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ARTICLE

Adaptability and stability of black bean genotypes for Rio de Janeiro, by GGE biplot analysis

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Abstract: *The study of adaptability and yield stability is essential for the selection and recommendation of new cultivars. Thus, this study determined the adaptability and yield stability of black bean genotypes for cultivar recommendation using a GGE biplot. To this end, nine trials were carried out at different locations in the state of Rio de Janeiro. Eleven genotypes were evaluated in three growing seasons, in a randomized block design, with three replications. Adaptability and stability of grain yield were analyzed by the GGE biplot method. The effects of genotypes, environments and of the genotype - environment interaction were significant, which explained the different responses of the genotypes to the tested environments. The GGE biplot analysis revealed Macaé as an ideal district for testing and high yield, adaptability, and stability of performance were observed for genotype CNFP 15290, which can be recommended for grain production in the state of Rio de Janeiro.*

Keywords: *Grain yield, G×E interaction, multivariate analysis,* Phaseolus vulgaris

INTRODUCTION

Common bean (*Phaseolus vulgaris* L.) is a widely distributed and commonly consumed species throughout the world. In this scenario, Brazil stands out, with the third place in the ranking of bean-producing countries in 2020 (FAO 2020). In 2020/21, the production in Brazil reached 3 million tons. Of this total yield, 509 thousand tons consisted of black bean (CONAB 2022). It is worth emphasizing that, despite the country's leading position, the demand for this food product is far from being supplied. In addition, the yield of this grain (1,045 kg ha^{-1}) in Brazil is still low when compared to the crop yield potential, which could exceed 4,000 kg ha^{-1} (Souza et al. 2019).

In Rio de Janeiro, common bean accounts for 0.15% of the total amount produced in the Southeast Region (IBGE 2020). Although this is one of the largest national centers of common bean marketing, the demand still exceeds

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the supply. To mitigate this problem, the state of Rio de Janeiro imports the product from neighboring states, e.g., Espírito Santo, Minas Gerais and São Paulo (CEASA 2010). This panorama serves as a map to choose adequate strategies to optimize the sustainability of common bean cultivation in the state.

One of the main challenges for breeding programs is the search for new cultivars that combine high yield, adaptability and stability (Borém et al. 2017). Thus, the GGE biplot method integrates the main effects of the genotype (G) and genotype x environment interaction (GE), which removes the main effect from the environment (E) and integrates the genotypic main effect to the effect of G×E interaction. Biplot graphs are generated to visually represent a data matrix (Yan and Holland 2010, Silva and Benin 2012). This may be a support to evaluate genotype performance at various sites in a fundamental and efficient way, as well as to identify and quantify the environmental effects on one or more agronomic traits of interest of a group of genotypes (Yan and Kang 2003).

When the G×E interaction is associated with a complex part, the classification of genotypes between environments is significantly altered, indicating the presence of genotypes with a good performance in one environment, but not in others (Cruz and Castoldi 1991). The G×E interaction effects are considered one of the main difficulties of selection in breeding programs. The reason is that, if there were no interactions, a single trial would be sufficient to provide universal results about a genotype.

This GGE biplot method has been used for different crops, and proved efficient for the evaluation and selection of genotypes with high yield performance combined with stability in different environments (Cruz et al. 2020, Gonçalves et al. 2020, Rocha et al. 2020). In this context, this study tested whether black bean genotypes can present different responses to multiple environments, in an analysis by the GGE biplot. The objective was to determine the adaptability and yield stability of black bean genotypes via GGE biplot, with a view to recommend the best for grain production in the state of Rio de Janeiro, Brazil.

MATERIAL AND METHODS

Test location and genotypes

Eleven black bean genotypes were evaluated, three of which were control cultivars (BRS Campeiro (G1), BRS Esplendor (G2), IPR Uirapurú (G3)), and eight test lines (CNFP 15289 (G4), CNFP 15290 (G5), CNFP 15292 (G6), CNFP 15302 (G7), CNFP 15304 (G8), CNFP 15310 (G9) CNFP 15359 (G10) and CNFP 15361 (G11)), developed at Embrapa Rice and beans (BRS cultivars and CNFP lines) and from the Instituto Agronômico do Paraná (cv IPR Uirapurú).

Three trials were carried out in three growing seasons (2013, 2014 and 2015), at the State Enterprise for Agricultural Research of Rio de Janeiro (PESAGRO-RIO), in three districts of the state: Araruama, Campos dos Goytacazes and Macaé. The respective soils were classified as Dystrophic Red-Yellow Podzolic, Pdzolic Yellow Alic and Alic Red-Yellow Latosol. The nine environments in these districts were Araruama 2013 (E1), Campos 2013 (E2), Macaé 2013 (E3), Araruama 2014 (E4), Campos 2014 (E5), Macaé 2014 (E6), Araruama 2015 (E7), Campos 2015 (E8) and Macaé 2015 (E9). A map of Rio de Janeiro (Figure 1) explains where sampling was performed in the trials.

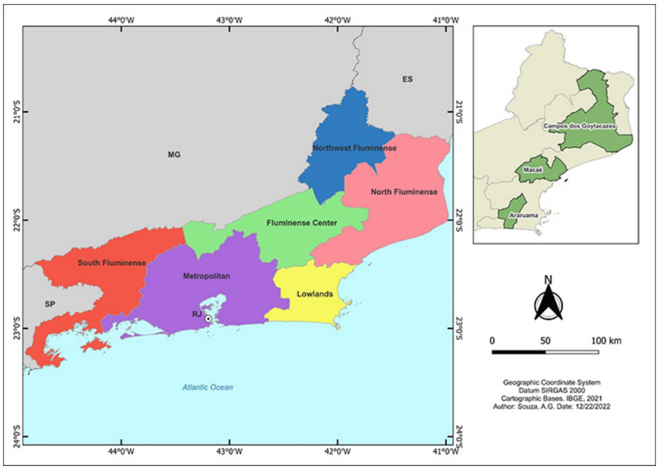

Figure 1. Spatial distribution of the mesoregions in the state of Rio de Janeiro and map of the location of the districts where three annual trials for the value for cultivation and use (VCU) of black bean were installed from 2013 to 2015.

Experimental design and yield evaluation

During the trials, the cultural and phytosanitary treatments recommended for the crop were applied, as well as sprinkler irrigation whenever necessary, as proposed by Carneiro et al. (2015). The experiments were sown between March and April of each year and harvested shortly after the physiological maturity of seeds, the last step of the reproductive phase of the plants (stage R9). At the end of R9, the seed moisture content was about 15%, i.e., adequate for harvesting, which should coincide with the moment of maximum grain dry matter.

The trials were arranged in an experimental design of randomized blocks with three replications, with a total of 297 plots. Each plot consisted of four 4 m rows spaced 0.50 m apart, with a total plant population of 300 thousand ha^{-1}. Yield data from the two center rows were taken into consideration, disregarding the border rows. A border area surrounded the experimental area completely to minimize environmental effects.

Statistical and GGE biplot analyses

Individual analysis of variance was performed for each environment to assess the homogeneity of residual variances, by the following model:

$Y_{ij} = \mu + G_i + B_j + \varepsilon_{ij}$, where Y_{ij} is the observed value of the i-th genotype in the j-th block; μ the overall mean; G_i the fixed effect of the i-th genotype; B_j the random effect of the j-th block; and ε_{ij} the error associated with the i-th genotype in the j-th block. Meeting the ANOVA assumptions (Pimentel 2002), combined analysis of variance was performed in a factorial arrangement, grouping the three study locations and the three years, i.e., creating nine study environments, to identify possible genotype x environment interactions. The following statistical model was used:

$Y_{ijk} = \mu + G_i + {}^{B}/_{A_{jk}} + A_j + GA_{ij} + \varepsilon_{ijk}$, where Y_{ijk} is the observed value relative to the i-th genotype in the j-th environment and the k-th block; μ the overall study mean; G_i the fixed effect of the i-th genotype; ${}^{B}/_{A_{jk}}$ the effect of the kth block within the jth environment; A_j the random effect of the j-th environment; GA_{ij} the fixed effect of the interaction of the i-th genotype with the j-th environment, and ε_{ijk} the error associated with the observation Y_{ijk}, $\varepsilon_{ijk} \sim NID\ (0, \sigma^2)$. After detecting significance of the G×E interaction by the F test, the interaction was partitioned into a simple and complex part, as proposed by Cruz and Castoldi (1991), by the following expression:

$\sqrt{(1-r)^3 Q_1 Q_2}$, where Q_1 and Q_2 are the mean squares of genotypes in pairs of environments; and r is the correlation between the genotype means across the nine environments. Thereafter, adaptability and stability of black bean genotypes was estimated by GGE Biplot multivariate analysis, according to the model:

$Y_{ij} = \mu + G_i + E_j + GE_{ij}$, where Y_{ij} is the mean yield of the i-th genotype in the j-th environment; μ the overall mean; G_i the effect of the i-th genotype; E_i the effect of the j-th environment; and GE_{ij} the effect of the interaction between the i-th genotype and in the j-th environment (Yan 2001). The GGE biplot model does not separate genotypic effects (G) from effects of the genotype-environment interaction (G × E), maintaining them together in two multiplicative terms, represented by the following equation:

$Y_{ij} = \mu + \beta_j = g_{i1}e_{j1} + g_{i2}e_{j2} + \varepsilon_{ij}$, where Y_{ij} is the expected performance of genotype i in environment j; μ is the overall mean of observations; β_j the main effect of environment j; g_{i1} and e_{j1} are the main scores of i-th genotype in the j-th environment, respectively; g_{i2} and e_{j2} are secondary scores of i-th genotype in the j-th environment, respectively; and ε_{ij} is the unexplained residue of both effects. Thus, the GGE biplot model was constructed by simple dispersion of g_{i1} and g_{i2} for genotypes, and e_{j1} and e_{j2} for environments, by singular value decomposition (SVD), by the equation:

$Y_{ij} = \mu - \beta_j = \lambda_1\xi_{i1}\ \eta_{j1} + \lambda_2\xi_{i2}\ \eta_{j2} + \varepsilon_{ij}$, where λ_1 and λ_2 are the highest eigenvalues of the first and second principal components PC1 and PC2, respectively; ξ_{i1} and ξ_{i2} the eigenvectors of the i-th genotype of PC1 and PC2, respectively; and η_{j1} and η_{j2} the eigenvectors of the j-th environment of PC1 and PC2, respectively (Yan 2001). For statistical data analysis, analysis of variance was initially carried out with software Genes (Cruz 2016). On the other hand, GGE Biplot analysis was performed using R software (R Core Team 2019), using the functions available in the Metan package (Olivoto and Lúcio 2020).

RESULTS AND DISCUSSION

The combined analyses of variance showed significant differences ($p \leq 0.01$) between the effects of genotypes, environments, and G×E interaction (Table 1), denoting differences in the grain yield response between genotypes. The differences between environments were sufficient to discriminate the genotypes and the different responses of

Table 1. Summary of the combined analysis of variance for grain yield of 11 black bean genotypes evaluated in nine different environments in the state of Rio de Janeiro, in 2013, 2014 and 2015

Source of variation	**df**	**MS** (kg ha^{-1})		
Blocks / Environments	18	201840.13		
Genotypes (G)	10	1274989.31**		
Environments (E)	8	5269589.04**		
G×E	80	138024.14**		
Residual	180	62336.74		
Mean		1762.21		
CV (%)	11.20			
MSR+/ MSR-	6.24			
Mean environments				
Araruama	2209.03(*E1*)	1565.27(*E4*)	1065.27(*E7*)	
Campos dos Goytacazes	1706.09(*E2*)	1635.97(*E5*)	1426.09(*E8*)	
Macaé	2075.76(*E3*)	1853.27(*E6*)	2323.15(*E9*)	
Mean genotypes	**Araruama**	**Campos dos Goytacazes**	**Macaé**	**Overall mean**
BRS Campeiro	1601	1739	2339	1893
BRS Esplendor	1592	1785	2004	1794
IPR Uirapurú	1418	1356	1741	1505
CNFP 15289	1608	1441	2462	1837
CNFP 15290	1849	1731	2414	1998
CNFP 15292	1548	1475	1874	1632
CNFP 15302	1545	1461	1783	1596
CNFP 15304	1579	1573	2223	1792
CNFP 15310	1790	1685	2182	1886
CNFP 15359	1490	1439	1623	1517
CNFP 15361	1724	1798	2277	1933

** Significant at $p \leq 0.01$ by the F test. MSR+/ MSR-: ratio between the largest and the smallest residual mean square.

genotypes in the different environments. The development of the genotypes was not similar in the environments due to the edaphoclimatic differences between the environments tested, due to the different conditions of altitude, location and climate.

The ratio between the highest and lowest residual mean square was 6.24, demonstrating that the residual variances were homogeneous and therefore suitable for the use of combined analysis of variance (Cruz and Regazzi 2003). Grain yield is a polygenic trait, i.e., governed by many genes and heavily influenced by environmental factors, which interfere with the experimental variation coefficient (Resende and Duarte 2007). However, the coefficient of variation (11.20) was low, which indicates good experimental precision.

The GGE Biplot multivariate analysis was used to represent the patterns related to interaction, adaptability, and stability, which was impossible by the standard analysis of variance. Initially, principal component (PC) analysis was carried out, where PC1 is correlated to the main genotype effect, while PC2 represents the fraction of grain yield associated with the G×E interaction. The highest eigenvalues of PC1 and PC2, together, accounted for 78.19% of the total variation in grain yield (Figure 2). Therefore, these results revealed that multivariate analysis of principal components explained a major proportion of the sum of squares of genotypes and G×E interaction, which proves the high efficiency of the methodology (Santos et al. 2017).

The GGE biplot analysis represented by "which-won-where" (Figure 2) shows which genotypes had a superior development in specific environments. According to this graph, the genotypes G1 (BRS Campeiro), G2 (BRS Esplendor), G4 (CNFP 15289), G5 (CNFP 15290), G7 (CNFP 15302), G10 (CNFP 15359) and G11 (CNFP 15361), assigned to the vertices of the polygon, were the most responsive to the respective environments near their vertices. However, they may perform better or worse in one or more environments (Yan and Tinker 2006), in other words, they are more suitable for specific recommendations. Genotypes G7 (CNFP 15302) and G10 (CNFP 15359) were not grouped in any of the tested environments. They are considered unfavorable for the environments in which they were tested, and will not be recommended (Karimizadeh et al. 2013). On the other hand, the other genotypes located within the polygon were less responsive to environmental stimuli and, therefore, more suitable when the objective is broad adaptation (Karimizadeh et al. 2013, Melo et al. 2020).

The analysis of the biplot "mean vs. stability" (Figure 3), explains that the greater the projection of a genotype in relation to the PC1 axis, the lower its stability, while on the contrary, the farther away the genotype is from the PC2 axis, the higher-yielding it tends to be (Melo et al. 2020). The arrow highlights a higher mean performance observed among the genotypes (Yan 2001).

Thus, G4 (CNFP 15289) was the most unstable of the evaluated genotypes. However, it had an advantageous performance compared to other genotypes grown in environment E9 (Macaé 2015). Genotypes G3 (IPR Uirapurú), G5 (CNFP 15290), G8 (CNFP 15304), and G10 (CNFP 15359) had a highly stable performance, although, the grain yield of the second was higher. In addition, the genotypes G1 (BRS Campeiro), G5 (CNFP 15290) and G11 (CNFP 15361) stood out with greater stability combined with higher yields. The yield of the lines G5 (CNFP 15290) and G11 (CNFP 15361) exceeded that of cvs. G1 (BRS Campeiro), G2 (BRS Esplendor), and G3 (IPR Uirapurú).

For Yan and Tinker (2006), high genotype stability is only significant when combined with a good mean performance. Thus, the genotypes G10 (CNFP 15359) and G3 (IPR Uirapurú), with high stability due to their low projections on the PC1 axis, are not desirable options for grain production in these study regions, since they were not high-yielding, in spite of stable. However, genotype G5 (CNFP 15290) had high stability as well as high yield performance, which indicates an excellent selection option, since it even exceeded the control cultivars G1 (BRS Campeiro), G2 (BRS Esplendor), and G3 (IPR Uirapurú) in both aspects.

The biplot graph "discrimination vs. representativeness" (Figure 4) shows the selection of environments of greater discrimination of genotypes and representativeness. This fact was confirmed by Santos et al. (2017), in their observation that an ideal environment should discriminate superior genotypes and be representative among the other tested environments. According to Yan and Holland (2010), the biplot shows the discriminatory power of a test environment based on the length of its vector. In addition, the higher the PC1value, the greater the ability to discriminate the

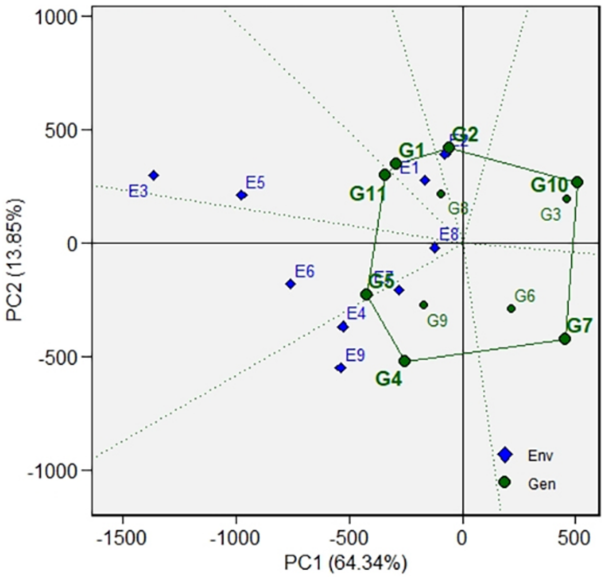

Figure 2. GGE biplot representing a "which-won-where" pattern of black bean genotypes and environments for grain yield (kg ha^{-1}). Environments: E1 – Araruama 2013; E2 – Campos 2013; E3 – Macaé 2013; E4 – Araruama 2014; E5 – Campos 2014; E6 – Macaé 2014; E7 – Araruama 2015; E8 – Campos 2015; E9 – Macaé 2015. Genotypes: G1 – BRS Campeiro; G2 – BRS Esplendor; G3 – IPR Uirapurú; G4 – CNFP 15289; G5 – CNFP 15290; G6 – CNFP 15292; G7 – CNFP 15302; G8 – CNFP 15304; G9 – CNFP 15310; G10 – CNFP 15359; G11 – CNFP 15361.

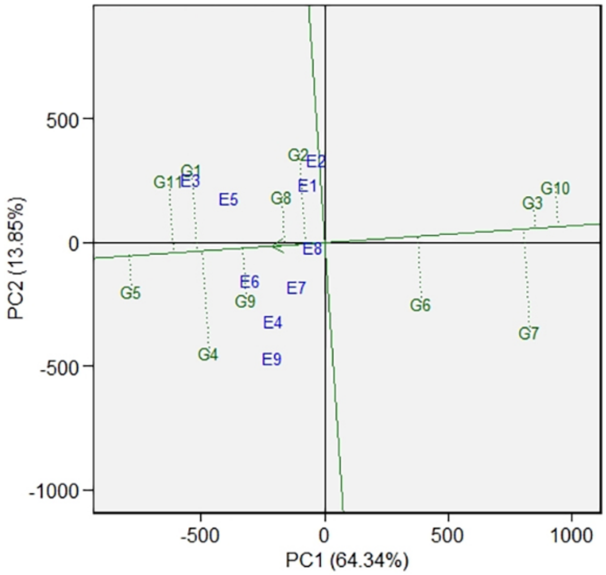

Figure 3. GGE biplot representing "mean vs. stability" of black bean genotypes and environments for grain yield (kg ha^{-1}). Environments: E1 – Araruama 2013; E2 – Campos 2013; E3 – Macaé 2013; E4 – Araruama 2014; E5 – Campos 2014; E6 – Macaé 2014; E7 – Araruama 2015; E8 – Campos 2015; E9 – Macaé 2015. Genotypes: G1 – BRS Campeiro; G2 – BRS Esplendor; G3 – IPR Uirapurú; G4 – CNFP 15289; G5 – CNFP 15290; G6 – CNFP 15292; G7 – CNFP 15302; G8 – CNFP 15304; G9 – CNFP 15310; G10 – CNFP 15359; G11 – CNFP 15361.

variable, while the greater the representativeness, the lower is PC2 (Yan and Kang 2003, Yan and Tinker 2006). In this way, based on the vector length, the longer vectors for the environments E3 (Macaé 2013), E5 (Campos dos Goytacazes 2014), and E9 (Macaé 2015) suggested a greater discriminatory power; E6 (Macaé 2014) and E4 (Araruama 2014) showed moderate discriminatory power; and E1 (Araruama 2013), E2 (Campos dos Goytacazes 2013), E7 (Araruama 2015) and E8 (Campos dos Goytacazes 2015) lower discriminatory power (Figure 4). This suggests that environments with short vectors are less discriminating, which means that all genotypes tend to carry similarly little or no information about the genotypic differences that can be revealed in a given environment and, therefore, should not be used as test environments (Melo et al. 2020).

The authors Yan and Tinker (2006) classified environments in three ways: the first classification as discriminative and representative (useful for the selection of adapted genotypes); the second classification as discriminative and unrepresentative (useful to rule out unstable genotypes); and third classification as non-discriminatory and non-representative (to be avoided as test environments). Regarding representativeness, the environments that form the smallest angles with the mean-environment axis (MEA), which corresponds to the line that crosses the mean environment, and the origin of the biplot, will be more representative. Thus, the results indicated that the environments E3 (Macaé 2013), E5 (Campos dos Goytacazes 2014), E6 (Macaé 2014), and E9 (Macaé 2015) were discriminative and representative. As all environments in Macaé (E3, E6 and E9) were discriminative, this site seems to be ideal for the selection of superior adapted genotypes. None of the environments was simultaneously non-discriminatory and non-representative, avoiding the discarding of environments based on this criterion.

An ideal genotype is one with a high mean performance for the studied trait combined with high stability in all tested environments (Yan and Tinker 2006, Melo et al. 2020). During the evaluation of different genotypes, it is used as a reference to identify an ideotype, i.e., one that is represented by a point located in the center of the concentric circles, considered the most desirable (Figure 5). Thus, genotype G5 (CNFP 15290) was closest to an ideotype, had a high stability of performance and yield, which indicates it as promising for grain production in the state of Rio de Janeiro.

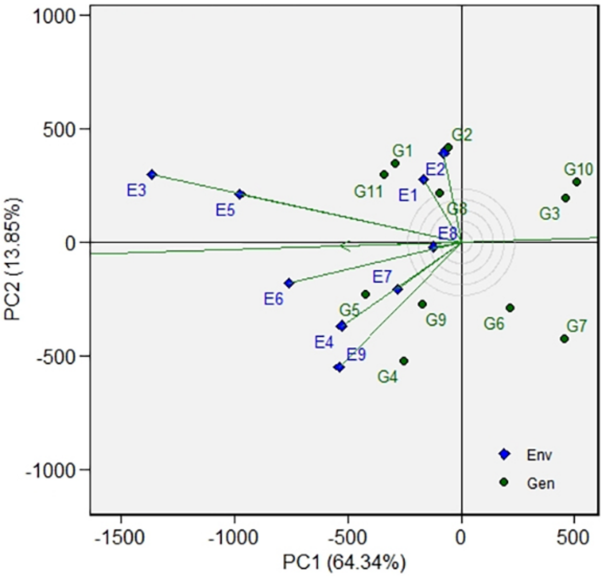

Figure 4. GGE biplot representing "discriminativeness vs. representativeness" of black bean genotypes and environments for grain yield (kg ha^{-1}). Environments: E1 – Araruama 2013; E2 – Campos 2013; E3 – Macaé 2013; E4 – Araruama 2014; E5 – Campos 2014; E6 – Macaé 2014; E7 – Araruama 2015; E8 – Campos 2015; E9 – Macaé 2015. Genotypes: G1 – BRS Campeiro; G2 – BRS Esplendor; G3 – IPR Uirapurú; G4 – CNFP 15289; G5 – CNFP 15290; G6 – CNFP 15292; G7 – CNFP 15302; G8 – CNFP 15304; G9 – CNFP 15310; G10 – CNFP 15359; G11 – CNFP 15361.

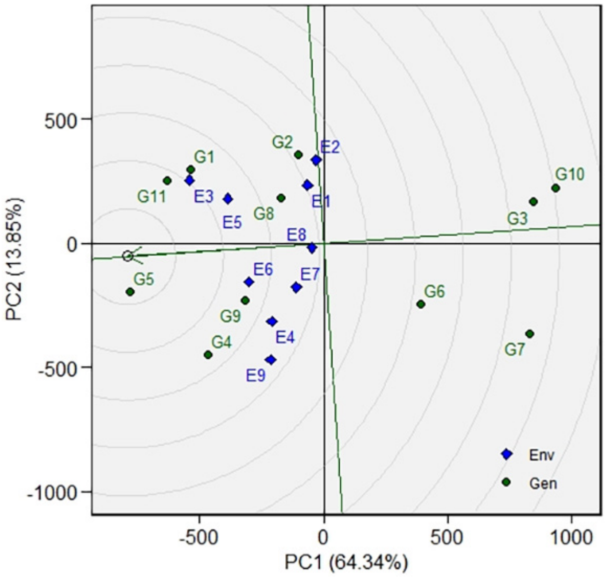

Figure 5. GGE biplot representing the ranking of black bean genotypes (ideal genotype) for grain yield (kg ha^{-1}). Environments: E1 – Araruama 2013; E2 – Campos 2013; E3 – Macaé 2013; E4 – Araruama 2014; E5 – Campos 2014; E6 – Macaé 2014; E7 – Araruama 2015; E8 – Campos 2015; E9 – Macaé 2015. Genotypes: G1 – BRS Campeiro; G2 – BRS Esplendor; G3 – IPR Uirapurú; G4 – CNFP 15289; G5 – CNFP 15290; G6 – CNFP 15292; G7 – CNFP 15302; G8 – CNFP 15304; G9 – CNFP 15310; G10 – CNFP 15359; G11 – CNFP 15361.

The genotypes G3 (IPR Uirapurú), G7 (CNFP 15302), and G10 (CNFP 15359), located in the last concentric circles, i.e., furthest from the ideotype, had the poorest performance. Therefore, the recommendation of the best genotypes must be based on high yield performance and stability.

Thus, when analyzing the GGE biplots, genotype G5 (CNFP 15290) was adaptable to local conditions and had stable yields, with higher means than the control cultivars G1 (BRS Campeiro), G2 (BRS Esplendor) and G3 (IPR Uirapurú).

CONCLUSIONS

Genotype CNFP 15290 was considered an ideotype in view of the superior performance in relation to the overall mean and high adaptability and stability, as well as indicated for future evaluations in common bean breeding programs. The district of Macaé discriminated the genotypes better and was more representative. Genotype CNFP 15290 can be recommended for grain production in the state of Rio de Janeiro due to its high performance stability, adaptability, and yield.

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