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GGE Biplot and REML/BLUP based-analysis of yield stability and adaptability for common beans in multi-environment trials

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ABSTRACT: Prior to releasing new varieties, one of the most common aims in breeding is to study genotype by environmental interactions. Using the analysis obtained from these initial processes, a multitude of varieties based on their relative performance through different environments is produced. Herein we assessed the link-up between GGE Biplot and REML/BLUP based-methods in a commercial panel of 32 bean genotypes, which included 17 carioca bean genotypes and 15 black bean genotypes. The assessment was conducted during 2009 in four different locations of Pernambuco State, Brazil. Regarding the locations, São João and Araripina showed to be highly representative and non-discriminatory, while Arcoverde was the most discriminatory and well-represented favoring the selection of widely adapted genotypes. The selection of genotypes was consistent by using both methods and the final conclusion shows outstanding performance. Considering a high yield stability and adaptability, the following genotypes showed outstanding performance: the black types included CNFP (11995, 11983, 11985 and 11991), and the carioca types are CNFC (11951 and 11954). Understanding genotype by environmental interactions enabled us to identify potential genotypes for releasing.

Key words: heritability; genotype by environment interaction; mixed models; *Phaseolus vulgaris* L.

Análise baseada em GGE Biplot e REML/BLUP da estabilidade de produção e adaptabilidade para feijoeiro comum em ensaios multi-ambientais

RESUMO: Antes do lançamento de novas cultivares, um dos objetivos mais comuns no melhoramento de plantas é estudar a interação dos genótipos com os ambientes. Utilizando a análise obtida desses processos iniciais, foi produzida uma multiplicidade de genótipos com base em seu desempenho relativo através de diferentes ambientes. Neste trabalho, avaliamos a ligação entre os métodos baseados em GGE Biplot e REML / BLUP em ensaios de competições com 32 genótipos de feijão, que incluiu 17 genótipos de feijão carioca e 15 genótipos de feijão preto. A avaliação foi realizada durante o ano de 2009 em quatro locais diferentes do estado de Pernambuco, Brasil. Quanto aos locais, São João e Araripina mostraram-se altamente representativos e não discriminatórios, enquanto Arcoverde foi o mais discriminatório e bem representado, favorecendo a seleção de genótipos amplamente adaptados. A seleção dos genótipos foi consistente utilizando ambos os métodos e a conclusão final mostra um excelente desempenho. Considerando uma alta adaptabilidade e estabilidade de produção, os seguintes genótipos apresentaram desempenho superiores: os tipos preto incluíram CNFP (11995, 11983, 11985 e 11991), e os tipos carioca são CNFC (11951 e 11954). A compreensão da interação genótipo por ambiente nos permitiu identificar possíveis cultivares para lançamento.

Palavras-chave: herdabilidade; interação genótipos x ambientes; modelos mistos; *Phaseolus vulgaris* L.

Introduction

The common bean is one of the most widespread crops around the world. Brazil is the largest bean consumer in the world and the third largest producer with the production of thirty-two hundred tons over three harvest seasons throughout the year (Conab, 2017). However, the Brazilian production of beans is not enough to meet the domestic market demand (Conab, 2017). Thus, bean-breeding programs assume the challenges and initiative in developing new cultivars for obtaining greater grain yield which may decrease importation of beans from abroad.

Since beans are a widely cultivated crop in different regions in Brazil, an analysis of adaptability and stability become necessary to make a safe recommendation of high yield genotypes. Among the many methods for explaining the genotype and environment interaction (GxE), the GGE Biplot and the REML/BLUP (Best Linear Unbiased Prediction) are highlighted by the practicality to interpret results and the accuracy in selecting genotypes (Santos et al., 2017).

The graphs in a GGE biplot analysis are built from the main components where only the environments are considered as being of fixed effect, so that the first and second components represent the yield proportion due to the genotype characteristics and due to the GxE interaction, respectively (Yan, 2001; Miranda et al., 2009; Yan & Holland, 2010). In this sense, this analysis provides a better understanding of GxE interaction, enabling an accurate prediction for the average performance of genotypes in different environments, as well as to identify which genotypes are more stable (Badu-Apraku et al., 2012; Santos et al., 2017).

On the other hand, REML/BLUP analysis incorporates the study of productivity, adaptability and genotypic stability simultaneously by using the method of harmonic mean of relative performance of genotypic values (MHPRVG), as proposed by Resende (2002). This methodology is based on the analysis of the genetic values by means of mixed models, considering the genotypic effects as random and providing stability and genotypic adaptability rankings; this method allows for analyzing unbalanced data and non-orthogonal designs with heterogeneity of variances (heteroscedasticity).

The GGE Biplot and REML/BLUP methods have been used separately to investigate the genotype-environment interaction for different crops, but there are no reports of their use for common beans. Thus, the objective of this work was to evaluate the performance and association between the GGE biplot and REML/BLUP methods to select different common bean genotypes which simultaneously combine high grain yield, adaptability and stability.

Material and Methods

The trials were conducted in 2009 at the experimental stations of The *Instituto Agronômico de Pernambuco* (*IPA*), in four municipalities: Araripina, Arcoverde, Caruaru and São João. Araripina presents predominantly soft-wavy topography,

altitude of 622m, an average temperature of 23.7 ºC, rainfall index of 645.2 mm (APAC, 2017), and yellow-red-dystrophic latosol soil (Embrapa, 2013); Arcoverde presents wavy topography, annual average temperature of 22.2 °C, rainfall index of 640.7 mm, eutrophic-regolithic neosol soil (Embrapa, 2013); Caruaru presents wavy topography, altitude of 554 m, annual average temperature of 21.7 °C, rainfall index of 707 mm (APAC, 2017) and neosol soil (Embrapa, 2013); São João presents wavy topography, altitude of 716 m, average annual temperature of 21.1 °C, rainfall index of 955.8 mm (APAC, 2017), and regosol soil.

Thirty-two (32) common bean genotypes were evaluated (Table 1) in the agricultural year of 2009, from which 17 were from the 'Carioca' group and 15 were from the 'Black' group. The experiment was arranged in a randomized block design with three replications, totaling 384 plots. Each experimental unit consisted of 4 lines of 4 m, spacing of 50 x 20 cm, totaling a population of 100,000 plants ha^{-1}. The data collection was performed in the two central rows, while the borderlines were neglected. Before implementing the experiments, the analyzed soil received a sowing fertilization (200 kg ha^{-1} of chemical fertilizer NPK 04-20-20, according to Cavalcanti, 2008). Soil preparation was carried out in a conventional way with plowing and light harrowing.

Table 1. Common bean genotypes, commercial type and their origins.

Order	Genotypes	Type	Origin
1	BRS 9435 Cometa	Carioca	Embrapa
2	BRS Estilo	Carioca	Embrapa
3	BRS Pérola	Carioca	Embrapa
4	CNFC 11944	Carioca	Embrapa
5	CNFC 11945	Carioca	Embrapa
6	CNFC 11946	Carioca	Embrapa
7	CNFC 11948	Carioca	Embrapa
8	CNFC 11951	Carioca	Embrapa
9	CNFC 11952	Carioca	Embrapa
10	CNFC 11953	Carioca	Embrapa
11	CNFC 11954	Carioca	Embrapa
12	CNFC 11956	Carioca	Embrapa
13	CNFC 11959	Carioca	Embrapa
14	CNFC 11962	Carioca	Embrapa
15	CNFC 11966	Carioca	Embrapa
16	CNFC 8017	Carioca	Embrapa
17	IPR Juriti	Carioca	IAPAR
18	BRS Campeiro	Preto	Embrapa
19	BRS Esplendor	Preto	Embrapa
20	BRS Supremo	Preto	Embrapa
21	CNFP 11973	Preto	Embrapa
22	CNFP 11976	Preto	Embrapa
23	CNFP 11978	Preto	Embrapa
24	CNFP 11979	Preto	Embrapa
25	CNFP 11983	Preto	Embrapa
26	CNFP 11984	Preto	Embrapa
27	CNFP 11985	Preto	Embrapa
28	CNFP 11991	Preto	Embrapa
29	CNFP 11994	Preto	Embrapa
30	CNFP 11995	Preto	Embrapa
31	IAC Diplomata	Preto	IAC
32	IPR Uirapuru	Preto	IAPAR

Grain yields were obtained in all the experiments during the harvest period carried out 90 days after planting. This data was used to estimate the genetic parameters to evaluate adaptability and stability using the GGE biplot and REML/BLUP procedure.

The GGE Biplot multivariate analysis was conducted using the ggplot2 software package (Wickham, 2016) considering the following model: $Y_{ij} - \mu - \beta_j = g1_ie1_j + gi2e2_j + \varepsilon_{ij}$, where Y_{ij} is the expected performance of genotype i in the environment j; μ is the general constant of the observations; β_j is the main effect of the environment j; $g1_i$ and $e1_j$ are the major scores for the ith genotype in the jth environment, respectively; $gi2$ and $e2_j$ are the secondary scores for the ith genotype in the jth environment, respectively; and ε_{ij} is the unexplained residue by both effects. The GGE Biplot plot was performed by simple dispersion of $g1_i$ and $gi2$ for genotypes and $e1_j$ and $e2_j$ for environments by means of the Decomposition in Singular Values (DSV) using the following equation: $Y_{ij} - \mu - \beta_j = \lambda_1\xi_{i1}\eta_{1j} + \lambda_2\xi_{i2}\eta_{2j} + \varepsilon_{ij}$, where λ_1 and λ_2 are the largest eigenvalues of the first and second major PCA1 and PCA2 components, respectively; ξ_{i1} and ξ_{i2} are the eigenvector of the ith genotype for PCA1 and PCA2, in that order; and η_{1j} and η_{2j} are the eigenvectors of the jth environment for PCA1 and PCA2, respectively.

The following statistical model was considered for evaluation via REML/BLUP: $y = Xr + Zg + Wi + e$, where: y refers to a data fixed effects-vector (block averages between locations); r refers to the vector of the effects of the local-repetition combinations added to the general average of fixed effects; g refers to genotypic effects of genotypes (random); i refers to effects of the genotype x environment interaction (random) and of errors (e) or wastes (random); and X, Z and W refer to the incidence matrices for r, g and i, respectively. The equations that make the mixed model equivalent to the prediction of r, g and i are:

$$\begin{bmatrix} X'X & X'Z & X'W \\ Z'X & Z'Z+\lambda_1 & Z'W \\ W'X & W'Z & W'W+\lambda_2 \end{bmatrix} \begin{bmatrix} \hat{r} \\ \hat{g} \\ \hat{i} \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \\ W'y \end{bmatrix}$$

where:

$$\lambda_1 = \frac{1 - h_g^2 - h_i^2}{h_g^2}$$

and

$$\lambda_2 = \frac{1 - h_g^2 - h_i^2}{h_i^2}$$

where:

h_i^2 - coefficients of determination for the effects of the genotype x environment interaction; and

h_g^2 - individual broad sense heritability at block level.

The Univariate Mixed Model was used in the study on the interaction between genotypes (G) and environments (E) (Resende, 2002). This model is composed of the main effects (G) and the (G x E) interaction by means of G + GE, so as to obtain the multivariate BLUP. The BLUP of the G x E effects was used to eliminate the noise from the genotype x environment interaction.

The MHPRVG method was used for genetic evaluation by the highest values of the harmonic mean of the genotypic values (Resende, 2002).

$$MHPRVG = \frac{n}{\sum_{j=1}^{n} \frac{1}{Vg_{ij}}}$$

where:

n - number of locations where the genotype i was evaluated; and,

Vg_{ij} - genotypic value of the genotype i in the location j, expressed as the ratio of the mean of this location.

The genotypes with the best performance were assessed in three different ways for the MHPRVG method: selection based on the predicted genetic value by the mean behavior in all locations, in the situation, without interaction; selection based on the predicted genetic value considering the behavior of the genotypes in each location in the situation with the effect of the mean interaction; and the simultaneous selection for yield, stability (MHVG) and adaptability (PRVG). Model 54 of the Selegen computer system (Resende, 2016) was used to evaluate lineages and cultivars in complete block designs in several locations and one observation per plot. A joint analysis was conducted for each common bean group in the agricultural year of 2009 by the MHPRVG method.

Results and Discussion

The joint deviance analysis for common bean trials was conducted by taking the effects of genotypes and environments when they were significant ($p \leq 0.01$) by the Chi-square test, indicating that the genotypes differed genetically for grain yield (Table 2) and that the environments

Table 2. Analysis of deviance for grain yield in common bean genotypes of the Carioca (17) and Black (15) beans assessed 90 days after emergence in the municipalities of Araripina, Arcoverde, Caruaru and São João, Pernambuco state, in the agricultural year of 2009.

Effect	Deviation[1]	LRT Chi-Square (χ^2)
Genotypes	5588.02 +	7.9 **
Genotypes x environments interaction	5682.45	102.35 **
Environments	5644.18	64.08 **
Residual	-	-
Complete Model	5580.12	-

[1]Deviance of adjusted model without the cited effects; distribution for 1 degree of freedom. LRT, likelihood; **significant by the chi-square test at 1% (6.63) probability.

were contrasting, respectively. However, the significance of the genotype x environment interaction indicates that there was divergent behavior of the genotypes in the different environments in which they were assessed. Due to inconstancy in the classification of genotypes, it was necessary to split the genotype x environment interaction using the adaptability and stability analyzes (Farias Neto et al., 2013).

The GGE biplot analysis allowed us to identify mega-environments and to select the best genotypes for each group

formed, taking into account that the genotypes are far from the origin and those which belong to the vertices of the mega-environments showed better performance. Thus, the GGE biplot grouped the environments in four mega-environments presenting six genotypes of the Carioca group, including: CNFC (11946, 11966, 11945, 11962 and 8017) and IPR Juriti; in addition to four black genotypes, which were: CNFC (11984 and 11995), IAC Diplomata and BRS Supremo located in the vertices of the mega-environments (Figure 1A and 1B).
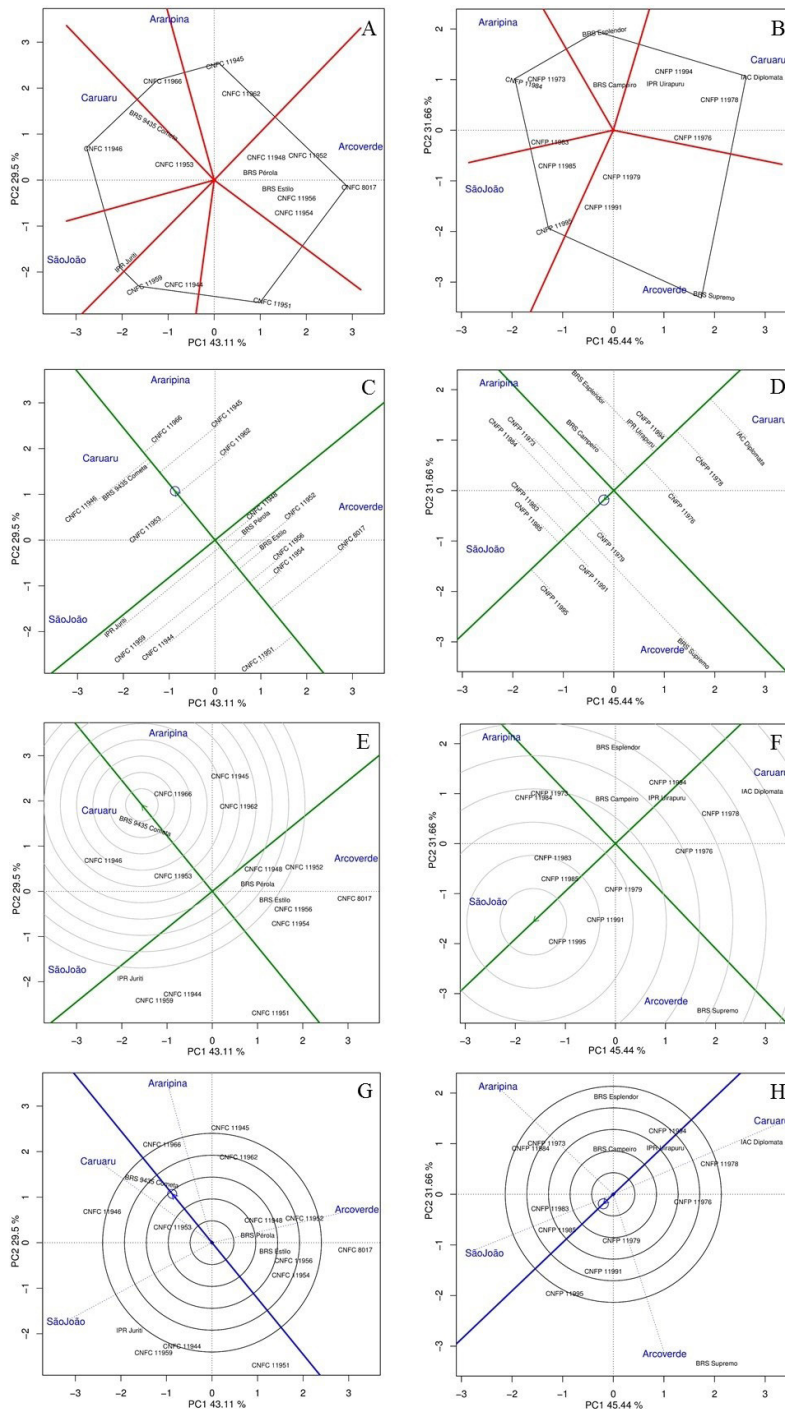

Figura 1. GGE biplot representing the "which-won-where" for Carioca bean genotypes (A), black bean genotypes (B), means x stabilities for Carioca bean genotype (C) and means x stabilities for black bean genotypes (D), estimate of an ideal Carioca bean genotype (E), estimate of an ideal black bean genotype (F), discrimination and representativeness of Carioca bean genotype (F) and discrimination and representativeness of Carioca bean genotype (G) of the environments for grain yield (kg ha⁻¹).

The CNFC (11952, 11948, 11956, 11954, 11953 and 11962), BRS Estilo, BRS 9435 Cometa and BRS Pérola Carioca cultivars are within the formed mega- environments, however they presented smaller vectors and exhibit greater interaction with the environments in which they are located (Figure 1A). The same is shown for the CNFP (11973, 11976, 11978, 11979, 11983, 11985, 11991 and 11994) and IPR Uirapuru (Figure 1B) black bean genotypes. It is also worth noting that the genotypes located in the groups that do not contain environments are considered unfavorable for the environments in which they were tested and we do not recommend them (Karimizadeh et al., 2013).

We also assessed the productivity and stability of the genotypes (Figures 1C and 1D) based on the Average Environment Coordination (AEC), represented by the circle formed in the "*means x stabilities*" biplot. It is possible to identify the genotypes therein which are above or below the average and which have less influence of the environment. This was followed by only six Carioca genotypes, as follows: CNFC (11945, 11946, 11953, 11962 and 11966) and BRS 9435 Cometa; as well as eight black bean genotypes: CNFP (11973, 11979, 11983, 11984, 11985, 11991, 11995) and BRS Supremo, where these showed yields above the general average.

Regarding stability, the interaction of the genotype with the environment is stronger as the greater the projection of the genotype is to the axis and the more unstable the genotype is. Thus, in addition to presenting above-average productivity, the genotypes CNFC 11966 and BRS 9435 Cometa of the Carioca group were classified as more stable for the tested environments. Likewise, the CNFC 11959, BRS Estilo and IPR Juriti carioca bean genotypes showed to have high productivity and stability. It can be noticed that environments previously considered unfavorable for the groups of tested environments generally showed below-average productivity, in addition to being classified as unstable.

In order to consider a genotype to be ideal, it must show a relatively higher productivity yield in all environments. In the GGE biplot, this genotype was defined by the largest length of the vector, represented by an arrow in the center of the concentric circle (Figure 1E and1F). although only representative, this genotype served as a reference for the evaluation of the others. According to the productivity ranking, the BRS 9435 Cometa and CNFC 11966 cultivars of Carioca beans, and CNFP 11995 of the black group were considered to be the closest to "ideal", presenting high averages of yields and good stability.

Discrimination and representativeness for tested environments are important measures in providing reliable information. The discrimination and representativeness of the environments is observed by the graphs denoted by "Discriminant vs. Representative" (Figure 1G and 1H). The capacity to discriminate is visualized by the length of the vector connected to the environment, which is proportional to the standard deviation within the respective environment. Thus, the smaller the vector, the lower the relationship between yield and stability (Yan et al., 2007). However, the ability of being

representative is dependent on the angle formed with AEA, so those environments with smaller angles are considered the most representative (Yan & Tinker, 2006). In this sense, taking into account the environments for bean culture, Carioca and São João were highly representative and non-discriminatory environments. Arcoverde was considered the most discriminating environment with good representativeness, with characteristics favoring the selection of widely adapted genotypes. Araripina was classified as non-representative and the least discriminant, and can be discarded for not providing safe information (Yan & Tinker, 2006; Yan et al., 2007).

The correlation coefficient between the studied environments indicates positive correlation, negative or lack of correlation if the angles formed are acute, obtuse or straight, respectively. It is noted that Araripina had a positive correlation with Caruaru, indicating that the variability among the genotypes is the only one responsible for the observed productivity difference. São João presented negative correlation with Arcoverde, proving that the interaction between genotypes and environments interferes in the classification of genotypes in different environments. The same correlation was obtained between the municipalities of São João and Araripina, which presented the highest angles. Araripina and Arcoverde presented as uncorrelated.

Regarding the results obtained with the black beans, São João was considered the most discriminating and representative environment, and Caruaru was highly representative and non-discriminatory. Araripina and Arcoverde were classified as the least representative and discriminating. Regarding the correlations, Araripina presented negative correlation with Arcoverde and Caruaru. Also, São João presented high correlation with Araripina, lack of correlation with Arcoverde and negative correlation with Caruaru. Altogether, these results show that Pernambuco state presents edaphoclimatic differences which influence the yield and selection of the genotypes in each environment. Therefore, genotype information obtained for one of these environments cannot be taken into account for others.

It is necessary to consider that the GGE Biplot method only captures a small percentage of the total variability which can compromise the analysis, since the patterns are obtained with less precision and with the use of mixed models being necessary. The REML/BLUP method was used for better analysis of the results. This methodology allowed us to interpret genotypic values by estimates of adaptability and stability (Silva et al., 2011). The selection of the best genotypes was performed by three different strategies. In the first one, the five best genotypes were selected based on the average performance in all environments and with the free genotypic values of the interaction, where it was possible to perceive that the Carioca bean genotypes with the highest genetic gains were CNFC 11946 (137.47%), CNFC 11948 (132.81%), CNFC 11954 (125.25%) and CNFC 11962 (122.19%) (Table 3). Of these, only CNFC 11946 did not agree with the biplot GGE analysis. For black beans, the highest genetic gains were from CNFC (11983, 11991, 11995) genotypes and the

Table 3. Estimates of genetic gain predicted for grain yield of 32 common bean genotypes considering the average performance of the environments in the State of Pernambuco.

Order	Carioca genotypes	$g^{(1)}$	$u + g$	Gain	New mean	$u+g+gem$
1	CNFC 11951	121.52	2011.84	143.35	2033.68	2080.27
2	CNFC 11946	96.34	1986.67	137.47	2027.80	2040.92
3	CNFC 11948	95.55	1985.88	132.82	2023.14	2039.68
4	CNFC 11954	89.57	1979.89	125.25	2015.58	2030.33
5	CNFC 11962	88.55	1978.88	122.19	2012.52	2028.74
6	CNFC 11966	81.89	1972.22	119.09	2009.42	2018.33
7	CNFC 11952	25.00	1915.32	96.92	1987.24	1929.40
8	BRS Pérola	14.39	1904.71	92.79	1983.12	1912.81
9	CNFC 11956	9.98	1900.31	88.85	1979.17	1905.93
10	CNFC 8017	-4.35	1885.97	81.29	1971.62	1883.52
11	BRS Estilo	-12.14	1878.18	77.40	1967.73	1871.35
12	CNFC 11953	-43.53	1846.80	68.89	1959.21	1822.29
13	BRS 9435 Cometa	-55.94	1834.38	64.26	1954.59	1802.88
14	IPR Juriti	-63.28	1827.05	59.71	1950.04	1791.41
15	CNFC 11945	-81.23	1809.10	54.85	1945.18	1763.36
16	CNFC 11959	-114.98	1775.34	49.19	1939.52	1710.60
17	CNFC 11944	-119.05	1771.28	43.76	1934.09	1704.24

Order	Black genotypes	$g^{(1)}$	$u + g$	Gain	New mean	$u+g+gem$
1	CNFP 11995	171.75	2062.08	171.75	2062.08	2158.79
2	CNFP 11983	157.64	2047.97	164.69	2055.02	2136.73
3	CNFP 11991	151.88	2042.21	160.42	2050.75	2127.73
4	BRS Esplendor	134.95	2025.28	154.05	2044.38	2101.27
5	BRS Campeiro	134.38	2024.71	150.12	2040.45	2100.38
6	CNFP 11985	131.34	2021.66	146.99	2037.32	2095.62
7	CNFP 11984	92.84	1983.17	128.82	2019.15	2035.45
8	CNFP 11979	75.68	1966.01	115.99	2006.32	2008.63
9	BRS Supremo	62.14	1952.46	112.40	2002.73	1987.45
10	CNFP 11994	51.75	1942.08	108.61	1998.94	1971.22
11	CNFP 11973	40.01	1930.34	104.58	1994.90	1952.87
12	CNFP 11976	38.66	1928.98	100.91	1991.24	1950.75
13	CNFP 11978	8.29	1898.62	85.19	1975.51	1903.28
14	IPR Uirapuru	-22.98	1867.35	73.38	1963.71	1854.41
15	IAC Diplomata	-234.87	1655.46	22.33	1912.66	1523.20

$g^{(1)}$: genotypic effect; $u + g$: predicted genotypic value; $u+g+gem$: mean genotypic value in the environments.

controls, which did not stand out in the GGE bilot, which were: BRS Esplendor and BRS Campeiro.

The second selection strategy was to consider the best genotypes screened for the four specific environments (Table 4). With this strategy, the IPR Juriti (São João), CNFC 11954, CNFC 8017 (Arcoverde), CNFC 11966 and CNFC 11962 (Araripina) Carioca genotypes and the CNFP 11995 (São João), CNFP 11991 (Arcoverde) and CNFP 11983 (Araripina) Black genotypes are among the best, according to the GGE biplot method. For Caruaru, none of the six best genotypes selected from Carioca and black beans were common among the methodologies.

The third method considered herein was MHPRVG, where the CNFC (11946, 11948, 11951, 11952, 11954, CNFC 11962, 11966) and CNFP (11983, 11985, 11995) cultivars for the Carioca group were the most suitable and stable genotypes. For the black beans, CNFP (11979, 11984, 11991), BRS Campeiro and BRS Esplendor (Table 5) genotypes were the most suitable and stable. Only one Carioca (CNFC 11966) and five of the black group CNFP (11979, 11983, 11985, 11991, CNFP 11995) were also selected by GGE biplot analysis as having high productivity and good stability, while the controls were superior.

The Carioca bean lines CNFC 11946 and CNFC 11966 obtained the best genotypic values throughout the environments and for the average environment, according to the REML/BLUP and GGE biplot analysis (Table 3). These lines are also the best according to the harmonic mean relative genetic value performance (MHPRVG), which simultaneously considers the attributes productivity, adaptability and stability. The black genotypes which stood out in all the methods used were: CNFP 11983, CNFP 11991, and CNFP 11995.

It is noteworthy that there is agreement between the GGE Biplot and REML/BLUP methods in discriminating the best cultivars, a fact also observed by Silva et al. (2011) and Santos et al. (2017). The use of the mixed model procedure unifies the selection of the best genotypes by the attributes: productivity, adaptability and stability. The GGE biplot provides a description of the discriminative power of the environments for the specific genotypes and informs the similar environments. Thus, the combination of the REML/BLUP and GGE Biplot methods enabled selecting more productive, stable and responsive genotypes for common beans in Brazil for both broad and specific adaptation, and this will allow breeders to make a reliable selection of the best genotypes.

Table 4. Estimates of genetic gain predicted for grain yield of common bean cultivars in four environments in Pernambuco state.

Order	Carioca genotypes	$g+ge$	$u+g+ge$	Gain	New mean	Black genotypes	$g+ge$	$u+g+ge$	Gain	New mean
					Caruaru					
1	CNFC 11954	374.18	1573.06	374.19	1573.06	CNFP 11983	141.65	1340.52	275.51	1474.39
2	CNFC 11951	352.67	1551.55	363.43	1562.30	CNFP 11985	136.19	1335.06	260.03	1458.91
3	CNFC 11952	313.77	1512.64	346.88	1545.75	CNFP 11995	54.24	1253.11	218.51	1417.39
4	CNFC 8017	300.08	1498.96	335.18	1534.05	CNFP 11984	-35.94	1162.93	119.98	1318.85
5	BRS Pérola	291.91	1490.79	326.53	1525.40	BRS Supremo	-54.52	1144.35	112.04	1310.92
6	CNFC 11962	236.22	1435.09	311.47	1510.35	CNFP 1199	-57.28	1141.59	104.68	1303.56
					São João					
1	CNFC 11946	181.53	2142.27	251.49	2212.23	CNFP 11995	339.91	2300.65	339.91	2300.65
2	CNFC 11951	160.52	2121.27	234.34	2195.09	CNFP 11984	311.33	2272.07	325.62	2286.36
3	IPR Juriti	132.09	2092.83	225.05	2185.79	CNFP 11991	307.19	2267.93	319.47	2280.22
4	CNFC 11959	115.37	2076.12	215.91	2176.65	CNFP 11973	239.85	2200.59	299.57	2260.31
5	CNFC 11966	90.68	2051.42	198.24	2158.98	CNFP 11979	236.23	2196.97	286.90	2247.64
6	BRS 9435 Cometa	75.16	2035.90	190.03	2150.78	BRS Esplendor	202.75	2163.49	272.87	2233.62

Continued from Table 4

Order	Carioca genotypes	g+ge	u+g+ge	Gain	New mean	Black genotypes	g+ge	u+g+ge	Gain	New mean
					Arcoverde					
1	CNFC 11962	227.79	2425.99	343.95	2542.15	CNFP 11995	491.44	2689.64	491.44	2689.64
2	CNFC 11951	197.18	2395.38	314.97	2513.17	BRS Campeiro	434.56	2632.76	463.00	2661.20
3	CNFC 11966	189.49	2387.69	303.56	2501.76	CNFP 11978	359.14	2557.34	428.38	2626.58
4	CNFC 11954	81.07	2279.26	250.61	2448.81	BRS Esplendor	357.06	2555.25	410.55	2608.75
5	CNFC 11946	61.13	2259.33	238.77	2436.97	CNFP 11991	351.61	2549.81	398.76	2596.96
6	CNFC 8017	44.14	2242.34	218.01	2416.21	CNFP 11976	274.94	2473.14	378.12	2576.32
					Araripina					
1	CNFC 11948	406.96	2610.46	421.20	2624.69	CNFP 11983	449.90	2653.39	449.90	2653.39
2	CNFC 11946	373.93	2577.42	405.71	2609.20	CNFP 11985	418.92	2622.41	434.41	2637.90
3	CNFC 11966	324.71	2528.20	385.12	2588.61	BRS Esplendor	409.03	2612.52	425.95	2629.44
4	CNFC 11956	222.99	2426.48	345.73	2549.22	BRS Campeiro	375.54	2579.03	412.07	2615.56
5	CNFC 11954	116.39	2319.88	306.91	2510.40	CNFP 11994	359.04	2562.53	399.05	2602.54
6	CNFC 11962	93.85	2297.34	295.70	2499.19	CNFP 11991	348.09	2551.58	392.68	2596.17

g+ge: genotypic effect per environment; u+g+ge: genotypic value predicted with capitalization of the interaction with the environments.

Table 5. Stability and adaptability (MHPRVG and MHPRVG * MG) of genotypic values for grain yield of 32 common bean genotypes evaluated at 90 days after emergence in the 2009 agricultural year.

Order	Carioca genotypes	MHPRVG	MHPRVG*MG
1	BRS Estilo	0.9970	1884.6311
2	CNFC 11953	0.9632	1820.6874
3	CNFC 11944	0.9064	1713.4214
4	CNFC 11959	0.9011	1703.3472
5	IPR Juriti	0.9518	1799.1589
6	BRS 9435 Cometa	0.9517	1798.9900
7	CNFC 11946	1.0652	2013.5846
8	CNFC 11966	1.0438	1973.2153
9	CNFC 11956	1.0008	1891.7936
10	CNFC 11945	0.9332	1763.9914
11	CNFC 11948	1.0794	2040.4834
12	CNFC 11952	1.0325	1951.7058
13	CNFC 11954	1.0863	2053.3842
14	CNFC 11951	1.1133	2104.5760
15	CNFC 8017	1.0065	1902.5369
16	BRS Pérola	1.0254	1938.3077
17	CNFC 11962	1.0803	2042.0497

Order	Black genotypes	MHPRVG	MHPRVG*MG
1	CNFP 11985	1.1060	2090.7310
2	CNFP 11984	1.0609	2005.5412
3	BRS Campeiro	1.0811	2043.7179
4	CNFP 11995	1.1275	2131.4141
5	CNFP 11979	1.0361	1958.5822
6	BRS Esplendor	1.0734	2029.0690
7	CNFP 11991	1.0988	2077.0456
8	CNFP 11978	0.9548	1804.9065
9	CNFP 11976	0.9673	1828.5792
10	IPR Uirapuru	0.9214	1741.6665
11	CNFP 11994	0.9978	1886.1108
12	CNFP 11973	1.0190	1926.1624
13	CNFP 11983	1.1263	2129.1272
14	BRS Supremo	1.0344	1955.4153
15	IAC Diplomata	0.7972	1506.8770

MHPRVG: harmonic mean relative performance of genotypic values; MHPRVG * MG: refers to MHPRVG multiplied by the overall average in all environments.

Conclusion

There was concordance between the GGE Biplot and REML/BLUP methods in identifying the best common bean genotypes.

CNFC 11946 and CNFC 11966 Carioca bean cultivars presented high productivity, good adaptability and stability.

CNFP 11983, CNFP 11991, and CNFP 11995 black bean genotypes were selected based on GGE biplot and REML/BLUP analyzes.

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