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Genotype × environment interaction, adaptability, and stability of soybean genotypes in a new production region of Brazil

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Research Article

Keywords: Glycine max, plant breeding, mixed-model, REML/BLUP

Posted Date: July 8th, 2026

DOI: https://doi.org/10.21203/rs.3.rs-10207522/v1

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Additional Declarations: No competing interests reported.

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Abstract

Soybean yield is strongly influenced by environmental conditions, making the understanding of genotype × environment (G×E) interaction essential for accurate cultivar recommendation. This study aimed to evaluate the adaptability and stability of soybean genotypes for grain yield in the northern region of Rio de Janeiro State, Brazil, a promising area for soybean expansion. Eight genotypes were evaluated in a randomized complete block design with four replications across five environments, defined by the combination of locations and growing seasons (2019/2020 and 2020/2021), in the municipalities of Campos dos Goytacazes and Macaé. Adaptability and stability were assessed based on the REML/BLUP approach. A significant and predominant G×E interaction was detected, accounting for most of the variation in grain yield and indicating differential genotype responses across environments. The genotypes 95R95IPRO, BMX COMPACTA IPRO, and TMG7061IPRO showed superior performance, combining high grain yield, adaptability, and stability, as identified by the HMRPGV method. Consistency among the predicted genotypic values free of interaction (μ + g), HMGV (stability and yield), and RPGV (adaptability) further supported the superior performance of 95R95IPRO and BMX COMPACTA IPRO. These results highlight the potential of these genotypes for cultivation in the target region and reinforce the importance of mixed-model approaches in soybean breeding programs.

Introduction

Soybean (*Glycine max* (L.) Merrill) is one of the most important crops worldwide, with Brazil currently ranking as the leading global producer. Its production plays a pivotal role in the national economy, as evidenced by the 2024/2025 growing season, in which soybean occupied 46.1 million hectares and produced 147.7 million tons, accounting for approximately 49.6% of the total grain production in the country (Conab, 2025).

Globally, soybean is highly valued as a source of protein and vegetable oil. The grains exhibit high nutritional quality, with protein content ranging from 38 to 42% and oil content between 18 and 22%, in addition to containing essential amino acids and unsaturated fatty acids (James; Yang 2016; Patil et al.; 2018; Zhang et al. 2018).

The increasing global demand for soybean has driven the expansion of cultivation into new agricultural frontiers in Brazil (Rocha et al. 2022). In this context, recent studies have identified the northern and northwestern regions of Rio de Janeiro State as promising areas for soybean production, with more than 300 thousand hectares considered suitable for mechanized cropping systems (Zilli et al., 2021; Zilli et al., 2022).

However, the performance of soybean genotypes is strongly influenced by edaphoclimatic conditions, resulting in significant genotype × environment (G×E) interaction (Possobom et al., 2020; Cruz et al., 2021). Therefore, evaluating genotype performance across environments is essential for the identification of broadly adapted and stable cultivars.

Several statistical approaches have been proposed to assess G×E interaction, adaptability, and stability. Among them, mixed models based on restricted maximum likelihood and best linear unbiased prediction (REML/BLUP) stand out due to their high accuracy in predicting genotypic values (Resende, 2016; Olivoto et al., 2017). These

methods have been widely applied in soybean breeding programs (Gonçalves et al., 2020; Carvalho et al., 2021; Costa et al., 2025).

Despite the recent expansion of soybean cultivation into new regions, studies addressing the adaptability, stability, and yield performance of soybean genotypes under the specific edaphoclimatic conditions of Rio de Janeiro State remain scarce. This gap highlights the need for research to support genotype recommendation and production strategies in this emerging production region.

Therefore, this study aimed to evaluate the genotype × environment interaction, as well as the adaptability, stability, and grain yield performance of soybean genotypes grown under the edaphoclimatic conditions of northern Rio de Janeiro State, Brazil, using mixed models (REML/BLUP).

Materials and methods

Genetic material

Genetic material evaluated in this study consisted of commercial soybean cultivars (Table 1). These genotypes were selected based on their previously demonstrated superior agronomic performance in Brazilian regions with edaphoclimatic conditions analogous to those observed in the present study.

Table 1. Characteristics of soybean genotypes evaluated in the study

Genotypes	RMG[1]	Growth habit	Trait[2]
55I57RSF IPRO (BMX ZEUS IPRO)	5.5	Indeterminate	Intacta RR2 PRO
M5917IPRO	5.9	Indeterminate	Intacta RR2 PRO
95R95IPRO	5.9	Indeterminate	Intacta RR2 PRO
TMG7061IPRO	6.1	Indeterminate	Intacta RR2 PRO
BRS 544RR	6.2	Indeterminate	RR
63I64RSF IPRO (BMX GARRA IPRO)	6.3	Indeterminate	Intacta RR2 PRO
65I65RSF IPRO (BMX COMPACTA IPRO)	6.5	Indeterminate	Intacta RR2 PRO
BRS 7780IPRO	7.7	Semi-determinate	Intacta RR2 PRO

[1]RMG = Relative Maturity Group.
[2]Genetically Modified Trait = Intacta RR2 PRO – insect resistance and tolerance to glyphosate herbicide; RR – tolerance to glyphosate herbicide (Roundup Ready soybean).

Experimental sites and growing conditions

The study was conducted in the northern region of Rio de Janeiro State, Brazil, on commercial farms located in the municipalities of Macaé and Campos dos Goytacazes. Yield performance was evaluated through multi-environment trials carried out across five experimental environments during the 2019/2020 and 2020/2021 growing seasons (Table 2).

Meteorological data for both growing seasons, as well as the physicochemical properties of the soils at the five experimental sites, are provided in Supplementary Tables 1 and 2, respectively.

Table 2. Climatic and soil characterization of the experimental environments across the 2019/2020 and 2020/2021 growing seasons.

Code	Growing seasons	Sowing date	Rainfall (mm)	Temp. (˚C)	Geographical coordinates	Alt. (m asl)	Soil class
E1	2020/2021	05/11/2020	774	26,9	21°43'41" S 41°12'41" W	7	Fluvic cambisol
E2	2020/2021	28/10/2020	699	26,4	21°45'41" S 41°15'22" W	8	Fluvic cambisol
E3	2020/2021	30/10/2020	976	26,1	21°33'47" S 41°18'52" W	48	Yellow latosol
E4	2019/2020	30/10/2019	1434	25,5	22°17'15" S 41°55'33" W	13	Haplic gleysol
E5	2020/2021	23/10/2020	1203	26,0	22°17'15" S 41°54'01" W	11	Haplic gleysol

E = Environment; Temp. = Temperature average; Alt. = Altitude; E1 = Farm Abadia, Campos dos Goytacazes, E2 = Farm Ayrizes, Campos dos Goytacazes, E3 = Farm Guandu, Campos dos Goytacazes; E4 and E5 = Farm Primus, Macaé.

Experimental design and crop management

The experiments were conducted using a randomized complete block design with four replications. Each experimental plot consisted of five 5-m-long rows spaced 0.5 m apart. The three central rows were considered as the harvestable area (4.5 m^2), excluding 1.0 m at each end of the rows to minimize border effects. Sowing was performed at a density of 16 seeds per linear meter, corresponding to an estimated plant population of 320,000 plants ha^{-1}.

The soil was prepared using conventional tillage (plowing and harrowing). The seeds were co-inoculated with *Bradyrhizobium* strains (a mix of strains SEMIA 5079 and BR 29) was applied at a rate of five doses per hectare, ensuring 1.5 to 2 million cells per soybean seed, and 100 mL ha^{-1} at concentration 10^8 of *Azospirillum brasilense* (strains AbV-5 and AbV-6). The inoculants were applied directly to the seeds, moments before sowing, following the technical recommendations and sowing was carried out immediately after inoculation. Planting fertilization consisted of a mixture of 100 kg ha^{-1} of P_2O_5 and 80 kg ha^{-1} of K_2O, using single superphosphate and potassium chloride as

sources, along with 50 kg ha^{-1} of FTE BR-12 as a source of micronutrients. Potassium was applied half at sowing and half approximately 30 days after plant emergence, in alignment with agronomic guidelines (Sediyama et al., 2015). All crop management practices were undertaken according to crop requirements, following (Seixas et al. 2020).

Harvesting was carried out at full maturity (R8 stage), defined as the point at which approximately 95% of the pods had reached their mature color. Plants from the harvestable area of each plot were mechanically threshed, and grain weight was determined using a precision balance. Grain yield (GY), corresponding to the grain yield of plants after harvest and processing, with grain weights adjusted to 13% moisture and the value extrapolated to kg ha^{-1}.

Genetic and statistical analyses

The grain yield data were analyzed using the Selegen REML/BLUP software (Resende, 2016). The variance components estimates and the genotypic values was obtained via REML/BLUP methodology, used the following linear mixed model:

$$\mathbf{y = Xr + Zg + Wi + e}$$

where **y** is the vector of data, **r** is effects of blocks within different environments (assumed as fixed) summed to the general mean, $\mathbf{g} \sim N(\mathbf{0}, \mathbf{I}\sigma_g^2)$ is the vector of genotypic effects, **i** $\sim N(\mathbf{0}, \mathbf{I}\sigma_p^2)$ is the vector of the G × E interaction effects, and $\mathbf{e} \sim N(\mathbf{0}, \mathbf{I}\sigma^2)$ is the vector of errors or residuals. **X**, **Z**, and **W** are the incidence matrices for these effects.

The significance of the random effects was evaluated by deviance analysis using the Likelihood Ratio Test (LRT), assuming a χ^2 distribution for the test statistic (Resende, 2016).

The estimated components included genotypic variance ($\hat{\sigma}_g^2$), variance of the G×E interaction ($\hat{\sigma}_{ge}^2$), residual variance ($\hat{\sigma}_e^2$) and phenotypic variance ($\hat{\sigma}_p^2$). Based on these components, the genetic parameters were obtained using the following estimators:

genotype mean-based heritability

$$\hat{h}^2 = \frac{\hat{\sigma}_g^2}{\hat{\sigma}_g^2 + \frac{\hat{\sigma}_{ge}^2}{e} + \frac{\hat{\sigma}_e^2}{re}}$$

selective accuracy

$$SA = \sqrt{\hat{h}^2}$$

and the genotypic correlation of genotype performance across environments

$$\hat{r}_{ge}^2 = \frac{\hat{\sigma}_g^2}{\hat{\sigma}_g^2 + \hat{\sigma}_{ge}^2}$$

where *e* is the number of environments and *r* is the number of replications.

Selection for yield, adaptability, and stability was based on the following equations:

harmonic mean of genotypic values (HMGV), ranks genotypes by yield and stability

$$HMGV = \frac{n}{\sum_{j=1}^{n} \frac{1}{GV_{ij}}}$$

relative performance of genotypic values (RPGV), selects genotypes for greater genotypic adaptability

$$RPGV = \frac{1}{n} \sum_{j=1}^{n} \frac{GV_{ij}}{A_j}$$

harmonic mean of the relative performance of genotypic values (HMRPGV), simultaneously evaluates the grain yield, stability, and adaptability of soybean genotypes

$$\text{HMRPGV} = \frac{n}{\sum_{j=1}^{n} \frac{1}{\text{RPGV}_{ij}}}$$

where, n is the number of environments in which genotype i was evaluated; GV_{ij} is the genotypic value (BLUP) of genotype i in environment j and A_j is the average grain yield in environment j.

Results and Discussion

The genotype effect was not statistically significant (Table 3), indicating the absence of consistent differences among the overall means of the evaluated materials. This finding may be attributed to the use of commercial cultivars, which generally have a similar genetic base and exhibit high yield potential, thereby limiting the extent of variability among them. On the other hand, the genotype-by-environment (G×E) interaction showed significant effects ($p<0.01$), indicating differential responses of soybean genotypes across environments. Similar significant interactions have been reported in previous soybeans studies (Carneiro et al., 2019; Albuquerque et al., 2022). The significant effect of G×E interaction suggests that grain yield varies among genotypes, leading to potential shifts in ranking across evaluated environments. This highlights the importance of selecting superior genotypes specific to environmental conditions rather than relying solely on average performance. Thus, this interaction influences genotype selection during breeding program stages and cultivar recommendations.

Grain yield is a polygenic quantitative property, meaning itis governed by multiple genes with minor effects and strongly influenced by the environment factors (Mbuma et al. 2022). In this study, phenotypic variance of grain yield was predominantly explained by the G×E interaction, contributing approximately 80% to the phenotypic expression.

The variance components of the interaction surpassed the genotypic variance component, emphasizing the greater influence of the interaction on the total variance. This finding aligns with similar estimates in soybean studies (Albuquerque et al., 2022).

The mean genotype heritability coefficient was 0.03 for GY (Table 3), indicating that GY exhibited low heritability and was strongly influenced by environmental factors and genotype-by-environment (G × E) interactions in its phenotypic expression. Selection accuracy is a parameter associated with reliability in the evaluation and prediction of genotypes, as it measures the correlation between the genotypic values predicted from experimental data and the true genotypic values. In this study, the accuracy was 0.18, which is considered low. This low value can be mainly attributed to the high G×E interaction observed, indicating a strong influence of the environment on genotype performance and reduced consistency of genotypic expression across environments. The experimental coefficient of variation (CVe) is one of the most widely accepted methods for evaluating experimental precision. In this study, the CVe was 10.76%, a value within the acceptable range for soybean experiments and lower than those reported under different edaphoclimatic conditions (Torres et al., 2018; Moitinho, 2021).

As regards the CVg/CVe ratio, an ideal scenario would present high values, indicating a greater genetic variability. In this study, however, the ratio was low, denoting reduced genetic variability, with most of the phenotypic variation attributed to environmental factors. Gonçalves et al. (2020) examined 16 soybean genotypes in eight environments and also found a relative coefficient lower than 1.0, indicating a stronger interaction of the grain yield trait with environmental variations.

The genotypic correlation between environments (rge = 0.01) was very low, indicating a lack of consistency in genotype performance across environments. This result suggests that genotypes exhibited different responses depending on environmental

conditions, with a likely occurrence of changes in ranking between environments. Such behavior characterizes the predominance of complex genotype × environment interactions (Costa et al., 2015), in which the relative performance of genotypes is not maintained. This scenario makes it difficult to accurately classify and recommend superior cultivars (Olivoto et al., 2019), as genotype performance becomes environment-specific rather than stable across conditions.

Table 3. Deviance analysis, chi-square test (χ^2), estimation of variance components, and genetic parameters for grain yield in eight soybean genotypes evaluated in five environments in the municipalities of Campos dos Goytacazes and Macaé in the years 2019, 2020, and 2021.

Effect	**Deviance** [(1)]	**LRT (Chi-squared)** [(2)]
Genotype (G)	1924.79	0.00^{ns}
Genotype × environment interaction (G × E)	2045.72	120.93^{**}
Complete	1924.79	
Variance components and genetic parameters		
Genotypic variance ($\hat{\sigma}_g^2$)	3726.70	
Variance of G × E interaction ($\hat{\sigma}_{ge}^2$)	518077.23	
Environmental variance ($\hat{\sigma}_e^2$))	124612.87	
Phenotypic variance ($\hat{\sigma}_p^2$)	646416.80	
genotype mean-based heritability ($\hat{h}^2$)	0.032	
Selection accuracy (SA)	0.18	
Coefficient of determination of the G × E (R^2)	0.80	
Genotypic correlation between environments ($\hat{r}_{ge}^2$)	0.01	
Coefficient of genotypic variation (CVg)	1.86	
Coefficient of experimental variation (CVe)	10.76	
Relative coefficient of variation (CVg/Cve)	0.17	
Overall mean (μ): kg ha^{-1}	3281.15	

[(1)] Deviance of the model adjusted for this effect. [(2)] LRT, likelihood ratio test.
** and * Significant by the Chi-square test at $p<0.01$ and $p<0.05$, respectively.

Genotypic values for grain yield

Table 4 showed the ranking of genotypic values for grain yield in five cultivation environments, with an average yield of 3281.15 kg ha^{-1}. The standout genotypes, namely

95R95IPRO, M5917IPRO, BMX COMPACTA IPRO, and BRS 7780IPRO, exhibited higher grain yields (3294.97, 3286.56, 3285.74, and 3285.32 kg ha^{-1}, respectively), displaying the highest genotypic values for the environment without G×E interaction effect (μ+g). When utilizing genotypic values (μ+g) for ranking, they can be extrapolated to environments different from those of evaluation, as this estimate does not account for the effect of G×E interaction (Maia et al. 2009; Gonçalves et al. 2014). Consequently, a consistent response is anticipated across diverse environments.

The genetic gain, represented by the difference between the genotypic value of the genotype and the general average, was more expressive for the genotype 95R95IPRO, with 13.82 kg ha^{-1}. The new average, resulting from the addition of this gain to the general average, reinforces the productive potential of this genotype. Most genotypes presented a new average higher than the general average, except for BRS 544RR, indicating its lower suitability for high-yield environments.

The predicted genotypic values without considering the genotype × environment interaction (μ + g) indicate the average performance of the genotypes in non-specific environments. The genotypes 95R95IPRO, M5917IPRO, BMX COMPACTA IPRO, BRS 7780IPRO and TMG7061IPRO stood out with values higher than the general average of 3281.15 kg ha^{-1}. These results suggest that these genotypes have a high genetic potential for grain yield, regardless of environmental variations.

The genetic gain reached up to 13.82 kg ha^{-1} for genotype 95R95IPRO, resulting in a new mean of 3294.97 kg ha^{-1} for grain yield. All genotypes selected based on the new mean maintained the same ranking as those chosen by the interaction-free genotypic value (μ + g). Of the evaluated genotypes, 87.5% exhibited a new mean exceeding the overall mean, except for genotype BRS 544RR, which showed a lower grain yield (3259.41 kg ha^{-1}).

When incorporating the genotype × environment interaction (μ + g + gem), a change in the predicted values was observed, reflecting the influence of the environments on the expression of grain yield. The genotypes 95R95IPRO, M5917IPRO, BMX COMPACTA IPRO, BRS 7780IPRO and TMG7061IPRO remained the most productive, indicating stability and broad adaptability. On the other hand, genotypes such as BMX ZEUS IPRO and BRS 544RR presented lower values, suggesting sensitivity to environmental variations.

By applying the mean genotypic value in the environments (μ + g + gem), where the genotype and environment interaction is considered, the ranking of the best genotypes aligned with those selected based on the highest genotypic values free from interaction (μ + g). This emphasis is particularly noteworthy for five genotypes: 95R95IPRO, M5917IPRO, BMX COMPACTA IPRO, BRS 7780IPRO, and TMG 7061IPRO, all surpassing the average grain yield (Table 4). The top five genotypes selected in all environments, considering the mean genotypic value of the environments, exceeded the national average soybean yield in the 2023/2024 harvest, which stood at 3202 kg ha^{-1} (Conab, 2025). This demonstrates the viability of the selection strategy using this method. While the two selection methods are similar in terms of ranking, the predicted values are always higher for the mean of the environments.

Table 4. Ranking and predicted genotypic values free from interaction with environments for the grain yield in eight soybean genotypes evaluated in five environments in the municipalities of Campos dos Goytacazes and Macaé in the years 2019, 2020, and 2021.

Rank	Genotypes	g	μ + g	Gain[1]	New mean	μ + g + ge_m
1	95R95IPRO	13.82	3294.97	13.82	3294.97	3679.30
2	M5917IPRO	5.41	3286.56	9.62	3290.77	3437.02
3	BMX COMPACTA IPRO	4.59	3285.74	7.94	3289.09	3413.36
4	BRS 7780IPRO	4.17	3285.32	7.00	3288.15	3401.31
5	TMG7061IPRO	4.02	3285.17	6.40	3287.56	3396.96
6	BMX GARRA IPRO	-3.32	3277.83	4.78	3285.93	3185.45
7	BMX ZEUS IPRO	-6.95	3274.20	3.11	3284.26	3081.05
8	BRS 544RR	-21.75	3259.41	0.00	3281.15	2654.78
			Mean: 3281.15 kg ha^{-1}			

[1] genetic gain (kg ha^{-1}); g: additive genetic effect; μ + g: predicted genotypic value (free from interaction); μ + g + ge_m: mean genotypic value across environments.

The analysis of genotypic values with and without interaction provides valuable information for genetic improvement programs. Genotypes with high performance and stability, such as those mentioned above, are ideal candidates for large-scale recommendations. However, the presence of significant interaction highlights the importance of considering specific environments in genotype selection, aiming to maximize yield under particular conditions. An alternative method for genotype selection involves considering performance specific to each location. This is achieved by analyzing the predicted genotypic values in each environment (μ + g + ge). It becomes apparent that there is a shift in the ranking of the best genotypes depending on the cultivation site, illustrating the impact of the G × E interaction.

Examining the predicted genotypic values for grain yield across all environments reveals that the BRS 7780IPRO genotype excelled as the top performer in environments E2 (Ayrizes), E3 (Guandu), and E4 (Primus 2019/2020) (Figure 1). Genotype 95R95IPRO exhibited outstanding performance among the top three selected genotypes

in Campos dos Goytacazes (Abadia) and in the two environments in Macaé. Additionally, it featured prominently in the ranking based on the average yield across all environments, as represented by the interaction-free genotypic value ($\mu + g$).

In a study conducted with soybeans in the northern region of Rio de Janeiro, Zilli et al. (2022) assessed 54 soybean cultivars across five harvests. Cultivars BRS 7780IPRO and 95R95IPRO exhibited grain yields surpassing 6000 kg ha^{-1}. In the same investigation, during 11 evaluations in the region, genotype 95R95IPRO demonstrated an average yield of 3743 kg ha^{-1}, a performance closely aligned with those estimated by the methodology of genotypic values. The results from these cultivars indicated a certain adaptation to the region's conditions, resulting in grain yields surpassing the current national average. When the G × E interaction is considered ($\mu + g + ge_m$), it is advisable to cultivate these genotypes in areas demonstrating the same pattern of genotype and environment interaction used in this experimental network.

The gains in grain yield - genotypes marked with triangles were used to estimate selection gain in each environment - for the three best genotypes in each location (Figure 1), relative to the respective location averages, are 18, 21, 9, 10, and 17% for the environments of Abadia, Ayrizes, Guandu, Primus 2019/2020, and Primus 2020/2021, respectively. Conversely, the lowest grain yields were observed in the municipality of Campos dos Goytacazes: 2608 kg ha^{-1} (Abadia), 2031 kg ha^{-1} (Ayrizes), and 1344 kg ha^{-1} (Guandu).

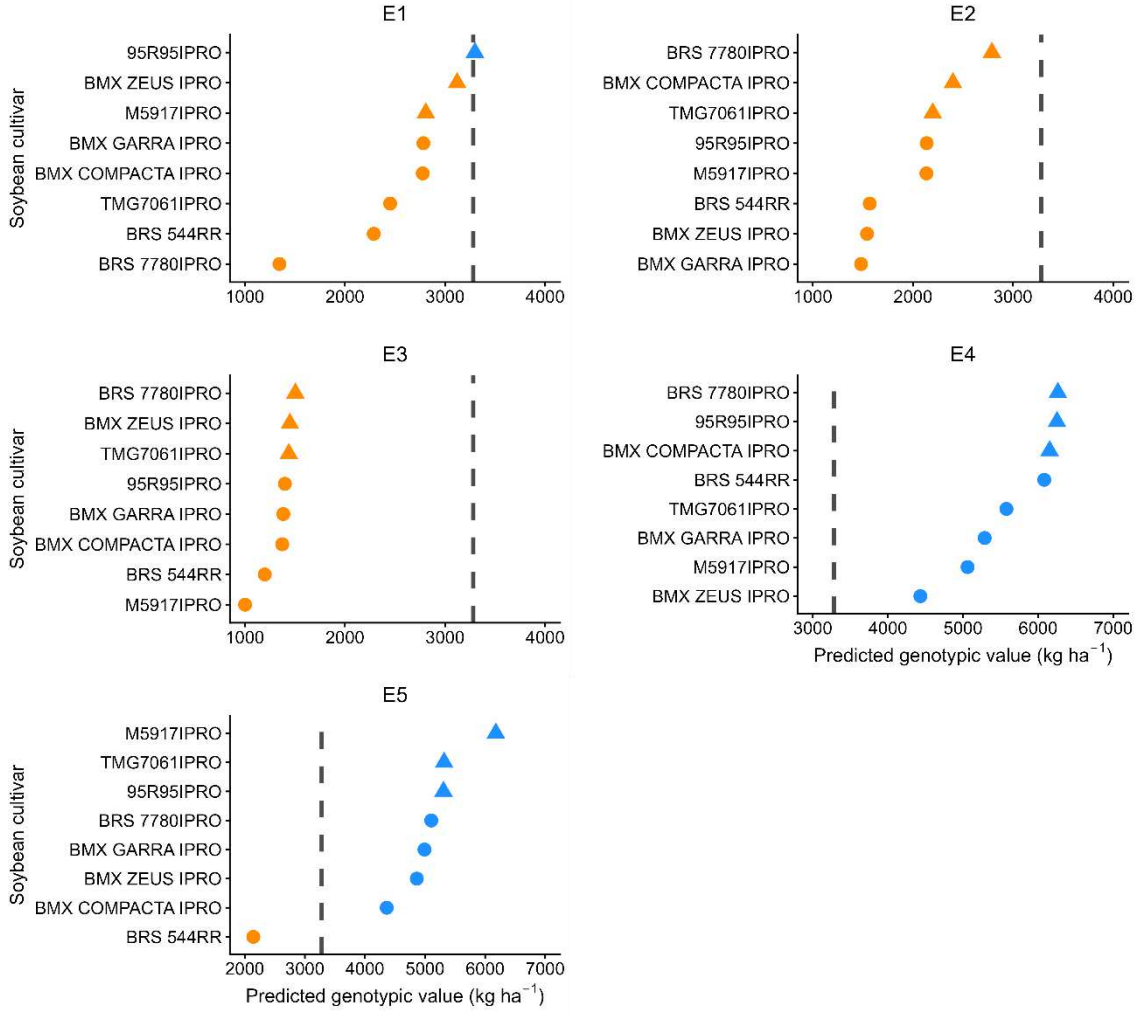
Across the tested environments, the highest grain yields occurred in the municipality of Macaé, with an average yield of 5638 kg ha^{-1} (2019/2020 growing season) and 4782 kg ha^{-1} (2020/2021 harvest), respectively. All genotypes (except BRS 544RR in the 2020/2021 harvest) in Macaé achieved grain yields exceeding the national average for the 2020/2021 harvest, which stood at 3526 kg ha^{-1}. Genotype BRS

7780IPRO exhibited the highest grain yield (6263 kg ha^{-1}) in Primus 2019/2020. In contrast, M5917IPRO had the lowest production performance, yielding 1002 kg ha^{-1} in the Guandu location (E3), in Campos dos Goytacazes.

The variations in yield across environments may be attributed to the climatic and soil peculiarities of each location (Supplementary tables 1 and 2). It is observed that the cumulative volume of rainfall on all farms throughout the harvests theoretically met the soybean's water requirements. These farm precipitation values are above the minimum total water requirement of the soybean crop, which varies between 450 and 800 mm $cycle^{-1}$ depending on climatic conditions, crop management, and cycle duration (Neumaier et al. 2020).

However, there was a marked difference in rainfall distribution between locations, with Macaé experiencing better distribution compared to Campos dos Goytacazes. Temperature data indicated generally higher maximum values (average of 31.2 ºC) in Campos compared to Macaé (average of 30.0 ºC) (Supplementary table 1). These values are within the acceptable standard and, preliminarily, demonstrate no adverse effects on crop development.

Figure 1. Predicted genotypic values for grain yield (kg ha^{-1}) of eight soybean cultivars evaluated in five environments.



E1: Abadia farm, Campos dos Goytacazes, 2020/2021 growing season; E2: Ayrizes Farm, Campos dos Goytacazes, 2020/2021 growing season; E3: Guandu farm, Campos dos Goytacazes, 2020/2021 growing season; E4: Primus farm, Macaé, 2019/2020 growing season; E5: Primus farm, Macaé, 2020/2021 growing season. The dashed line represents the overall mean across environments. Blue symbols indicate genotypes with performance above the overall mean, while the orange symbol indicates below-average performance. Genotypes marked with triangles were used to estimate selection gain in each environment.

Adaptability and stability

Table 5 presents the performance of genotypes concerning stability (HMGV), genotypic adaptability (RPGV and RPGVμ), and simultaneous stability and adaptability (HMRPGV and HMRPGVμ) for the soybean grain yield trait across the study environments. As defined by Breda et al. (2025), stability refers to a genotype's ability to remain highly predictable even in the face of environmental variations, while adaptability is understood as its capacity to capitalize on environmental changes.

The harmonic mean of genotypic values (HMGV) classifies genotypes based on both yield and stability values. Consequently, a higher HMGV value is associated with lower standard deviation in genotypic performance between environments (Gonçalves et al. 2014). Applying this criterion, the most notable genotypes are 95R95IPRO, BMX COMPACTA IPRO, TMG7061IPRO, BMX ZEUS IPRO, and BRS 7780IPRO. Four out of these five genotypes are among the top performers identified through the combined analysis of genotypic values (excluding M5917IPRO), indicating a degree of consensus between these assessment methodologies.

The relative performance of genotypic values (RPGV) estimates adaptability across different environments, expressing genotypic values as a ratio of the overall mean for each location. Using this approach, the most outstanding genotypes—95R95IPRO, BMX COMPACTA IPRO, TMG7061IPRO, and BRS 7780IPRO—demonstrate the capacity to respond to improvements in environmental conditions. Notably, these three prominent genotypes recommended by HMGV align with those identified by RPGV.

Genotypes 95R95IPRO, BMX COMPACTA IPRO, and TMG7061IPRO demonstrated outstanding performance in simultaneous selection for grain yield, stability, and adaptability, securing the top three positions. The results of HMGV, RPGV, and HMRPGV reveal that two of the three best-performing genotypes also ranked highest

375 in yield based on the average across the environments associated with the predicted
376 genotypic value (Table 5). The rankings of these genotypes remained consistent across
377 interaction-free predicted genotypic value (μ + g) and HMRPGV methodologies,
378 aligning with the rankings reported by Gonçalves et al. (2020) for various commercial
379 soybean lines and cultivars. According to Cruz et al. (2021), this consistency is linked to
380 the selection of genotypes with greater stability and adaptability across the tested
381 environments simultaneously, indicating high productivity, adaptive contribution, and
382 predictability across the five environments of the northern region of Rio de Janeiro. The
383 observed maintenance of the ranking of genotypes in the three methodologies suggests a
384 degree of agreement between these approaches.

385 The top three genotypes identified by the HMRPGVμ criterion (HMRPGV
386 multiplied by the overall mean across all locations) exhibited grain yields of 3641 kg ha^{-1}
387 (95R95IPRO), 3434 kg ha^{-1} (BMX COMPACTA IPRO), and 3394 kg ha^{-1}
388 (TMG7061IPRO), surpassing the overall mean (3281 kg ha^{-1}) by 11%, 5%, and 3%,
389 respectively. These genotypes fall within the Maturity Groups classification (5.8 to 7.0),
390 which has been adapting to the study region (Batista et al. 2020; Zilli et al. 2022; Souza
391 Filho et al. 2023) and more recently with the implementation of the Climate Risk Zoning
392 (Zarc) for soybean, which defines the most appropriate sowing periods for the crop and
393 those associated with lower probabilities of losses due to climatic risk, among other
394 factors. Gonçalves et al. (2020) assessed the adaptability and stability of soybean grain
395 yield through a mixed REML/BLUP model across two harvests and eight environments.
396 Their findings showed consistency with our study concerning the selection via HMRPGV
397 and predicted genetic gains, with agreement in ranking the best genotypes. Gains relative
398 to the mean were more pronounced than those observed in the current study.

399 The HMRPGV methodology, which considers genotype effects as random, offers

400 the advantage of handling unbalanced data, heterogeneity of variances, and varying
401 numbers of environments for selection (Resende et al. 2007). Ensuring stability across
402 cultivation years is essential for new genetic materials and current cultivars, ensuring
403 genetic gains and contributing as genetic sources for breeding programs.
404

Table 5. Genotypic stability (HMGV), adaptability (RPGV and RPGVμ), stability, and adaptability of genotypic values (HMRPGV and HMRPGVμ) for grain yield (kg ha^{-1}) in eight soybean genotypes evaluated in five environments in the municipalities of Campos dos Goytacazes and Macaé in 2019, 2020, and 2021.

Genotype	HMGV	Genotype	RPGV	RPGVμ	Genotype	HMRPGV	HMRPGVμ
95R95IPRO	2726.33	95R95IPRO	1.12	3659.04	95R95IPRO	1.11	3641.65
BMX COMPACTA IPRO	2636.24	BMX COMPACTA IPRO	1.05	3459.00	BMX COMPACTA IPRO	1.05	3434.08
TMG7061IPRO	2597.38	TMG7061IPRO	1.04	3408.10	TMG7061IPRO	1.03	3394.78
BMX ZEUS IPRO	2392.27	BRS 7780IPRO	1.04	3403.15	M5917IPRO	0.98	3210.54
BRS 7780IPRO	2356.29	M5917IPRO	1.01	3321.94	BMX GARRA IPRO	0.94	3093.17
BMX GARRA IPRO	2329.79	BMX ZEUS IPRO	0.97	3173.87	BMX ZEUS IPRO	0.94	3074.30
M5917IPRO	2291.84	BMX GARRA IPRO	0.96	3154.79	BRS 7780IPRO	0.93	3039.20
BRS 544RR	1968.59	BRS 544RR	0.81	2669.32	BRS 544RR	0.74	2442.64

HMGV: harmonic mean of genotypic values; **RPGV**: relative performance of genotypic values; **RPGVμ**: relative performance of genotypic values for grain yield; **HMRPGV**: harmonic mean of the relative performance of genotypic values; **HMRPGVμ**: harmonic mean of the relative performance of genotypic values for grain yield.

Conclusion

The G x E variation found in this study highlights the importance of considering environmental specificities in the selection and recommendation of cultivars.

The genotypes 95R95IPRO, M5917IPRO, BMX COMPACTA IPRO, BRS 7780IPRO and TMG 7061IPRO stood out for presenting average yields above the general average (3281.15 kg ha^{-1}) and consistent performance in multiple environments. These genotypes demonstrated potential to be recommended in breeding programs aiming at broad adaptability.

The analysis of predicted genotypic values, both free and considering the interaction with the environment, revealed changes in the ranking of genotypes, evidencing the need to use methods that evaluate the stability and adaptability of genotypes for different environmental conditions.

The results obtained reinforce the importance of considering the G × E interaction in soybean genetic improvement programs. Genotype selection must be carried out based on analyses that consider both the average performance and the stability and adaptability of the genotypes to different cultivation environments.

Funding

Additionally, acknowledgment is given to the funding support from Fundação de Amparo à Pesquisa do Estado do Rio de Janeiro - FAPERJ, Conselho Nacional de Desenvolvimento Científico e Tecnológico - CNPq, and Associação Nacional de Promoção e Inovação da Indústria de Biológicos ANPII-Bio.

Declarations

Ethics approval Not applicable.

Competing interests

The authors declare no conflicts of interest.

Abbreviations: G×E, genotype-by-environment; GY, Grain yield; HMGV, harmonic mean of genotypic values; HMRPGV, harmonic mean of the relative performance of genotypic values; HMRPGVμ, harmonic mean of the relative performance of genotypic values for grain yield; REML/BLUP, restricted maximum likelihood and best linear unbiased prediction; RPGV, relative performance of genotypic values; RPGVμ, relative performance of genotypic values for grain yield.

Supplemental material: the supplementary material consists of tables in Excel format, as indicated in the Materials and Methods section, provided to support the interpretation of the results and to characterize the field experimental sites.

References

Albuquerque JRT, Lins HA, Santos MG, Freitas MAMD, Oliveira FSD, Souza ARE, Silveira LM, Nunes GHS, Barros Júnior AP, Vieira PFMJ (2022) Adaptability and stability of soybean (*Glycine max* L.) genotypes in semiarid conditions. **Euphytica** 218:61. https://doi.org/10.1007/s10681-022-03014-w

Batista JN, Silva E, Souza EWS, Silva RKG, Mendonça LP, Cruz D, Rocha RS, Entringer GC, Guareschi RF, Souza Filho BF, Jantalia CP, Zilli JE, Gravina GA (2020) Avaliação de cultivares de soja quanto à fixação biológica do nitrogênio na região Norte Fluminense. In: **Anais do Congresso Fluminense de Pós-Graduação** 1. Galoá. https://doi.org/10.17648/congresso-fluminense-pg-2020-127339

Breda VSM, Daher RF, Santana JGS, Ambrósio M, Vidal AKF, ... Costa ES (2025) Genotype × environment interaction and estimates of grain yield adaptability and stability in black common bean genotypes in Brazil. **Crop Sci** 65:e70213. https://doi.org/10.1002/csc2.70213

Carneiro AK, Bruzi AT, Pereira JLAR, Zambiazzi EV (2019) Stability analysis of pure lines and a multiline of soybean in different locations. **Crop Breed Appl Biotechnol** 19:395–401. https://doi.org/10.1590/1984-70332019v19n4a55

Carvalho MP, Nunes JAR, Carmo EL, Simon GA, Moraes RNO (2021) Adaptability and stability of conventional soybean by GGE biplot analysis. **Pesq Agropec Trop** 51:e67995. https://doi.org/10.1590/1983-40632021v5167995

Cavassim JE (2014) Classificação em grupos de maturidade relativa para a soja comparando metodologias de estabilidade. Tese de Doutorado, Universidade Federal do Paraná.

Companhia Nacional de Abastecimento (2025) Portal de informações agropecuárias. https://portaldeinformacoes.conab.gov.br/safra-serie-historica-graos.html

Costa AF, Leal NR, Ventura JA, Gonçalves LSA, Amaral Júnior AT, Costa H (2015) Adaptability and stability of strawberry cultivars using a mixed model. **Acta Sci Agron** 37:435–440. https://doi.org/10.4025/actasciagron.v37i4.19502

Costa APL, Moitinho ACR, Silva AP, Amaral LO, Souza JS, Unêda-Trevisoli SH (2025) Comparative analysis of adaptability and stability of soybean genotypes for cultivar registration and protection. **Braz J Biol** 85:e286817. https://doi.org/10.1590/1519-6984.286817

Cruz DP, Gravina GA, Vivas M, Entringer GC, Souza YP, Rocha RS, Silva RKG (2021) Combined selection for adaptability, genotypic stability and cowpea yield from mixed models. **Ciênc Rural** 51:e20200540. https://doi.org/10.1590/0103-8478cr20200540

Gonçalves GMC, Ferreira-Gomes RL, Lopes ACA, Vieira PFMJ (2020) Adaptability and yield stability of soybean genotypes by REML/BLUP and GGE biplot. **Crop Breed Appl Biotechnol** 20:e302020211. https://doi.org/10.1590/1984-70332020v20n2a33

Gonçalves GM, Viana AP, Amaral Junior AT, Resende MDV (2014) Breeding new sugarcane clones by mixed models under genotype by environmental interaction. **Sci Agric** 71:66–71. https://doi.org/10.1590/S0103-90162014000100009

James AT, Yang A (2016) Interactions of protein content and globulin subunit composition of soybean proteins in relation to tofu gel properties. **Food Chem** 194:284–289. https://doi.org/10.1016/j.foodchem.2015.08.019

Maia MCC, Resende MDV, Paiva JR, Cavalcanti JJV, Barros LM (2009) Seleção simultânea para produtividade, adaptabilidade e estabilidade genotípica em clones de caju por modelos mistos. **Pesq Agropec Trop** 39:43–50.

Mbuma NW, Gerrano AS, Lebaka N, Labuschagne M (2022) Interrelationship between grain yield components and nutritional quality traits in cowpea genotypes. **S Afr J Bot** 150:34–43. https://doi.org/10.1016/j.sajb.2022.07.006

Moitinho ACR (2021) Estimativa de parâmetros genéticos e análise multivariada na seleção de genótipos de soja oriundos do cruzamento de genitores tipo grão × tipo alimento. Dissertação de Mestrado, Universidade Estadual Paulista.

Neumaier N, Farias JRB, Nepomuceno AL, Mertz-Henning LM, Foloni J, Moraes LAC, Gonçalves S (2020) Ecofisiologia da soja. In: Seixas CDS, Neumaier N, Balbinot Junior AA, Krzyzanowski FC, Leite RMVB (eds) **Tecnologias de produção de soja**, pp 33–54. Embrapa Soja.

534 Olivoto T, Lúcio AD, Silva JA, Sari BG, Diel MI (2019) Mean performance and stability
535 in multi-environment trials II: Selection based on multiple traits. **Agron J** 111:2961–
536 2969. https://doi.org/10.2134/agronj2019.03.0221
537 Olivoto T, Nardino M, Carvalho IR, Follmann DN, Ferrari M, Szareski VJ, Pelegrin AJ,
538 Souza VQ (2017) REML/BLUP and sequential path analysis in estimating genotypic
539 values and interrelationships among simple maize grain yield-related traits. **Genet Mol**
540 **Res** 16:gmr16019525. https://doi.org/10.4238/gmr16019525
541 Patil G, Vuong TD, Kale S, Valliyodan B, Deshmukh R, Zhu C, Nguyen HT (2018)
542 Dissecting genomic hotspots underlying seed protein, oil, and sucrose content in an
543 interspecific mapping population of soybean using high-density linkage mapping. **Plant**
544 **Biotechnol J** 16:1939–1953. https://doi.org/10.1111/pbi.12929
545 Possobom MTF, Rodrigues HS, Ferreira RAC, Ludke WH, Cruz CD, Schuster I, Silva
546 FL (2020) Interação genótipo × ambiente. In: Matsuo E, Cruz CD, Sediyama T (eds)
547 **Aplicações de técnicas biométricas no melhoramento genético da soja**, pp 153–164.
548 Mecenas.
549 Resende MDV, Duarte JB (2007) Precisão e controle de qualidade em experimentos de
550 avaliação de cultivares. **Pesq Agropec Trop** 37:182–194.
551 Resende MDV (2016) Software SELEGEN-REML/BLUP: A useful tool for plant
552 breeding. **Crop Breed Appl Biotechnol** 16:330–339. https://doi.org/10.1590/1984-
553 70332016v16n4a49
554 Rocha CB, De Majo C, Dutra S (2022) A geo-historical analysis of expanding soybean
555 frontiers in the Brazilian Cerrado. **HALAC** 12:217–252. https://doi.org/10.32991/2237-
556 2717.2022v12i2.p217-252
557 Sediyama T, Felipe LS, Borém A (2015) **Soja: do plantio à colheita.** Editora UFV.
558 Seixas CDS, Neumaier N, Balbinot Junior AA, Krzyzanowski FC, Leite RMVBC (eds)
559 (2020) **Tecnologias de produção de soja.** Embrapa Soja.
560 Souza Filho BF, Zilli JE, Viana AR, Batista JN, Alves BJR, Jantalia CP, Caballero SSU,
561 Zito RK (eds) (2023) **A cultura da soja no Norte Fluminense – safra 2022/2023:**
562 **Resultados experimentais.** PESAGRO-RIO.
563 Torres FE, Benites SB, Ribeiro LP, Correa AM, Silva Junior CA, Teodoro PE (2018)
564 Selection of soybean genotypes for Cerrado/Pantanal ecotone via REML/BLUP. **Biosci J**
565 34:333–340. https://doi.org/10.14393/BJ-v34n2a2018-37207
566 Zhang J, Wang X, Lu Y, Bhusal SJ, Song Q, Cregan PB, Yen Y, Brown M, Jiang GL
567 (2018) Genome-wide scan for seed composition provides insights into soybean quality

improvement and the impacts of domestication and breeding. **Mol Plant** 11:460–472. https://doi.org/10.1016/j.molp.2017.12.016

Zilli JE, Batista JN, Guareschi RF, Zito RK (eds) (2022) **Avaliação de cultivos de soja no Norte Fluminense.** Embrapa Agrobiologia.

Zilli JE, Polidoro JC, Alves BJR, Lumbreras JF (eds) (2021) **Produção da soja e do milho como um caminho para o desenvolvimento do agronegócio da região Norte Fluminense.** Embrapa Solos.

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