	0.56 ± 0.20	0.73 ± 0.24	0.54 ± 0.20	0.79 ± 0.25	0.94 ± 0.27	0.46 ± 0.19
c^2_b	0.01	0.04	0.02	0.05	0.02	0.01	0.05
$h^2_{m\ lin}$	0.93	0.73	0.86	0.73	0.89	0.97	0.66
Ac	0.96	0.84	0.92	0.85	0.94	0.98	0.81
CV _g	11.27	4.48	17.92	16.16	16.01	14.50	4.18
CV _e	4.26	2.57	10.16	10.86	7.62	3.45	4.23
CV _g /CV _e	2.65	1.50	1.76	1.48	2.10	4.20	0.99
SEP	1.40	1.74	5.95	0.41	0.66	79.46	0.50
M	48.29	115.49	89.18	2.22	12.93	3.300.14	20.81
Season 2							
σ^2_g	26.48	12.10	204.69	0.26	3.14	188006.01	0.83
σ^2_b	0.66	1.27	8.78	0.02	0.07	10321.16	0.03
σ^2_e	5.30	10.16	70.28	0.21	0.57	82569.31	0.26
σ^2_f	32.45	23.54	283.76	0.50	3.78	280896.49	1.12
h^2	0.81 ± 0.25	0.51 ± 0.20	0.72 ± 0.24	0.51 ± 0.20	0.82 ± 0.25	0.66 ± 0.23	0.73 ± 0.24
c^2_b	0.02	0.05	0.03	0.05	0.01	0.03	0.02
$h^2_{m\ lin}$	0.90	0.70	0.85	0.70	0.91	0.81	0.86
Ac	0.95	0.83	0.92	0.84	0.95	0.90	0.92
CV _g	9.68	2.89	19.83	19.50	13.11	12.93	4.23
CV _e	4.33	2.64	13.38	13.47	5.59	8.56	2.37
CV _g /CV _e	2.24	1.09	1.48	1.44	2.35	1.51	1.78
SEP	1.55	1.89	5.47	0.27	0.51	183.98	0.33
M	53.14	120.34	62.65	1.57	13.51	3353.03	21.51

¹notes from 1 to 5; σ^2_g : Genotypic variance; σ^2_b : Between-block variance; σ^2_e : Environmental residual variance; σ^2_f : Phenotypic variance; h^2 : Heritability of genotypic effects; c^2_b : coefficient of determination of block effects; $h^2_{m\ lin}$: heritability of lineage mean; Ac: accuracy of genotype selection; CV_g: coefficient of genetic variation; CV_e: coefficient of environmental variation; CV_g/CV_e: Ratio; SEP: standard deviation of the predicted genotypic value; μ : Overall mean.

Days to Maturity (NDM %), the CV_g was as low as 2.89, while for APM in different seasons, it was as high as 19.83. These variations in CV_g demonstrate the diverse genetic potential within the evaluated soybean population for these agronomic traits.

In Table 3, it can be seen from the MHVG results that in Season 1, the coefficient of environmental variation (CV_e) ranged from 2.57% (NDM) to 10.86% (AC), while in Season 2 it ranged from 2.64% (NDM) to 13.47% (Ac). Because the variables are the same and the range of variation is similar, the cultivars behave similarly in the environments studied. Similar results were obtained by Tadege et al., (2014).

Except for OIL (Table 3), which varied between environments about the average h^2 value in Season 1, the other variables remained with high heritability values. As the variable PG that when presenting a value of $h^2 = 94\%$, indicates prospects of success by the phenotypic selection, confirmed with values greater than 1.0 (one) presented by all variables in the quotient CV_g/CV_e. This is an indication of a good condition for the selection of genotypes for the trait, provided by the indication of greater genetic than environmental variance. However, the high h^2 value for PG may also be influenced by the significant G x E interaction variance detected in the study, as well as by the substantial genetic variance resulting from the

broad genetic variability of the lines, which originate from a wide range of sources (Table 1). These factors should be considered when interpreting the results, as they emphasize the complex interplay between genetic diversity and environmental interactions.

value for PG may also be influenced by the significant G x E interaction variance detected in the study, as well as by the substantial genetic variance resulting from the broad genetic variability of the lines, which originate from a wide range of sources (Table 1). These factors should be considered when interpreting the results, as they emphasize the complex interplay between genetic diversity and environmental interactions.

The success achieved by high soybean yields is directly linked to several factors such as soil heterogeneity, experimental material, the competition between and between plots, sampling and plot size, etc. The accuracy values (Table 3) for the two environments showed values of up to 98% in PG. These accuracy values indicate credibility and safety in selecting superior genotypes for the characters evaluated (Pimentel-Gomes, 2000).

The mixed model analysis allows for the evaluation of genotypes across environments, ranking them according to the variables analyzed (Gonçalves et al., 2014). To better determine the most stable and adapted genotypes, the MHPRGV method was used to predict the genotypic values of OIL and PG, aiming to select the ten best genotypes in Seasons 1 and 2

According to Carvalho et al. (2016), stable genotypes are not necessarily more productive. However, genotypes 32 and 30 (Table 4) lead the ranking of the adaptability and stability analysis as the most productive genotypes and showed better performance by the Mean Harmonic Relative Performance of Genotypic Values (MHPRVG) analysis by the mixed model's method using REML/BLUP.

The stability of a genotype is characterized by its consistent performance across various environments, showing resilience to changes in environmental conditions. This is how Alves et al. (2018) define the concept. In the context of this study, genotypes 32, 30, 50, and 24 have demonstrated stability, consistently ranking among the top ten genotypes over two growing seasons. This

Table 4. Mean Harmonic Analysis of the Relative Performance of Genotypic Values (MHPRVG), for descending classification of the 10 best genotypes evaluated in Seasons 1 and 2. Jaboticabal, SP.

Genotype	<i>g</i>	<i>u + g</i>	GA	New Mean	Genotype	<i>g</i>	<i>u + g</i>	GA	New Mean
Grain Production (kg ha ⁻¹)									
Environment 1					Environment 2				
32	1529.30	4829.40	1529.30	4829.40	32	891.20	4244.20	891.20	4244.20
30	1329.10	4629.20	1429.20	4729.30	30	817.70	4170.70	854.40	4207.50
44	775.30	4075.50	1211.20	4511.40	35	703.20	4056.30	804.00	4157.10
38	680.20	3980.30	1078.50	4378.60	2	646.80	3999.80	764.70	4117.80
41	612.50	3912.60	985.30	4285.40	21	574.60	3927.60	726.70	4079.70
50*	539.30	3839.40	910.90	4211.10	18	506.80	3859.90	690.10	4043.10
34	446.30	3746.50	844.60	4144.70	40	478.00	3831.00	659.80	4012.80
42	423.10	3723.20	791.90	4092.00	26	476.50	3829.60	636.90	3989.90
29	391.00	3691.10	747.30	4047.50	50*	399.70	3752.70	610.50	3963.50
24	352.30	3652.50	707.80	4008.00	24	314.90	3668.00	580.90	3934.00
Oil content (%)									
8	2.43	23.24	2.43	23.24	44	1.55	23.07	1.55	23.07
44	1.11	21.92	1.77	22.58	33	1.38	22.90	1.47	22.98
50*	1.06	21.87	1.53	22.34	50*	1.03	22.55	1.32	22.84
48*	0.99	21.81	1.40	22.21	8	0.98	22.50	1.24	22.75
16	0.84	21.66	1.29	22.10	17	0.95	22.47	1.18	22.70
17	0.75	21.57	1.20	22.01	4	0.89	22.41	1.13	22.65
33	0.74	21.56	1.13	21.95	35	0.77	22.29	1.08	22.60
4	0.71	21.53	1.08	21.89	49*	0.68	22.20	1.03	22.55
46	0.70	21.52	1.04	21.85	34	0.62	22.14	0.98	22.50
37	0.57	21.39	0.99	21.80	37	0.60	22.12	0.95	22.46

g: additive genetic effect; *u+g*: additive genetic value; GA: accumulated genetic gain; *u*: overall average: yield = 3326.59; oil content = 21.16.

*: controls.

repeated performance is indicative of their stability and adaptability, aspects which are crucial for reliable agricultural production, as detailed in Table 4.

From the analysis of the predicted genotypic values for grain yield (Table 4), the predicted gains from selecting the ten superior genotypes with higher means based on the additive effect obtained genetic gains ranging from 707.8 kg ha⁻¹ to 1529.3 kg ha⁻¹ in Season 1 and from 580.9 kg ha⁻¹ to 891.2 kg ha⁻¹ in Season 2.

The ten best genotypes selected in the two environments considering the New Average obtained for grain production, exceeded the average soybean yield obtained in the State of São Paulo (CONAB, 2020). Evidence that the most productive genotypes selected were also the most stable and adapted by this method.

Due to the need to select superior genotypes from the point of view of productivity, combined with specific traits for the consumer market, such as high oil content (Peluzio et al., 2014), the genotypes were classified according to the performance presented in the two seasons (Table 4) for OIL.

By the MHPRVG method, it was possible to verify that the conduction of the experiments was favorable in relation to the stability of the environments. The oil content obtained constancy in the phenotypic variability. The genotypes 8; 44; 50; 17; 33; 4 and 37, remained in the selection among the ten best in both environments for oil content. For the productivity character, genotypes 32, 30, 50, and 24 showed greater productive stability in both environments.

In order to aid the visual selection of the best genotypes, the GGE biplot method was used, which has as a parameter the plotting of the scores associated with the environments and the genotypes, presenting the values of the projections on the ordinate and abscissa axes, generating an ordering by stability and productive performance (Soares et al., 2017).

The oil content scores, it is observed that within the mega-environment formed are inserted the genotypes 44; 50; 4; 17; 49; 37; 38, and 26 (Figure 6). Genotype 26 is in the center of the limiting circle of adaptability and stability, coinciding with the overall mean of the experiment. At the vertex of the polPGon is genotype 44, indicating its superiority over the environments and the other genotypes.

For Season 2 (the crop year 2019/2020) (Figure 5) the ranking is 44>17>4>49>26, while in Environment 1 (the crop year 2018/2019) the genotypes with the best adaptability and stability were 44>50>37>38>26. Genotype 8 despite presenting superiority among the genotypes in oil content is represented outside the limiting circle. This indicates that it did not show adaptability and stability in any environment. The same occurred with genotype 9, which showed the lowest oil content.

In the biplot representation of the yield, the polPGon is fully inserted in the limiting circle of adaptability and stability (Figure 7). Indicating no genotypes with discrepant values for more or less.

Within the mega-environment formed, genotype 32 stands out for being inserted in the vertex of the polPGon. Showing its high productivity and high adaptability and stability, followed by genotype 30, which also presented

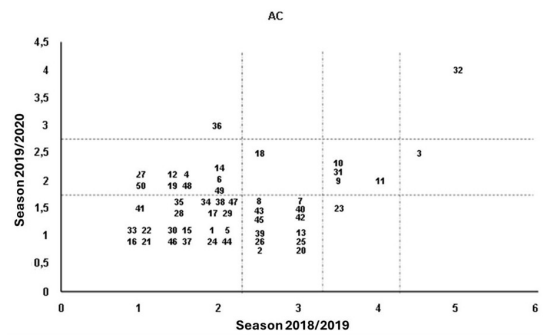


Figure 6. GGE biplot plot representing the scores of genotypes and environments from the oil content analysis. PC1 and PC2 = first and second principal components, respectively.

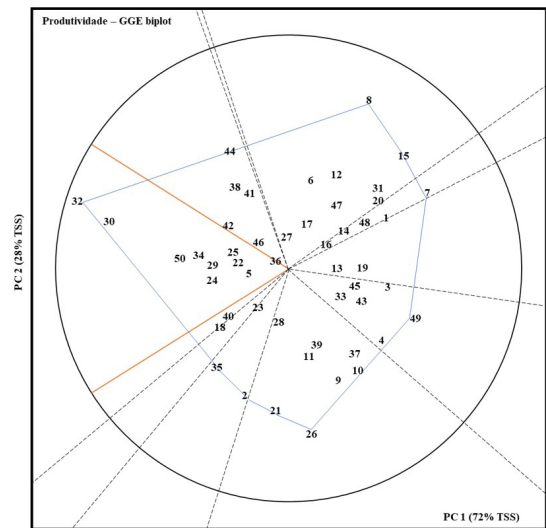


Figure 7. GGE biplot plot represents the scores of genotypes and environments from the yield analysis. PC1 and PC2 = first and second principal components, respectively.

these characteristics. Therefore, the ranking for best performance is as follows: 32>30>50>34>29>24>42>25>22>5>36. Except for genotypes 42 and 36 which showed better performance in Environment 1 (the crop year 2018/2019), the others obtained similar behavior in both environments (Figure 7). According to Andrade et al. (2016), for optimal genotype selection, one should jointly consider high productivity and high stability across environments. As well as the ideal test environment should be representative and be able to select genotypes well, highlighting the genotypes located closer to the ideotype, considering them as more desirable for selection (Freiria et al., 2018).

The existing adaptability and stability methods can present agreements and disagreements (Pereira et al., 2014). However, the GGE-biplot and MHPRVG methods were unanimous in considering the following genotypes as superior for grain yield: 24 ((Hartwig x BRS-134) x (Coodelec-201 x BRS MS Bacuri)); 29 (FT-Cometa x Bossier); 30 (BR-16 x Ocepar-5); 32 (JAB.00-05-5/4A2D

x M 7578 RR); 34 (JAB.00-05-5/4A2D x M 7908 RR); and 42 (JAB.00-01-21/4M1D x M 8336 RR). For oil content, the superior genotypes were: 4 (FT-Cometa x Bossier); 17 (EMBRAPA 48 x Conquista); 37 (JAB.00-05-1/5C3B x M 7639 RR); and 44 (JAB.04-1/5A4D x M 8230 RR). With the exception of genotype 24, derived from a quadruple cross, most of the superior genotypes come from two-parent crosses, where the RR parents used are newer compared to the conventional parents included in the breeding programs. This highlights the potential of modern RR materials to improve both grain yield and oil content performance.

For oil content, the MHPRVG method considered genotype 8 as superior to Environment 1. In turn, the GGE biplot method considered such genotype as not adapted, not being recommended for any environment. The genotypes that do not present favorable performance in all environments are disqualified when they are compared with the general average of the environments evaluated (Almeida Filho et al., 2014).

The GGE biplot method, as Yang et al. (2009) have noted, discerns only a minor fraction of the total variability inherent in genotype-environmental interactions. This limitation underscores the necessity for employing more robust statistical methodologies that can capture more nuanced patterns in the data. The Mixed Models by the MHPRVG method stand out in this regard, as they analyze the results in terms of direct genotypic values, offering a more precise depiction of genetic performance.

4. Conclusion

The analysis by GGE biplot and MHPRVG methods allows the selection of promising genotypes, highlighting genotypes 24; 29; 30; 32; 34, and 42 for productivity. And the genotypes 4; 17; 37 and 44 for oil content. And the association between MHPRVG and GGE biplot methods should be used and taken into consideration in the selection of promising soybean genotypes. Especially in the final stages of soybean genetic improvement programs.

Acknowledgements

This work was carried out with the support of the Coordination for the Improvement of Higher Education Personnel (CAPES) - Brazil - Funding Code 001.

References

- ALMEIDA FILHO, J.E., TARDIN, F.D., RESENDE, M.D.V., SILVA, F.F., GRANATO, Í.S.C. and MENEZES, C.B., 2014. Genetic evaluation of grain sorghum hybrids in Brazilian environments using the REML/BLUP procedure. *Scientia Agricola*, vol. 71, no. 2, pp. 145-150. <http://doi.org/10.1590/S0103-90162014000200009>.
- ALVES, R.S., DE CARVALHO ROCHA, J.R.A.S., TEODORO, P.E., DE RESENDE, M.D.V., HENRIQUES, E.P., SILVA, L.A., CARNEIRO, P.C.S. and BHERING, L.L., 2018. Multiple-trait BLUP: a suitable strategy for genetic selection of Eucalyptus. *Tree Genetics & Genomes*, vol. 14, no. 5, pp. 77. <http://doi.org/10.1007/s11295-018-1292-7>.
- ANDRADE, C.B., SILVA, A.J., FERRAUDO, A.S., UNÊDA-TREVISOLI, S.H. and DI MAURO, A.O., 2016. Strategies for selecting soybean genotypes using mixed models and multivariate approach. *African Journal of Agricultural Research*, vol. 11, no. 1, pp. 23-31. <http://doi.org/10.5897/AJAR2015.9715>.
- BERNARDO, R., 2020. Reinventing quantitative genetics for plant breeding: something old, something new, something borrowed, something BLUE. *Heredity*, vol. 125, pp. 375-385. <http://doi.org/10.1038/s41437-020-0312-1>. PMID:32296132.
- CARVALHO, L.P., FARIAS, F.J.C., MORELLO, C.D.L. and TEODORO, P.E., 2016. Uso da metodologia REML/BLUP para seleção de genótipos de algodoeiro com maior adaptabilidade e estabilidade produtiva. *Bragantia*, vol. 75, pp. 314-321. <https://doi.org/10.1590/1678-4499.275>.
- COLOMBARI FILHO, J.M., DE RESENDE, M.D.V., DE MORAIS, O.P., DE CASTRO, A.P., GUIMARÃES, É.P., PEREIRA, J.A., UTUMI, M.M. and BRESEGHELLO, F., 2013. Upland rice breeding in Brazil: a simultaneous genotypic evaluation of stability, adaptability and grain yield. *Euphytica*, vol. 192, no. 1, pp. 117-129. <http://doi.org/10.1007/s10681-013-0922-2>.
- COMPANHIA NACIONAL DE ABASTECIMENTO - CONAB, 2020 [viewed 30 April 2020]. *Acompanhamento da safra brasileira de grãos* [online]. Available from: <https://www.conab.gov.br/info-agro/safras/graos/boletim-da-safra-de-graos>
- CRUZ, C.D., 2013. Genes: um pacote de software para análise em estatística experimental e genética quantitativa. *Acta Scientiarum*, vol. 35, no. 3, pp. 271-276.
- EMPRESA BRASILEIRA DE PESQUISA AGROPECUÁRIA - EMBRAPA, 2018. *Indicações técnicas para a cultura da soja no Rio Grande do Sul e em Santa Catarina*. Pelotas: Embrapa Clima Temperado, 105 p.
- FREIRIA, G.H., GONÇALVES, L.S.A., FURLAN, F.F., FONSECA JUNIOR, N.S., LIMA, W.F. and PRETE, C.E.C., 2018. Statistical methods to study adaptability and stability in breeding lines of food-type soybeans. *Bragantia*, vol. 77, no. 2, pp. 253-264. <http://doi.org/10.1590/1678-4499.2017076>.
- GAZOTTO, L.A.C., CHARNAI, K., SANTOS, L.D.F., CARVALHO, M.N. and MORO, G.V., 2020. Correlation between grain yield in maize plant densities. *Cientifica*, vol. 48, no. 3, pp. 226-231. <http://doi.org/10.15361/1984-5529.2020v48n3p226-231>.
- GONÇALVES, G.M., VIANA, A.P., AMARAL JUNIOR, A.T. and RESENDE, M.D.V., 2014. Breeding new sugarcane clones by mixed models under genotype by environmental interaction. *Scientia Agricola*, vol. 71, no. 1, pp. 66-71. <http://doi.org/10.1590/S0103-90162014000100009>.
- GUO, B., SUN, L., JIANG, S., REN, H., SUN, R., WEI, Z., HONG, H., LUAN, X., WANG, J., WANG, X., XU, D., LI, W., GUO, C. and QIU, L.J., 2022. Soybean genetic resources contributing to sustainable protein production. *Theoretical and Applied Genetics*, vol. 135, no. 11, pp. 4095-4121. <http://doi.org/10.1007/s00122-022-04222-9>. PMID:36239765.
- KOMARIAH, A., WAHYUNI, D.S., RAMDHANI, RIA, E.R. and NOERTJAHYANI, 2023. Molecular analysis of Karawang local soybean genotypes with national superior varieties based on SSR analysis. *Brazilian Journal of Biology = Revista Brasileira de Biologia*, vol. 83, pp. e277744. <http://doi.org/10.1590/1519-6984.277744>. PMID:38055584.
- LEITE, W.S., PAVAN, B.E., MATOS FILHO, C.H.A., NETO, F.D.A., OLIVEIRA, C.B. and FEITOSA, F.S., 2016. Estimativas de parâmetros genéticos, correlações e índices de seleção para seis caracteres

- agronômicos em linhagens F8 de soja. *Comunicata Scientiae*, vol. 7, no. 3, pp. 302-310. <http://doi.org/10.14295/cs.v7i3.1176>.
- MATEI, G., WOYANN, L.G., MILIOLI, A.S., DE BEM OLIVEIRA, I., ZDZIARSKI, A.D., ZANELLA, R., COELHO, A.S.G., FINATTO, T. and BENIN, G., 2018. Genomic selection in soybean: accuracy and time gain in relation to phenotypic selection. *Molecular Breeding*, vol. 38, no. 9, pp. 117. <http://doi.org/10.1007/s11032-018-0872-4>.
- MELO, L.C., 2009. *Procedimentos para condução de experimentos de valor de cultivo e uso em feijoeiro comum*. Santo Antônio de Goiás: Embrapa Arroz e Feijão.
- PELUZIO, J.M., LOPES, L.A., CARVALHO, E.V., AFFÉRRRI, F.S. and DOTTO, M.A., 2014. Características agronômicas e divergência genética de cultivares de soja para percentagem de óleo nas sementes. *Revista de Ciências Agrárias*, vol. 57, no. 1, pp. 1-8. <http://doi.org/10.4322/rca.2013.058>.
- PEREIRA, H.S., BUENO, L.G., DEL PELOSO, M.J., ABREU, A.F.B., MOREIRA, J.A.A., MARTINS, M., WENDLAND, A., FARIA, L.C., SOUZA, T.L.P.O. and MELO, L.C., 2014. Agronomic performance and stability of andean common bean lines with white grains in Brazil. *Bragantia*, vol. 73, no. 2, pp. 130-137. <http://doi.org/10.1590/brag.2014.020>.
- PIMENTEL-GOMES, F., 2000. *Curso de estatística experimental*. 15th ed. Piracicaba: FEALQ.
- RAMALHO, M.A.P., ABREU, A.F.B., SANTOS, J.B. and NUNES, J.A.R., 2012. *Aplicações da genética quantitativa no melhoramento de plantas autógamas*. Lavras: UFLA, 522 p.
- RESENDE, M.D.V., 2007. *Selegen-Reml/Blup: sistema estatístico e seleção genética computadorizada via modelos lineares mistos*. Colombo: Embrapa Florestas, 359 p.
- SOARES, I.O., BRUZI, A.T., ZAMBIAZZI, E.V., GUILHERME, S.R., BIANCHI, M.C., SILVA, K.B., FRONZA, V. and TEIXEIRA, C.M., 2017. Stability and adaptability of soybean cultivars in Minas Gerais. *Genetics and Molecular Research*, vol. 16, no. 3, pp. 1-7. <http://doi.org/10.4238/gmr16039730>. PMID:28829903.
- STORCK, L. and RIBEIRO, N.D., 2011. Valores genéticos de linhas puras de soja preditos com o uso do método de Papadakis. *Bragantia*, vol. 70, no. 4, pp. 1-6.
- TADEGE, M.B., UTTO, H.Z. and AGA, A.A., 2014. Associação de métodos estatísticos usados para explorar a interação genótipo x ambiente (GEI) e estabilidade de cultivares. *African Journal of Agricultural Research*, vol. 9, no. 29, pp. 2231-2237.
- UNITED STATES DEPARTMENT OF AGRICULTURE – USDA, 2023 [viewed 21 May 2024]. *World agricultural production* [online]. Available from: <https://ipad.fas.usda.gov/>
- YAN, W., HUNT, L.A., SHENG, Q. and SZLAVNICS, Z., 2000. Cultivar evaluation and mega-environment investigation based on the GGE biplot. *Crop Science*, vol. 40, no. 3, pp. 597-605. <http://doi.org/10.2135/cropsci2000.403597x>.
- YANG, R.C., CROSSA, J., CORNELIUS, P.L. and BURGUEÑO, J., 2009. Biplot analysis of genotype x environment interaction: proceed with caution. *Crop Science*, vol. 49, no. 5, pp. 1564-1570. <http://doi.org/10.2135/cropsci2008.11.0665>.