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PLANT BREEDING

Adaptability and stability of corn genotypes for baby corn production via GGE biplot and REML

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ABSTRACT. Owing to the interaction between genotype and environment (G × E), selecting and developing high-yielding varieties with strong phenotypic adaptability and stability is paramount. Therefore, this study aimed to determine the efficiency of selection of corn genotypes for baby corn production based on productivity, adaptability, and stability. Eleven corn genotypes were evaluated in six municipalities in the state of Espírito Santo, Brazil in 2019. Superior genotypes were selected using the harmonic mean of the relative performance of the predicted genetic values (HMRPGV) and graphical analysis using the genotype main effect plus G × E (GGE) interaction biplot. Genotypes AG 1051 and BR 106 exhibited the best performance across environments. The HMRPGV method and ideotypes obtained through graphic analysis proved effective in selecting genotypes with high productive potential, responsiveness to environmental changes, and highly predictable behavior in the face of environmental stimuli.

Keywords: genotype x environment interaction; HMRPGV; ideotype; mixed models; *Zea mays* L.

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Introduction

Baby corn ears are juvenile, developing, and unpollinated corn (*Zea mays* L.) ears (Costa et al., 2020) which are consumed either fresh or in brine as snacks, pickles, salads, or used in the preparation of various dishes, such as risottos, soups, and stews.

Considered a vegetable due to the short period between sowing and harvesting, which varies based on sowing time, cultivar, and crop management, baby corn is generally harvested between 50 and 60 days after seedling emergence (Pereira Filho & Karum, 2008), specifically, two to three days after emergence of the style stigmata and preferably in the early hours of the day, when spikelet moisture is higher and ambient temperature is lower, such as to preserve their quality.

Despite the lack of commercial corn cultivars specifically developed for baby corn production, selection of the most suitable varieties is considered the most critical step for successful cultivation. Although sweet corn and popcorn cultivars have been widely used because of consumer market acceptance, a limitation in so doing is the rapid spikelet development of such cultivars, leading to a potential loss of commercial value (Nascimento et al., 2018). In addition to quality, plant traits such as height, earliness, flowering uniformity, and prolificacy are considered more important for baby corn production (Thakur et al., 2000).

An ideal genotype should combine high productivity with desirable agronomic traits. However, the study of selection gain is challenging due to the genotype × environment interaction. According to Cruz et al. (2014), this interaction influences cultivar recommendations and complicates breeding, as different criteria are necessary for the selection of superior materials using alternative methods to identify genetic superiority.

While studying genotype × environment interactions, the analysis of adaptability and stability provides valuable insights for selection. Adaptability is associated with the ability of a genotype to cope with environmental changes, whereas stability describes the predictability of genotypic behavior in response to environmental variation (Vidal et al., 2023).

Various statistical methods have been used to estimate adaptability and stability. One of these involves the Restricted Maximum Likelihood (REML)/Best Linear Unbiased Prediction (BLUP) method, an approach widely used for studies of this nature, as genetic evaluation is achieved by predicting the values of selection treatments (Resende, 2016). In this scenario, the harmonic mean of the relative performance of predicted genetic values (HMRPGV) proposed by Resende (2007) stands out as a method that allows simultaneous selection based on productivity, adaptability, and stability. Another notable methodology is based on principal components, and consists in a graphical analysis generated from a GGE Biplot (Yan et al., 2007). In this approach, graphs are generated from principal components, where the first and second components represent the proportion of baby corn yield due to genotype characteristics and G × E interactions, respectively (Olanrewaju et al., 2021).

Cropping for baby corn offers an excellent alternative for diversifying production and increasing profitability in family farming, as it renders greater earnings than those obtained from grain production (Nascimento et al., 2018). However, scientific data on baby corn cultivation, including the use of suitable cultivars, crop management, and fertilization, are lacking. Consequently, understanding the behavior of corn cultivars for baby corn production in different environments is paramount for selecting and recommending cultivars with wide adaptability, production stability, and high productivity, particularly in environments where family farming predominates.

Therefore, the objective of this study was to simultaneously determine selection efficiency based on high productivity, adaptability, and stability of corn genotypes for baby corn production in the state of Espírito Santo, Brazil, using the GGE biplot and REML/BLUP methodologies.

Material and methods

Eleven genotypes were assessed for baby corn production, including a double-hybrid as a control, four landraces, and six commercial varieties. Except for the hybrid, genotype selection was based on farmer preferences in the state of Espírito Santo, Brazil. These farmers commonly use open-pollinated varieties to produce corn grain for animal feed, cornmeal, and green corn production.

The experiment was laid in a randomized blocks design with eleven treatments four replicates. Each experimental unit consisted of four 6-m long rows spaced 1.0 m apart for a population density of 200,000 plants ha^{-1}. The effective sampling area encompassed the two central rows of each experimental plot, disregarding 0.5 m at both ends of the row, totaling 10 m². A border area surrounded each experimental plots to minimize environmental effects.

Assessments were conducted in 2019 on family farms in six municipalities representing all four mesoregions of the state of Espírito Santo: Alegre and Muqui in the south, Santa Teresa and Viana in the center, Governador Lindenberg in the northwest, and São Mateus on the north coast (Figure 1).

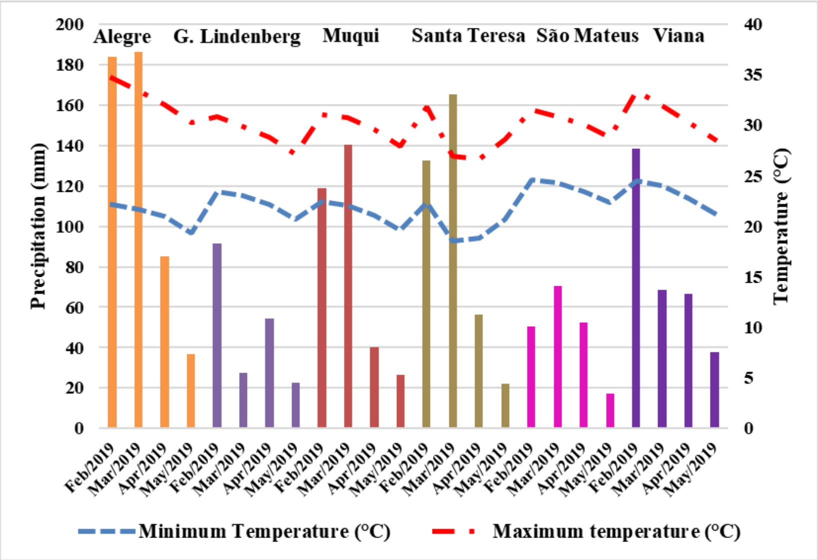

Figure 1. Meteorological data from the six municipalities in the state of Espírito Santo, Brazil, where 11 corn genotypes were evaluated for baby corn production in 2019. Source: Agritempo (2023).

The first baby corn harvest took place three days after the emergence of the styles-stigmata at 73 days after sowing (DAS). Following harvest, the spikelets were placed in thermal boxes at temperatures ranging from 5 to 12°C until the evaluation period. Subsequently, two harvests were conducted per week for a total of 11 harvests.

At sampling, spikelet weight (without straws or stigmas) was measured and converted to kg ha^{-1}. To meet commercial standards, baby corn must have a diameter between 10 and 18 mm and a length between 40 and 120 mm (Lucianetti & Bellettini, 2020).

Genotype adaptability and stability were estimated using the REML/BLUP procedure (Restricted Maximum Likelihood/Best Linear Unbiased Prediction), using the statistical model below: $y = X_b + Z_g + W_c + e$, where y is the vector of observed values, b is the effect of blocks within different environments (fixed), g is the effect of genotypes (random), c is the effect of the G × E interaction (random), e is the random error, and X, Z, and W represent the incidence matrices for b, g, and c, respectively.

The assumed distributions and structures of means (E) and variances (Var) were as follows:

$$\text{Var E}\begin{bmatrix} y \\ g \\ c \\ e \end{bmatrix} = \begin{bmatrix} Xb \\ 0 \\ 0 \\ 0 \end{bmatrix};\ \text{Var}\begin{bmatrix} g \\ c \\ e \end{bmatrix} =$$

As outlined by Resende (2016), the evaluation of model effects should not be tested using the F-test when using mixed models, as in the analysis of variance. Instead, a likelihood ratio test (LRT) conducted through deviance analysis is recommended. This analysis is applied to both balanced and unbalanced data, indicating the goodness of fit of the model used. In this context, deviance is a statistic derived from the ratio of likelihoods between the full model and a model that lacks the effect being tested.

Statistical model 54, involving the HMRPGV method for corn genotypes in baby corn production across multiple locations with one observation per plot, was used using the computational application SELEGEN – REML/BLUP to rank and select superior genotypes based concomitantly on productivity, adaptability, and stability (Resende, 2016). The HMRPGV method uses three strategies to select superior genotypes, focusing on stability and adaptability, and a simultaneous assessment of stability, adaptability, and productivity parameters.

To evaluate stability, the harmonic mean of genetic values (HMGV) was obtained using the following equation: $\text{HMGV}_\text{i} = n/\sum_{j=1}^{n}(1/Vg_{ij})$, where n is the number of environments in which genotype i was evaluated and Vg_{ij} is the genotypic value of genotype i in environment j, expressed as a proportion of the mean in that environment (Resende, 2007). For adaptability, the values for the relative performance of genetic values (RPGV) were obtained according to the following expression: $\text{RPGV}_\text{i} = 1/n\ x\ (\sum_{j=1}^{n} Vg_\text{ij})\ /M_\text{j}$, where M_j is the average yield in environment j. Simultaneous selection for productivity, adaptability, and stability was given by the HMRPGV statistic, according to the following expression: $\text{HMRPGV}_\text{i} = n/(\sum_{j=1}^{n} x\ 1)/Vg_\text{ij}$, where n is the number of locations where the i genotypes were evaluated, and Vg_{ij} is the genotypic value of genotype i in location j, expressed as a proportion of the mean at that location.

The ‘genotype main effect plus G × E (GGE) interaction biplot multivariate-analysis was performed using the GGE Biplot GUI package of the R statistical software (R Core Team, 2019), as per the following model: $Y_{ij} - \mu = G_i + E_j + GE_{ij}$ where Y_{1j} is the average yield of genotype i in environment j; μ is the overall mean; G_1 is the main effect of genotype i for environment j; and GE_{1j} is the specific interaction between genotype i and environment j (Yan et al., 2007; Yan & Holland, 2010).

The GGE Biplot methodology considers the main effect of genotypes and the G × E interaction, which are encompassed in two multiplicative terms, according to the following equation (Yan et al., 2000): $Y_{ij} - \mu - \beta_j = g_{1i}e_{1j} + g_{2i}e_{2j} + \varepsilon_{ij}$ where Y_{ij} is the expected performance of genotype i in environment j; μ is the overall mean of observations; β_j is the main effect of environment j; g_{1j} and e_{1j} are the main scores of genotype i in environment j, respectively; and ε_{ij} is the unexplained residual of both effects.

Biplot analysis is based on the principal component technique in which the first two components are represented by the axes of the multivariate analysis graph (Carvalho et al., 2021).

The graph of the GGE Biplot was generated by simple dispersion of g_{i1} and g_{i2} for genotypes and e_{j1} and e_{j2} for environments, using Decomposition into Singular Values (DVS) according to the following equation: $Y_{ij} = \mu - \beta_\text{j} = \lambda_1\xi_{i1}\eta_{1j} + \lambda_2\xi_{i2}\eta_{2j} + \varepsilon_{ij}$, where λ_1 and λ_2 are the largest eigenvalues of the first and second principal components, PC1 and PC2, respectively; ξ_{i1} and ξ_{i2} are the eigenvectors of genotype i of PC1 and PC2, respectively; and η_{1j} and η_{2j} are the eigenvectors of environment j of PC1 and PC2, respectively (Yan & Kang, 2019).

Statistical genetic analysis were performed using GENES software (Cruz, 2016) and the GGE BiplotGui package, using the R statistical software (R Core Team, 2019).

Results and discussion

The average baby corn yield of the eleven corn genotypes evaluated in this study reached 2,165.67 kg ha^{-1}, which was greater than the averages reported by Choudhary et al. (2019), Costa et al. (2020), and Kumar et al. (2020) (Table 1). Deviance analysis revealed significant effects of both genotype and the genotype × environment interaction (G × E), indicating variability among genotypes for baby corn yield and genotypic response to environment (Table 1).

Table 1. Summary of deviance analysis of 11 corn genotypes for baby corn yield evaluated in six municipalities in the state of Espírito Santo, Brazil, in 2019.

Effect	Deviance(1)	Chi-square(2)
Genotype	3,159.21	6.60*
Genotype × environment interaction	3,192.91	40.30*
Full model	3,152.61	-
Overall mean		2,165.67

(1)Deviance model adjusted without the cited effects; (2) significance at 5% probability using the chi-square test.

As shown in Table 2, there was a consensus in the ranking of most genotypes based on HMGV (stability), RPGV (adaptability), and HMRPGV (adaptability and stability). These results suggest that genetic values can be reliably predicted based on a unified performance standard simultaneously encompassing both stability and adaptability (Santos et al., 2018).

Table 2. Stability (HMGV), adaptability (RPGV and RPGV × OM), and stability and adaptability (HMRPGV and HMRPGV × OM) of genetic values of 11 corn genotypes for baby corn production, with prediction achieved by best linear unbiased prediction (BLUP) analysis, evaluated in six environments in the state of Espírito Santo, Brazil, in 2019.

Ranking	Genotype	HMGV	RPGV	RPGV (x OM)	HMRPGV	HMRPGV (x OM)
1	AG 1051	2,503.79	1.20	2,608.92	1.20	2,593.91
2	Aliança	2,205.23	1.07	2,320.81	1.06	2,293.66
3	BRS Eldorado	2,130.18	1.02	2,203.35	1.01	2,186.80
4	BR 106	2,116.24	1.05	2,279.63	1.03	2,234.96
5	Incaper 203	2,064.95	1.00	2,176.25	1.00	2,167.76
6	Celina	2,043.45	0.98	2,112.72	0.97	2,103.74
7	BRS Sol da Manhã	2,024.91	0.98	2,125.44	0.98	2,116.39
8	AL Bandeirante	1,986.06	0.97	2,101.90	0.96	2,074.63
9	Palha Roxa	1,965.96	0.95	2,061.65	0.95	2,050.89
10	Fortaleza	1,954.24	0.94	2,045.26	0.94	2,028.97
11	Emcapa 201	1,693.58	0.82	1,786.45	0.82	1,769.86

HMGV: harmonic mean of genotypic values; RPGV: relative performance of genetic values; HMRPGV: harmonic mean of the relative performance of predicted genetic values; and OM: overall mean.

Genotypes AG 1051, Aliança, and BR 106 showed outstanding performance according to the HMRPGV method, with yields surpassing 2,000 kg ha^{-1} (Table 2). This result suggests that these genotypes showed greater adaptability to the environments tested, as well as good predictability and high productivity. Conversely, cultivar Emcapa 201 exhibited the lowest values for the three measured parameters, indicating that it is not well suited for baby corn production.

The GGE biplot methodology offers the advantage of assisting in delimiting areas by identifying mega-environments, defined as groups of environments with similar G × E interactions, and consequently showing moderate changes in genotype ranking. Similarly, the "which-won-where" biplot visually groups environments and determines the genotypes with the best average performance in each environment (Yan & Tinker, 2006).

Figure 2 illustrates the grouping of the tested environments based on the G × E interactions among the best genotypes. The biplot originating from (0,0), is divided into six sectors. Within these sectors, the five evaluation environments were categorized into three groups based on the lines emanating from the biplot origin. The first group consisted of environments 4 (São Mateus) and 6 (Muqui), the second group included environments 1 (Alegre), 2 (Santa Teresa), and 5 (Viana), forming a mega-environment, and the third group comprised only environment 3 (Governador Lindenberg). Genotypes within the same sector were deemed to be the most adapted to that environment, whereas those within the polygon exhibited inferior performance. Thus, genotype 6 (AG 1051) was the most adapted to the mega-environment consisting in environments Alegre, Santa Teresa, and Viana, while genotypes 3 (BRS Eldorado) and 4 (Aliança) showed superior adaptation to the environments of São Mateus and Muqui. Finally, genotype 2 (BR 106) was the best adapted to the environment of the municipality of Governador Lindenberg.

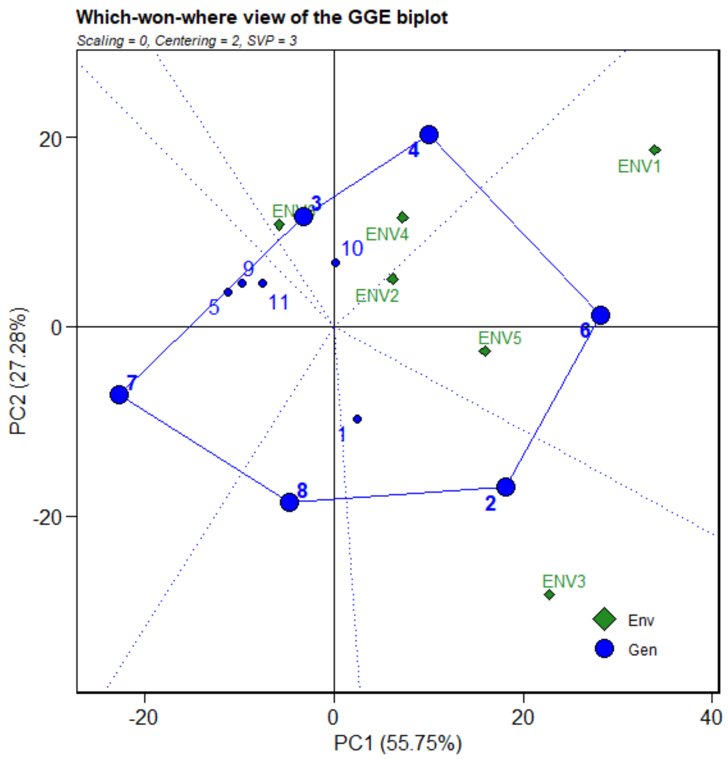

Figure 1. Which-won-where GGE biplot of corn genotypes and environments for baby corn yield (kg ha^{-1}). Gen – genotype: Gen.1 (Incaper 203), Gen. 2 (BR 106), Gen. 3 (BRS Eldorado), Gen. 4 (Aliança), Gen. 5 (Fortaleza), Gen. 6 (AG 1051), Gen. 7 (Emcapa 201), Gen. 8 (AL Bandeirante), Gen. 9 (Palha Roxa de Venda Nova do Imigrante), Gen. 10 (BRS Sol da Manhã), and Gen. 11 (Celina). Env – environment: Env. 1 (Alegre), Env. 2 (Santa Teresa), Env. 3 (Governador Lindenberg), Env. 4 (São Mateus), Env. 5 (Viana), and Env. 6 (Muqui).

According to Kumar et al. (2020), a larger proportion of the genotype effect relative to that of the G × E interaction implies that the performance of a genotype is less dependent on the environment, suggesting the existence of a relatively smaller number of mega-environments. In this study, the formation of two mega-environments indicates that the environment significantly influenced genotype performance, thus confirming the findings summarized in Table 1.

The vertices of the polygon were defined by the genotypes located farthest from the origin of the biplot, implying they were the genotypes with the best performance and greatest adaptation within their respective sectors, namely, genotypes 2, 3, 4, 6, 7, and 8 (Figure 2). Notably, among these, genotypes 7 (Emcapa 201) and 8 (AL Bandeirante) did not cluster in any of the six evaluated environments and, therefore, should be considered unfavorable for the tested groups of environments, indicating low productivity. The subpar performance of the Emcapa 201 cultivar, as depicted in Figure 2, corroborated the value estimated by the RPGV method (Table 2).

Souza et al. (2023) claimed that genotypes situated at the vertices of a polygon and do not cluster within any formed mega environment can be considered unfavorable for the tested environments and should not be recommended. Similarly, genotypes located within a polygon, as indicated by smaller vectors, exhibit lower performance and greater interaction with the environments in which they are found (Oliveira et al., 2018).

The analysis of the "mean vs. stability" biplot (Figure 3) underlined the fact that the greater the projection of a genotype in relation to the PC1 axis (abscissa axis), the lower its stability; conversely, the further away the genotype is from the PC2 axis (ordinate axis), the more yielding it tends to be. The arrow indicates the highest average performance among the evaluated genotypes (Yan et al., 2007).

Genotypes 2 (BR 106) and 4 (Aliança) showed higher yields than the overall mean of the evaluated genotypes; however, they were less stable. In contrast, in addition to showing higher yields than the overall mean of the experiment, genotype 6 (AG 1051) demonstrated the highest stability. The rest of the genotypes evaluated attained yields below the overall mean; however, among them, genotypes 5 (Fortaleza), 7 (Emcapa 201), and 9 (Palha Roxa de Venda Nova do Imigrante) showed the highest stability (Figure 3). These results are consistent with those observed in Table 2, where the most stable genotype according to the HMGV method was AG 1051, whereas the least stable were Fortaleza, Palha Roxa de Venda Nova do Imigrante, and Emcapa 201.

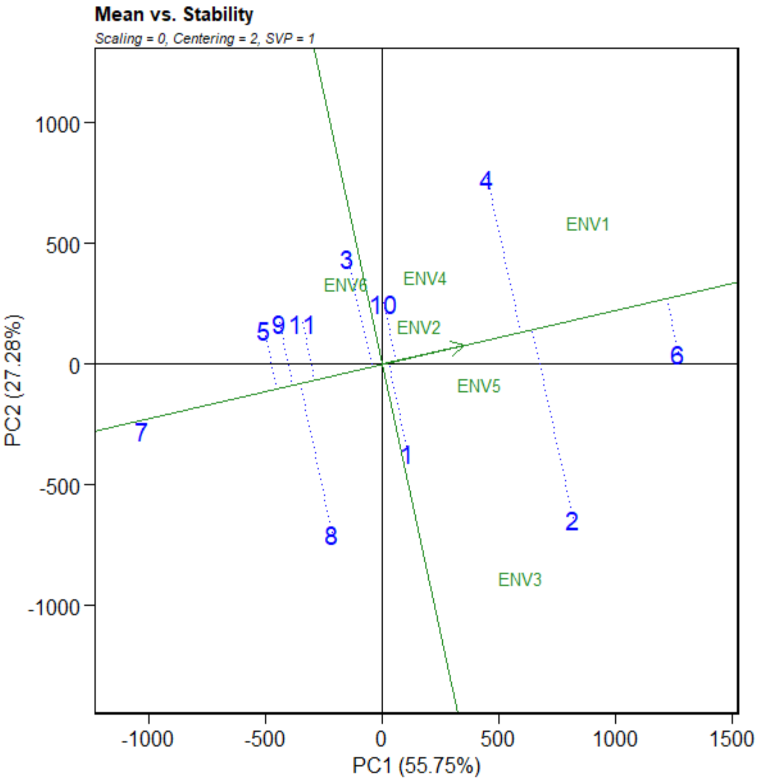

Figure 2. Mean vs. stability GGE biplot of corn genotypes and environments for baby corn yield (kg ha^{-1}). Gen – genotype: Gen.1 (Incaper 203), Gen. 2 (BR 106), Gen. 3 (BRS Eldorado), Gen. 4 (Aliança), Gen. 5 (Fortaleza), Gen. 6 (AG 1051), Gen. 7 (Emcapa 201), Gen. 8 (AL Bandeirante), Gen. 9 (Palha Roxa de Venda Nova do Imigrante), Gen. 10 (BRS Sol da Manhã), and Gen. 11 (Celina). Env – environment: Env. 1 (Alegre), Env. 2 (Santa Teresa), Env. 3 (Governador Lindenberg), Env. 4 (São Mateus), Env. 5 (Viana), and Env. 6 (Muqui).

Figure 4 illustrates the optimal conditions for evaluating corn genotypes for baby corn production. Environments 1 (Alegre) and 5 (Viana) were positioned near the first concentric circle and in proximity to the set, indicating that they were the most favorable environments and, consequently, deemed suitable. Conversely, environments 3 (Governador Lindenberg) and 6 (Muqui), which were situated farther from ideal conditions, were considered less conducive for assessing the performance of corn genotypes in baby corn production.

The ideal genotype is characterized by high average performance for the studied trait, coupled with stability across all tested environments (Oliveira et al., 2018). Santos et al. (2017) assert that while the ideal genotype is a theoretical model, it serves as a reference to identify an ideotype when evaluating genotypic performance in diverse environments. The ideotype is represented by a point located at the center of the concentric circles. Therefore, genotypes positioned closer to the center were deemed more desirable (Figure 5).

Figure 5 depicts the ideotype for baby corn productivity in the set of environments tested herein. Genotype 6 (AG 1051) was positioned within the first concentric circle, near the arrow, indicating it was the best genotype (ideotype), whereby it was classified as the ideal genotype. In turn, genotypes 2 (BR 106) and 4 (Aliança) were closer to the ideal genotypes, whereas genotypes 5 (Fortaleza), 7 (Emcapa 201), and 9 (Palha Roxa de Venda Nova do Imigrante), located in the outermost concentric circles, exhibited the lowest performance. Hence, the recommendation for the best genotypes is based on both high production performance and stability, aligning with the results in Table 2, which considers productivity, adaptability, and stability (HMRPGV). Consequently, the identified corn genotypes are recommended for baby corn production in the evaluated regions of the state of Espírito Santo, Brazil.

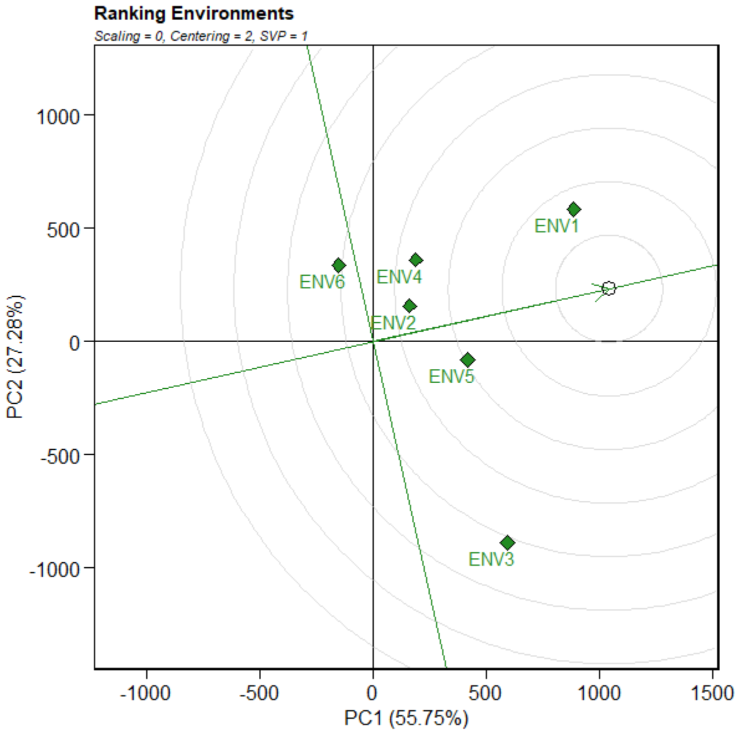

Figure 3. GGE biplot comparing all tested environments with the ideal environment. Env – environment: Env. 1 (Alegre), Env. 2 (Santa Teresa), Env. 3 (Governador Lindenberg), Env. 4 (São Mateus), Env. 5 (Viana), and Env. 6 (Muqui).

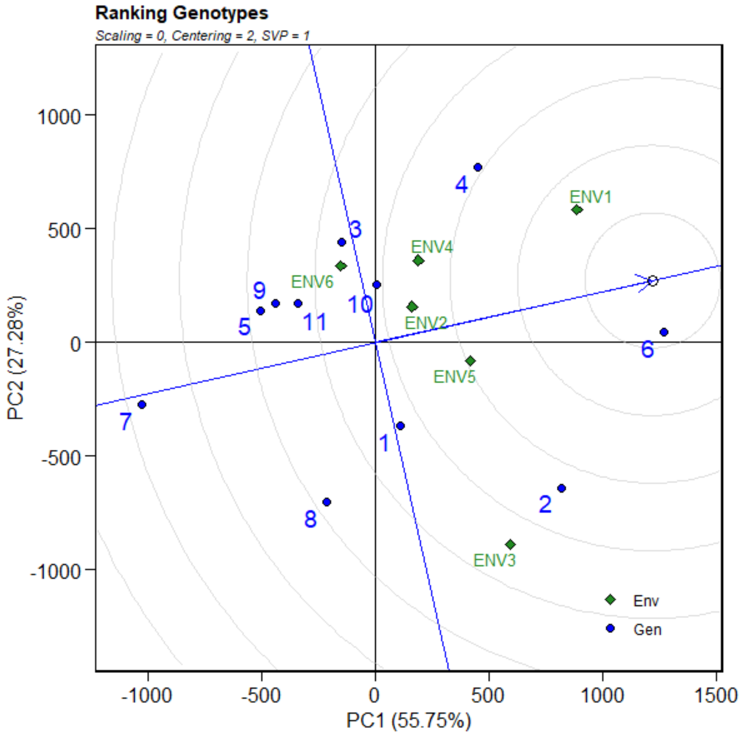

Figure 4. GGE Biplot comparing corn genotypes for baby corn production with the ideal genotype based simultaneously on productivity and stability. Gen – genotype: Gen.1 (Incaper 203), Gen. 2 (BR 106), Gen. 3 (BRS Eldorado), Gen. 4 (Aliança), Gen. 5 (Fortaleza), Gen. 6 (AG 1051), Gen. 7 (Emcapa 201), Gen. 8 (AL Bandeirante), Gen. 9 (Palha Roxa de Venda Nova do Imigrante), Gen. 10 (BRS Sol da Manhã), and Gen. 11 (Celina). Env – environment: Env. 1 (Alegre), Env. 2 (Santa Teresa), Env. 3 (Governador Lindenberg), Env. 4 (São Mateus), Env. 5 (Viana), and Env. 6 (Muqui).

In situations where low-level cropping technologies prevail, particularly in family farms, the use of hybrid corn seeds is economically unfeasible because of the high costs of fertilization and irrigation to achieve high productivity. However, the use of open pollinated varieties, either landraces or commercial, is an attractive alternative for these farmers (Nascimento et al., 2018).

Lima and Borém (2018) showed that open-pollinated varieties can be obtained through the free pollination of selected individuals, resulting in high heterozygosity and heterogeneity, but despite their greater productive stability and genetic variability, these varieties exhibit lower product uniformity. Moreover, yield is lower due to the limited exploitation of heterosis, with a maximum of 50% of the loci being heterozygous. On the other hand, the use of these varieties leads to a significant reduction in production costs, making them suitable for low-technology cropping systems with lower costs of fertilization, irrigation, and protection against pests, diseases, and weeds. Additionally, these varieties enable producers to produce their own seed each year, provided they do it correctly. Therefore, we recommend that low-income farmers use the Aliança landrace and the commercial variety BR 106 to produce baby corn under their growing conditions.

Conclusion

Based on simultaneous consideration of productivity, adaptability, and stability in baby corn production, Genotypes AG 1051, Aliança, and BR 106 showed the best performance across environments. The close agreement between the harmonic mean of the relative performance of genotypic values (HMRPGV) and the graphical analyses generated by the GGE Biplot method demonstrated their effectiveness in allowing for an optimized selection of high-yielding genotypes that are responsive to environmental stimuli and exhibit predictable responses to environmental variations. Therefore, these strategies are recommended for selecting corn genotypes for baby corn production.

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