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 incluíu 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 Arcoveiro 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 estabilidade e adaptabilidade 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). Entendendo a 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 ºC, 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 ºC, 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 ºC, 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.

| Order | Genotypes     | Type   | Origin       |
|-------|---------------|--------|--------------|
| 1     | BRS 9435 Cometa | Carioca | Embrapa      |
| 2     | BRS Estilo    | Carioca | Embrapa      |
| 3     | BRS Pêrola   | 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 Juri    | 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: \( Y_{ij} - \mu - \beta_j = g_{1i}e_{1j} + g_{2i}e_{2j} + \varepsilon_{ij} \), where \( Y_{ij} \) is the expected performance of genotype \( i \) in the environment \( j \); \( \mu \) is the general constant of the observations; \( \beta_j \) is the main effect of the environment \( j \); \( g_{1i} \) and \( e_{1j} \) are the major scores for the \( i \)th genotype in the \( j \)th environment, respectively; \( g_{2i} \) and \( e_{2j} \) are the secondary scores for the \( i \)th genotype in the \( j \)th environment, respectively; and \( \varepsilon_{ij} \) is the unexplained residue by both effects. The GGE Biplot plot was performed by simple dispersion of \( g_{1i} \) and \( g_{2i} \) for genotypes and \( e_{1j} \) and \( e_{2j} \) for environments by means of the Decomposition in Singular Values (DSV) using the following equation: \( Y_{ij} - \mu - \beta_j = \lambda_1 \xi_{1i} \eta_{1j} + \lambda_2 \xi_{2i} \eta_{2j} + \varepsilon_{ij} \), where \( \lambda_1 \) and \( \lambda_2 \) are the largest eigenvalues of the first and second major PCA1 and PCA2 components, respectively; \( \xi_{1i} \) and \( \xi_{2i} \) are the eigenvector of the \( i \)th genotype for PCA1 and PCA2, in that order; and \( \eta_{1j} \) and \( \eta_{2j} \) are the eigenvectors of the \( j \)th 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:

\[
\begin{align*}
X'X & \quad X'Z & \quad X'W \\
Z'X & \quad Z'Z + \lambda_1 & \quad Z'W \\
W'X & \quad W'Z & \quad W'W + \lambda_2 \\
\end{align*}
\]

where:

\[
\lambda_1 = \frac{1 - h_{1g}^2 - h_{1i}^2}{h_{1i}^2}
\]

and

\[
\lambda_2 = \frac{1 - h_{2g}^2 - h_{2i}^2}{h_{2i}^2}
\]

where:

- \( h_{1g} \) - coefficients of determination for the effects of the genotype x environment interaction; and
- \( h_{1i} \) - 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).

\[
\text{MHPRVG} = \frac{n}{\sum_{i=1}^{n} V_{gij}}
\]

where:

- \( n \) - number of locations where the genotype \( i \) was evaluated; and,
- \( V_{gij} \) - 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
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 Pêrola 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
controls, which did not stand out in the GGE biplot, 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, 11991, 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 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\(_+g\) | \(u+g\) | Gain | New mean | \(u+g+g+gem\) |
|-------|-------------------|--------|--------|------|----------|-------------|
| 1     | CNFC 11951        | 121.52 | 201.84 | 143.35 | 2033.68 | 2080.27     |
| 2     | CNFC 11946        | 94.34  | 198.67 | 137.47 | 2027.80 | 2040.92     |
| 3     | CNFC 11948        | 95.55  | 195.83 | 132.62 | 2023.14 | 2039.58     |
| 4     | CNFC 11954        | 89.57  | 197.88 | 125.25 | 2015.58 | 2030.33     |
| 5     | CNFC 11962        | 88.55  | 197.88 | 122.19 | 2012.52 | 2028.74     |
| 6     | CNFC 11966        | 81.89  | 197.22 | 119.09 | 2009.42 | 2018.33     |
| 7     | CNFC 11952        | 25.00  | 191.32 | 96.92  | 1987.24 | 1929.40     |
| 8     | BRS Pêrola        | 14.39  | 190.71 | 92.79  | 1983.12 | 1912.81     |
| 9     | 11956             | 9.98   | 190.31 | 88.85  | 1979.17 | 1905.93     |
| 10    | CNFC 8017         | -4.35  | 188.97 | 81.29  | 1971.62 | 1833.52     |
| 11    | BRS Estilo        | -12.14 | 187.18 | 77.40  | 1967.73 | 1871.35     |

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

| Order | Carioca genotypes | g\(_+g\) | \(u+g\)+| Gain | New mean | \(u+g+g+gem\) |
|-------|-------------------|--------|--------|------|----------|-------------|
| 1     | CNFP 11995        | 171.75 | 2062.08| 171.75| 2062.08  | 2178.99     |
| 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| 2019.21  | 1836.33     |
| 6     | CNFP 11985        | 131.34 | 2016.66| 146.59| 2037.32  | 2095.62     |
| 7     | CNFP 11984        | 92.84  | 1893.17| 128.82| 2019.15  | 2035.45     |
| 8     | CNFP 11979        | 75.68  | 1866.01| 115.59| 2006.32  | 2088.63     |
| 9     | BRS Superior      | 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  | 1828.98| 100.91| 1991.24  | 1950.75     |
| 13    | CNFP 11978        | 8.29   | 1898.62| 85.19 | 1755.51  | 1903.28     |
| 14    | IPR Uirapuru      | -22.98 | 1867.35| 73.38 | 1863.71  | 1854.41     |
| 15    | IAC Diplomata     | -234.87| 1655.46| 22.33 | 1912.66  | 1523.20     |

\(g\(_+g\)\): genotypic effect; \(u+g\): predicted genotypic value; \(u+g+g+gem\): mean genotypic value in the environments.

\(g\(_+g\)\): genotypic effect; \(u+g\): predicted genotypic value; \(u+g+g+gem\): mean genotypic value in the environments.

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Continued from Table 4

| Order | Carica genotypes | g+ge | u+g+ge | Gain | New mean | Black genotypes | g+ge | u+g+ge | Gain | New mean |
|-------|------------------|------|--------|------|----------|----------------|------|--------|------|----------|
|       |                  |      |        |      |          |                |      |        |      |          |
| 1     | CNFC 11962       | 227.79 | 2425.59 | 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 Espeldor | 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 |

Arcoverde

| Order | Carica genotypes | MHPRVG | MHPRVG * MG |
|-------|------------------|--------|-------------|
| 1     | CNFC 11962       | 0.8444 | 1884.6311  |
| 2     | CNFC 11951       | 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 8435 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 Pêrola       | 1.0254 | 1938.3077  |
| 17    | CNFC 11962       | 1.0803 | 2042.0497  |

Araripina

| 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 Espeldor    | 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 Ufrapu      | 0.9214 | 1741.6665  |
| 11    | CNFP 11994      | 0.9978 | 1866.1108  |
| 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.

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.

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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