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# Analysis of statistical methods to estimate genotype-by-environment interaction for yield-based selection of new bean cultivars and lines

# Análise de métodos estatísticos para estimativas da interação genótipos por ambientes no rendimento de grãos em cultivares e linhagens de feijão

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## Highlights

Analysis of genotype-by-environment (GxE) interaction using different methodologies.
Seven statistical methods were used to estimate GxE interaction.
Fourteen genotypes were tested in 23 environments in Paraná state, Brazil.

## Abstract

This study aimed to assess the statistical methods available to estimate genotype-by-environment (GxE) for yield-based selection of new bean cultivars and lines, and identify a testing strategy capable of reducing the number of test years and producing reliable results. Fourteen genotypes were tested in 23 environments in Paraná state, Brazil, over three consecutive years. The yield data obtained in each environment were submitted to homogeneity of variance analysis, normality testing, individual and pooled analysis of variance (ANOVA) of all the environments. GxE interaction was studied using linear, multivariate, and mixed model regression. Analyses were performed using data from two and three years of assessment. For linear and mixed model regression, the number of years analyzed did not affect result interpretation. However, in multivariate analysis, genotype behavior varied in the environments studied according to the number of years analyzed. The results obtained indicate that two years of assessment were sufficient to indicate new cultivars adapted to different environments.

**Key words:** Linear regression. Mixed models. Multivariate analysis. *Phaseolus vulgaris* L.

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## Resumo

Esse estudo teve por objetivo avaliar os métodos estatísticos disponíveis para as estimativas da interação genótipo por ambientes no rendimento de grãos em cultivares e linhagens de feijão, bem como estabelecer uma estratégia para a condução dos ensaios que visam avaliar a interação genótipos por ambientes, possibilitando a redução do número de anos de testes, com resultados confiáveis para embasar a indicação de novas cultivares. Um ensaio composto por 14 genótipos foi conduzido em 23 ambientes do estado do Paraná, Brasil, durante três anos consecutivos. Os dados de rendimento obtidos em cada ambiente foram submetidos a análise de homogeneidade de variâncias, teste de normalidade dos resíduos, análise de variância individual, e posteriormente foi efetuada a análise de variância conjunta dos ambientes. A interação genótipos por ambientes foi estudada utilizando diferentes métodos estatísticos: regressão linear, análise multivariada e modelos mistos. As análises foram efetuadas utilizando-se dados de dois e de três anos de avaliação. Para os métodos estatísticos que empregam a regressão linear e modelos mistos, o número de anos analisados não interferiu na interpretação dos resultados. Entretanto, na análise multivariada, o comportamento dos genótipos frente aos ambientes estudados variou de acordo com o número de anos analisados. Os resultados do estudo apontam que dois anos de avaliação foram suficientes para a indicação de novas cultivares adaptadas a diferentes ambientes.

**Palavras-chave:** Regressão linear. Modelos mistos. Análise multivariada. Phaseolus vulgaris L.

## Introduction

Common bean (*Phaseolus vulgaris* L.) is one of the most important legume crops worldwide, with its high protein and iron contents making it a vital dietary component for populations in Latin American, Asian and African countries. Global production in 2020 was 27.5 million metric tons, with India, Myanmar, Brazil, the United States and China as the leading producers (Food and Agriculture Organization [FAO], 2022).

Annual production in Brazil is 2,989.9 million metric tons across 2,859.3 million hectares, with Paraná state as the main domestic producer, followed by Minas Gerais, Goiás and Mato Grosso (Companhia Nacional de Abastecimento [CONAB], 2023). The legume is grown practically year-round, in different environments and production systems, making it subject to a range of environmental conditions, with genotype-by-environment (GxE) interaction an important aspect in assessing new cultivars (Rocha et al., 2010; Pontes et al., 2012; Domingues et al., 2013; Torga et al., 2013; Pereira et al. 2016).

GxE interaction occurs when genotype responses to the different environments tested differ statistically from those predicted by the mathematical model adopted. Thus, significant GxE interaction can be classified as simple when only the magnitude of the differences between genotypes changes and complex when the order of genotypes in the environments analyzed changes. The latter case makes the selection process more difficult, since the best genotype in an environment will remain superior in subsequent tests.

The effects of GxE interaction can be mitigated by identifying homogeneous and specific environments, whereby genotypes suited to each environment are selected based on their stability and adaptability.

Methods used to interpret the main effects of genotypes, the environment and their interaction include linear and mixed model regression, restricted maximum likelihood/best linear unbiased prediction (REML/BLUP), multivariate analysis, additive main effects, multiplicative interaction (AMMI) and genotype main effects + genotype environment interaction (GGE biplot) analysis.

AMMI analysis is a hybrid model that combines both the additive components for the main effects (genotypes and environments) and multiplicative components for interaction effects (Duarte and Vencovsky, 1999). According to Zobel et al. (1988), this method requires analysis of variance (ANOVA) and means to estimate additive main effects (overall mean, genotype and environment effects) and single value decomposition (SVD) or principal component analysis (PCA) to decompose interaction, constituting the multiplicative component of the model. The AMMI method provides a more detailed analysis of interaction and more precise estimates of genotypic responses, ensuring selection of the most productive genotypes and easy graphic interpretation of the results.

Another widely used method to study genotype adaptability and stability is a modification of AMMI analysis proposed by Yan et al. (2000), called the GGE biplot. Also referred to as the site regression (SREG) model by Cornelius et al. (1996) and Crossa and Cornelius (1997), the GGE biplot combines the additive effect of AMMI analysis with the multiplicative component (interaction) and submits these effects to principal component analysis (PCA). As described by Yan et al. (2000), SREG is a multiplicative regression model that combines ANOVA with PCA and demonstrates superior efficiency because it explains a greater proportion of the sum of squares for interaction when compared to pooled ANOVA (Yan, et al., 2000).

The REML/BLUP method is widely used to analyze data in plant and animal breeding programs. It allows comparisons between genotypes from different populations in different tests, adjusting the data for identifiable environmental effects and simultaneously predicting the individual genetic values (Resende, 2002). For interaction analysis using mixed models, Resende (2007) proposed REML/BLUP with simultaneous selection for yield, stability, and adaptability via the MHPRVG method (harmonic mean of relative performance of genetic values). In addition to the advantages mentioned, the MHPRVG can be used for unbalanced data, nonorthogonal designs and heterogeneous variances, which are common situations in field experiments that traditional techniques such as nonparametric regression and multiplicative models have difficulty addressing (Resende, 2007). As a result, mixed models are gaining ground in plant breeding programs.

This study aimed to assess the statistical methods available to estimate genotype-by-environment (GxE) for yield-based selection of new bean cultivars and lines, and identify a testing strategy capable of reducing the number of test years and producing reliable results.

## Materials and Methods

Data from common bean value for cultivation and use (VCU) testing conducted by the Institute for Rural Development of Paraná State - IAPAR-EMATER (IDR-Paraná) were used in the analyses. Fourteen genotypes were tested in 23 environments in four locations in Paraná state, Brazil: Guarapuava (25º 22' 12" S, 51º 36'00" W), Pato Branco (26°07'33.09" S, 52°39'02.68" W), Ponta Grossa (25º05'58" S, 50º 01'12" W) and Santa Tereza do Oeste (25°05'21.51" S, 53°35'27.84" W), over three consecutive crop years (2014/15, 2015/16 and 2016/17) in two growing seasons (wet and dry) (Table 1). The variable considered was grain yield, submitted to homogeneity of variance analysis, normality testing and individual and pooled ANOVA via the GENES program (Cruz, 2013), which was also used to obtain stability and adaptability estimates with the methods described by Eberhart and Russell (1966), Lin and Binns (1988), Annicchiarico (1992) and Wricke (1965). The SELEGEN program was used to estimate GXE interaction via the REML/BLUP method with MHPRVG, enabling simultaneous assessment of stability, adaptability, and average yield (Resende 2007). AMMI and GGE biplot analyses were performed in routines compiled in R (Frutos et al., 2014) and GENES software (Cruz, 2013).

**Table 1**
**List of the 23 environments in which 14 common bean genotypes were submitted to value for cultivation and use (VCU) testing in three crop years over two seasons, in four municipalities of Paraná state, Brazil**

| SEASON | LOCATION | ENVIRONMENTS | | |
|---|---|---|---|---|
| | | Crop Years | | |
| | | 2014/15 | 2015/16 | 2016/17 |
| WET | GUARAPUAVA | 1 | 8 | 16 |
| | PATO BRANCO | 2 | 9 | 17 |
| | PONTA GROSSA | 3 | 10 | 18 |
| | SANTA TEREZA | 4 | 11 | 19 |
| DRY | GUARAPUAVA | 5 | 12 | 20 |
| | PATO BRANCO | 6 | 13 | 21 |
| | PONTA GROSSA | 7 | 14 | 22 |
| | SANTA TEREZA | . | 15 | 23 |

Two datasets were compared in the present study, the first corresponding to two (2014/15 and 2015/16) and the second three consecutive crop years (2014/15, 2015/16 and 2016/17), in the same locations and seasons. The datasets were correlated using indices from the different methodologies applied to estimate phenotypic stability and adaptability.

## Results and Discussion

The pooled ANOVA results for the two datasets of two or three crop years (Table 2) showed statistically significant effects, with similar magnitude and significance (F test) between the datasets for all the sources of variation considered.

The overall means, genetic (CVg) and experimental coefficients of variation (CVe), (CVg/CVe) ratio and the ability to discriminate between genotypes, identified by the genotypic determination coefficient, also provided concordant information between the two datasets (Table 2). The correlation between the data sets (two and three crop years) for the 15 common environments was equal to 1 for the percentage contribution of each environment to the sum of squares of GXE interaction (Table 3).

Environments 1 to 7 correspond to year 1 (2014/15), 8 to 15 to year 2 (2015/16) and 16 to 23 to year 3 (2016/17). It was predicted that, each year, the sum of the respective contributions of each environment to GXE interaction would have similar magnitudes (Table 3). Thus, the expected contributions for each year were 50 and 33% for the two and three-year datasets, respectively. However, the environments contributed most to GxE interaction in crop year 2 (2015/16), making it possible to infer that the year and location contributed equally to interaction.

The correlation between the datasets for the 14 common genotypes was 0.688 for the sum of squares contribution of each genotype to GXE interaction, considering the environments within each genotype (Table 4). Genotype 2 contributed least to GxE interaction for both datasets, while contribution was greater than 8.0% for genotypes 8 and 3 for two-year data and for 11, 4, 3 and 8 for the three-year data set. However, this information was not sufficient to select promising genotypes for cultivation, with more detailed studies required.

**Table 2**

**A. Pooled analysis of variance of the variable grain yield (metric tons ha$^{-1}$) in value for cultivation and use (VCU) testing of common bean in the dry and wet seasons over three crop years, in Paraná state, Brazil**

| SV | 2 years (2014/15, 2015/16) | | | | | 3 years (2014/15, 2015/16, 2016/17) | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | DF | SQ | QM | F | Probability | DF | SQ | QM | F | Probability |
| Blocks/Env | 45 | 23.53 | 0.5229 | | | 69 | 37.24 | 0.5397 | | |
| Genotypes | 13 | 27.94 | 21,489 | 11.71 | 0** | 13 | 25.54 | 19,647 | 10.53 | 0** |
| Environments | 14 | 438.43 | 313,167 | 59.9 | 0** | 22 | 624.96 | 284,074 | 52.63 | 0** |
| GenxEnv | 182 | 100.15 | 0.5503 | 3.00 | 0** | 286 | 164.14 | 0.5739 | 3.07 | 0** |
| | | | | | | | | | | |
| Gen/Env | 195=<br>(13+182) | 128.08 | 0.6568 | 3.58 | 0** | 299=<br>(13+286) | 189.68 | 0.6344 | 3.40 | 0** |
| Env/Gen | 196=<br>(14+182) | 538.58 | 27,479 | 14.97 | 0** | 308=<br>(22+286) | 789.1 | 25,620 | 13.73 | 0** |
| | | | | | | | | | | |
| Residual | 585 | 107.35 | 0.1835 | | | 897 | 167.44 | 0.1867 | | |
| | | | | | | | | | | |
| Total | 839 | 697.4 | | | | 1287 | 1019.32 | | | |
| | | | | | | | | | | |
| Mean (Metric tons/ha) | 2,781 | | | | | 2,798 | | | | |
| Experimental CV (%) | 15.4 | | | | | 15.44 | | | | |
| Genotypic CV (%) | 6.51 | | | | | 4.97 | | | | |
| CVg/CVe | 0.42 | | | | | 0.32 | | | | |
| Gen. coeff. det. (%) | 91.46 | | | | | 90.5 | | | | |

**Table 3**

**Pooled analysis of variance of the variable grain yield (metric tons ha$^{-1}$) in value for cultivation and use (VCU) testing of common bean, involving two crop years with 15 environments and three years with 23, in the wet and dry seasons in Paraná state, Brazil, decomposing GxE interaction for genotype performance[1] in each environment**

| SV | 2 years (2014/15, 2015/16) | | | | | | | | 3 years (2014/15, 2015/16, 2016/17) | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | Contribution to SQ (%) | | | | | | | | Contribution to SQ (%) | | |
| | DF | SQ | QM | F | P | Individual | Per year | Cumulative | SV | DF | QM | F | P | Individual | Per year | Cumulative |
| Gen/Env | 195 =13+182 | 128.08 | 0.6568 | 3.58 | 0.00** | | | | Gen/Env | 299 =13+286 | 189.68 | 0.6344 | 3.40** | | | |
| Gen/Env 1 | 13 | 3.5 | 0.2691 | 1.47 | 0.13 | 2.73 | | | Gen/Env 1 | 13 | 3.26 | 0.251 | 1.34 | 1.72 | | |
| Gen/Env 2 | 13 | 3.18 | 0.2448 | 1.33 | 0.19 | 2.48 | | | Gen/Env 2 | 13 | 3.18 | 0.2448 | 1.31 | 1.68 | | |
| Gen/Env 3 | 13 | 18.65 | 14,344 | 7.82 | 0.00** | 14.56 | | | Gen/Env 3 | 13 | 18.65 | 14,344 | 7.68** | 9.83 | | |
| Gen/Env 4 | 13 | 2.32 | 0.1786 | 0.97 | 1 | 1.81 | | | Gen/Env 4 | 13 | 2.32 | 0.1786 | 0.96 | 1.22 | | |
| Gen/Env 5 | 13 | 7.22 | 0.5551 | 3.03 | 0.00** | 5.63 | | | Gen/Env 5 | 13 | 7.22 | 0.5551 | 2.97** | 3.8 | | |
| Gen/Env 6 | 13 | 2.47 | 0.1898 | 1.03 | 0.42 | 1.93 | | | Gen/Env 6 | 13 | 2.47 | 0.1898 | 1.02 | 1.3 | | |
| Gen/Env 7 | 13 | 3.08 | 0.2366 | 1.29 | 0.21 | 2.4 | 31.5 | 31.55 | Gen/Env 7 | 13 | 3.08 | 0.2366 | 1.27 | 1.62 | 21.1 | 21.18 |
| Gen/Env 8 | 13 | 21.6 | 16,615 | 9.05 | 0.00** | 16.86 | | | Gen/Env 8 | 13 | 21.6 | 16,615 | 8.90** | 11.39 | | |
| Gen/Env 9 | 13 | 1.91 | 0.1468 | 0.8 | 1 | 1.49 | | | Gen/Env 9 | 13 | 1.91 | 0.1468 | 0.79 | 1.01 | | |
| Gen/Env 10 | 13 | 39.69 | 30,531 | 16.64 | 0.00** | 30.99 | | | Gen/Env 10 | 13 | 39.69 | 30,531 | 16.36** | 20.92 | | |
| Gen/Env 11 | 13 | 10.99 | 0.8454 | 4.61 | 0.00** | 8.58 | | | Gen/Env 11 | 13 | 10.99 | 0.8454 | 4.53** | 5.79 | | |
| Gen/Env 12 | 13 | 4.68 | 0.3603 | 1.96 | 0.02** | 3.66 | | | Gen/Env 12 | 13 | 4.68 | 0.3603 | 1.93* | 2.47 | | |
| Gen/Env 13 | 13 | 2.75 | 0.2113 | 1.15 | 0.31 | 2.14 | | | Gen/Env 13 | 13 | 2.75 | 0.2113 | 1.13 | 1.45 | | |
| Gen/Env 14 | 13 | 5.22 | 0.4018 | 2.19 | 0.01** | 4.08 | | | Gen/Env14 | 13 | 5.22 | 0.4018 | 2.15** | 2.75 | | |
| Gen/Env 15 | 13 | 0.83 | 0.0641 | 0.35 | 1 | 0.65 | 68.4 | 100 | Gen/Env 15 | 13 | 0.83 | 0.0641 | 0.34 | 0.44 | 46.2 | 67.4 |
| | | | | | | | | | Gen/Env 16 | 13 | 6.58 | 0.5058 | 2.71** | 3.47 | | |
| | | | | | | | | | Gen/Env 17 | 13 | 5.44 | 0.4182 | 2.24** | 2.87 | | |
| | | | | | | | | | Gen/Env 18 | 13 | 7.05 | 0.5423 | 2.90** | 3.72 | | |
| | | | | | | | | | Gen/Env 19 | 13 | 3.51 | 0.2703 | 1.45 | 1.85 | | |
| | | | | | | | | | Gen/Env 20 | 13 | 8.12 | 0.6248 | 3.35** | 4.28 | | |
| | | | | | | | | | Gen/Env 21 | 13 | 1.27 | 0.0981 | 0.53 | 0.67 | | |
| | | | | | | | | | Gen/Env 22 | 13 | 27.36 | 21,043 | 11.27** | 14.42 | | |
| | | | | | | | | | Gen/Env 23 | 13 | 2.51 | 0.1928 | 1.03 | 1.32 | 32.6 | 100 |
| Total | | | | | | 100 | | | | | | | | 100 | | |

**Table 4**

**Summary of pooled analysis of variance of the variable grain yield (metric tons ha$^{-1}$) in value for cultivation and use (VCU) testing of common bean, involving two crop years with 15 environments and three years with 23, in the wet and dry seasons in Paraná state, Brazil, decomposing GxE interaction for the effect of the environments on genotype contribution to interaction**

| SV | 2 years (2014/15, 2015/16) | | | | | | 3 years (2014/15, 2015/16, 2016/17) | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | DF | SQ | QM | F | Probability | Contribution (%) | SV | DF | SQ | QM | F | Probability | Contribution (%) |
| Env/Gen | 196= (14+182) | 538.58 | 2,748 | 15 | 0** | | Env/Gen | 308= (22+286) | 789.1 | 2,562 | 13.7 | 0** | |
| Env/Gen 1 | 14 | 38.92 | 2,780 | 15.1 | 0** | 7.23 | Env/Gen 1 | 22 | 62.86 | 2,857 | 15.3 | 0** | 7.97 |
| Env/Gen 2 | 14 | 30.39 | 2,171 | 11.8 | 0** | 5.64 | Env/Gen 2 | 22 | 43.96 | 1,998 | 10.7 | 0** | 5.57 |
| Env/Gen 3 | 14 | 43.12 | 3,080 | 16.8 | 0** | 8.01 | Env/Gen 3 | 22 | 64.2 | 2,918 | 15.6 | 0** | 8.14 |
| Env/Gen 4 | 14 | 40.64 | 2,903 | 15.8 | 0** | 7.55 | Env/Gen 4 | 22 | 65.73 | 2,988 | 16 | 0** | 8.33 |
| Env/Gen 5 | 14 | 38.57 | 2,755 | 15 | 0** | 7.16 | Env/Gen 5 | 22 | 50.91 | 2,314 | 12.4 | 0** | 6.45 |
| Env/Gen 6 | 14 | 41.71 | 2,979 | 16.2 | 0** | 7.74 | Env/Gen 6 | 22 | 54.23 | 2,465 | 13.2 | 0** | 6.87 |
| Env/Gen 7 | 14 | 39.65 | 2,832 | 15.4 | 0** | 7.36 | Env/Gen 7 | 22 | 50.78 | 2,308 | 12.4 | 0** | 6.44 |
| Env/Gen 8 | 14 | 45.28 | 3,234 | 17.6 | 0** | 8.41 | Env/Gen 8 | 22 | 63.66 | 2,894 | 15.5 | 0** | 8.07 |
| Env/Gen 9 | 14 | 34.53 | 2,466 | 13.4 | 0** | 6.41 | Env/Gen 9 | 22 | 46.19 | 2,100 | 11.2 | 0** | 5.85 |
| Env/Gen 10 | 14 | 39.19 | 2,799 | 15.3 | 0** | 7.28 | Env/Gen 10 | 22 | 56.23 | 2,556 | 13.7 | 0** | 7.13 |
| Env/Gen 11 | 14 | 40.25 | 2,875 | 15.7 | 0** | 7.47 | Env/Gen 11 | 22 | 66.43 | 3,020 | 16.2 | 0** | 8.42 |
| Env/Gen 12 | 14 | 35.39 | 2,528 | 13.8 | 0** | 6.57 | Env/Gen 12 | 22 | 47.06 | 2,139 | 11.5 | 0** | 5.96 |
| Env/Gen 13 | 14 | 31.94 | 2,281 | 12.4 | 0** | 5.93 | Env/Gen 13 | 22 | 56.34 | 2,561 | 13.7 | 0** | 7.14 |
| Env/Gen 14 | 14 | 39.02 | 2,787 | 15.2 | 0** | 7.24 | Env/Gen 4 | 22 | 60.52 | 2,751 | 14.7 | 0** | 7.67 |
| | | | | | | | | | | | | | |
| Total | | | | | | 100 | | | | | | | 100 |
| Mean | | | | | | 7.14 | | | | | | | 7.14 |
| Minimum | | | | | | 5.64 | | | | | | | 5.57 |
| Maximum | | | | | | 8.41 | | | | | | | 8.42 |
| Variance | | | | | | 0.59 | | | | | | | 0.95 |
| Standard Deviation | | | | | | 0.77 | | | | | | | 0.98 |
| CV (%) | | | | | | 10.73 | | | | | | | 13.68 |

In phenotypic adaptability and stability studies using the Eberhart and Russell methodology (1966) (Table 5), the overall mean yield was approximately 2.8 metric tons $ha^{-1}$. The beta coefficient (ß1) in linear regression was 1 and the coefficient of determination approximately 80.0%. For the criteria assessed, correlations between the datasets were positive for the mean (ß0=0.91), linear regression coefficient (ß1=0.88) and coefficient of determination ($R^2$= 0.96), meaning that the data analyzed over two and three years are equivalent in terms of genotype selection.

**Table 5**

**Summary of stability and adaptability analysis, via the Eberhart and Russell method (1966), for the variable grain yield (metric tons $ha^{-1}$) of 14 common bean genotypes in value for cultivation and use (VCU) testing involving two crop years with 15 environments and three years with 23, in the wet and dry seasons in Paraná state, Brazil, highlighting the mean (ß0), linear coefficient of regression (ß1) coefficient of determination of the model ($R^2$ in %)**

| | 2 years (2014/15, 2015/16) | | | 3 years (2014/15, 2015/16, 2016/17) | | | Pearson's correlation between 2 and 3 years of data | | |
|---|---|---|---|---|---|---|---|---|---|
| Genotype | Mean(ß0) | ß1 | $R^2$ (%) | Mean(ß0) | ß1 | $R^2$ (%) | Mean(ß0) | ß1 | $R^2$ (%) |
| 1 | 2.642 | 0.9579 | 73.84 | 2.81 | 9986 | 70.82 | 0.9103 | 0.8885 | 0.9574 |
| 2 | 2.249 | 0.6939 | 49.62 | 2.419 | 0.7303 | 54.16 | | | |
| 3 | 2.773 | 1.0448 | 79.27 | 2.88 | 1.0917 | 82.86 | | | |
| 4 | 2.784 | 11005 | 93.31 | 2.794 | 1.1081 | 83.4 | | | |
| 5 | 2.866 | 1.0293 | 86.04 | 2.885 | 0.9928 | 86.42 | | | |
| 6 | 2.825 | 1.1095 | 92.43 | 2.866 | 1.0526 | 91.2 | | | |
| 7 | 2.971 | 1.0781 | 91.8 | 2.887 | 0.9871 | 85.64 | | | |
| 8 | 2.935 | 1.1814 | 96.53 | 2.897 | 1.116 | 87.33 | | | |
| 9 | 2.717 | 0.9869 | 88.34 | 2.625 | 0.9365 | 84.75 | | | |
| 10 | 2.856 | 0.85 | 57.73 | 2.818 | 0.872 | 60.36 | | | |
| 11 | 2.775 | 0.9555 | 71.03 | 2.77 | 0.9957 | 66.62 | | | |
| 12 | 2.728 | 0.984 | 85.68 | 2.696 | 0.9516 | 85.91 | | | |
| 13 | 2.753 | 0.939 | 86.46 | 2.786 | 1.0511 | 87.54 | | | |
| 14 | 3.066 | 1.0892 | 95.23 | 3.033 | 1.1161 | 91.89 | | | |
| | | | | | | | | | |
| Total | 38.94 | 14 | 1147.322 | 39.166 | 14.0002 | 111.88 | | | |
| Mean | 2.781 | 1 | 81.95 | 2.798 | 1 | 79.92 | | | |
| Variance | 0.036 | 0.0151 | 203.12 | 0.021 | 0.0114 | 141.85 | | | |
| CV (%) | 6.8 | 12.28 | 17.39 | 5.22 | 10.67 | 14.9 | | | |

The second methodology used, proposed by Lin and Binns (1988) (Table 6), showed positive correlations between datasets for the criteria analyzed, with values from 0.91 to 0.92 for Pi (overall), Pi (+) and Pi (-), demonstrating equivalent information for the two and three-year datasets. Genotype 14 was the closest to ideal in both datasets and genotype 2 the furthest.

**Table 6**

**Summary of stability and adaptability analysis, via the Lin and Binns method (1988) for the variable grain yield (metric tons ha$^{-1}$) of 14 common bean genotypes in value for cultivation and use (VCU) testing involving two crop years with 15 environments and three years with 23, in the wet and dry seasons in Paraná state, Brazil, highlighting distance to the ideal genotype (Pi, expressed in %) considering all the environments (overall Pi), or only the favorable (Pi +) or adverse environments (Pi -)**

| | 2 years (2014/15, 2015/16) | | | 3 years (2014/15, 2015/16, 2016/17) | | | Pearson's correlation between 2 and 3 years of data | | |
|---|---|---|---|---|---|---|---|---|---|
| Genotype | Pi (overall) % | Pi (+) | Pi (-) | Pi (overall) % | Pi (+) | Pi (-) | Pi (overall) % | Pi (+) | Pi (-) |
| 1 | 9.74 | 8.67 | 12.19 | 6.39 | 5.38 | 9.13 | 0.9221 | 0.9185 | 0.9102 |
| 2 | 25.81 | 27.39 | 22.17 | 18 | 18.74 | 15.99 | | | |
| 3 | 6.99 | 6.97 | 7.03 | 5.06 | 4.79 | 5.8 | | | |
| 4 | 5.11 | 3.75 | 8.24 | 7.63 | 7.63 | 7.63 | | | |
| 5 | 3.93 | 4.11 | 3.5 | 4.4 | 4.82 | 3.25 | | | |
| 6 | 3.88 | 2.37 | 7.36 | 4.13 | 3.48 | 5.91 | | | |
| 7 | 2.07 | 1.56 | 3.25 | 4.31 | 4.14 | 4.79 | | | |
| 8 | 2.22 | 1.53 | 3.82 | 3.64 | 2.88 | 5.7 | | | |
| 9 | 6.48 | 6.62 | 6.17 | 9.36 | 9.15 | 9.95 | | | |
| 10 | 9.92 | 13.33 | 2.06 | 10.34 | 13.15 | 2.69 | | | |
| 11 | 9.02 | 10.9 | 4.69 | 10.59 | 12.31 | 5.91 | | | |
| 12 | 6.55 | 5.05 | 10.01 | 7.47 | 6.47 | 10.2 | | | |
| 13 | 7.1 | 6.86 | 7.65 | 6.48 | 5.25 | 9.82 | | | |
| 14 | 1.19 | 0.9 | 1.84 | 2.2 | 1.82 | 3.24 | | | |
| | | | | | | | | | |
| Total | 100 | 100 | 100 | 100 | 100 | 100 | | | |
| Mean | 7,143 | 7,143 | 7,143 | 7,143 | 7,143 | 7,143 | | | |
| Variance | 36.74 | 47.26 | 27.8 | 16.31 | 22.2 | 13.05 | | | |
| CV (%) | 84.86 | 96.25 | 73.81 | 56.54 | 65.96 | 50.57 | | | |

In the methodology proposed by Annicchiarico (1992) (Table 7), correlations between the datasets were positive for the criteria evaluated, between 0.91 and 0.93 for Wi (overall), Wi (+) and Wi (-), indicating equivalence for the data collected over two and three years. Under this methodology, the genotype that produces the highest yields most frequently in the environments tested is considered ideal. The higher the Wi value (greater than 100), the better the performance and predictability of the genotype. Genotype 14 was the closest to ideal, with values greater than 100 overall for all the environments and in the favorable or adverse environments, whereas genotype 2 exhibited the worst performance.

**Table 7**

**Summary of stability and adaptability analysis, via Annicchiarico method (1992), for the variable grain yield (metric tons $ha^{-1}$) of 14 common bean genotypes in value for cultivation and use (VCU) testing involving two crop years with 15 environments and three years with 23, in the wet and dry seasons in Paraná state, Brazil, highlighting reliability in genotype selection (Wi, expressed in %) considering all the environments (overall Wi), or only the favorable (Pi +) or adverse environments (Pi -)**

| | 2 years (2014/15, 2015/16) | | | 3 years (2014/15, 2015/16, 2016/17) | | | Pearson's correlation between 2 and 3 years of data | | |
|---|---|---|---|---|---|---|---|---|---|
| Genotype | Wi (overall) % | Wi (+) | Wi (-) | Wi (overall) % | Wi (+) | Wi (-) | Wi (overall) % | Wi (+) | Wi (-) |
| 1 | 86.21 | 84.83 | 87.25 | 90.28 | 89.14 | 91.31 | 0.9351 | 0.9144 | 0.9275 |
| 2 | 69.47 | 73.47 | 65.52 | 75.93 | 80.25 | 71.98 | | | |
| 3 | 89.47 | 87.5 | 90.78 | 93.74 | 92.03 | 95.07 | | | |
| 4 | 93.19 | 89.76 | 96.34 | 90.84 | 91.9 | 89.94 | | | |
| 5 | 96.98 | 101.54 | 93.48 | 97.07 | 100 | 94.57 | | | |
| 6 | 95.69 | 93.7 | 97.95 | 96.84 | 95.39 | 98 | | | |
| 7 | 101.79 | 102.14 | 101.23 | 97.17 | 97.2 | 96.86 | | | |
| 8 | 98.65 | 94.2 | 103.36 | 95.12 | 91.94 | 98.43 | | | |
| 9 | 91.02 | 92.36 | 89.58 | 86.97 | 86.99 | 86.67 | | | |
| 10 | 92.41 | 102.86 | 84.97 | 90.72 | 101.32 | 83.15 | | | |
| 11 | 90.24 | 93.11 | 87.38 | 88.18 | 92.82 | 84.32 | | | |
| 12 | 90.92 | 88.21 | 92.98 | 89.91 | 88.29 | 91.24 | | | |
| 13 | 93.01 | 92.86 | 92.7 | 92.17 | 88.76 | 95.49 | | | |
| 14 | 105.57 | 105.41 | 105.74 | 102.42 | 100.85 | 103.71 | | | |
| | | | | | | | | | |
| Total | 1294.63 | 1301.94 | 1289.28 | 1287.37 | 1296.88 | 1280.73 | | | |
| Mean | 92.47 | 93 | 92.09 | 91.95 | 92.63 | 91.48 | | | |
| Variance | 70.38 | 70.9 | 97.12 | 38.88 | 35.27 | 64.17 | | | |
| CV (%) | 9.07 | 9.05 | 10.7 | 6.78 | 6.41 | 8.76 | | | |

The method proposed by Wricke (1965) (Table 8) showed positive correlations (0.92) for ecovalence in both datasets, with genotype 14 contributing least to GxE interaction, followed by genotype 6.

**Table 8**
**Summary of stability and adaptability analysis, via the Lin and Binns method (1988), for the variable grain yield (metric tons 8) of $ha^{-1}$ common bean genotypes in value for cultivation and use (VCU) testing involving two crop years with 14 environments and three years with 15, in the wet and dry seasons in Paraná state, Brazil, highlighting the contribution (Ecovalence, Wi) of each genotype to the sum of squares of genotype x environment interaction**

| | 2 years (2014/15, 15/16) | | 3 years (2014/15, 2015/16, 2016/17) | | Pearson's correlation between 2 and 3 years of data | |
|---|---|---|---|---|---|---|
| Genotypes | Ecovalence (Wi) | Wi (%) | Ecovalence (Wi) | Wi (%) | Ecovalance | Wi (%) |
| 1 | 10.23 | 10.22 | 18.34 | 11.18 | 0.9223 | 0.9223 |
| 2 | 18.24 | 18.22 | 23.4 | 14.25 | | |
| 3 | 9 | 8.99 | 11.38 | 6.93 | | |
| 4 | 3.03 | 3.03 | 11.43 | 6.97 | | |
| 5 | 5.41 | 5.4 | 6.92 | 4.21 | | |
| 6 | 3.53 | 3.53 | 4.9 | 2.98 | | |
| 7 | 3.44 | 3.44 | 7.3 | 4.45 | | |
| 8 | 2.6 | 2.6 | 8.67 | 5.28 | | |
| 9 | 4.03 | 4.03 | 7.22 | 4.4 | | |
| 10 | 17.27 | 17.25 | 23.02 | 14.02 | | |
| 11 | 11.72 | 11.7 | 22.18 | 13.51 | | |
| 12 | 5.07 | 5.07 | 6.74 | 4.1 | | |
| 13 | 4.44 | 4.44 | 7.14 | 4.35 | | |
| 14 | 2.11 | 2.11 | 5.51 | 3.36 | | |
| | | | | | | |
| Total | 100.15 | 100 | 164.14 | 100 | | |
| Mean | 7.15 | 7.14 | 11.72 | 7.14 | | |
| Variance | 28.74 | 28.65 | 47.73 | 17.72 | | |
| CV (%) | 74.94 | 74.94 | 58.93 | 58.93 | | |

The AMMI method uses multivariant analysis, adopting the additive main effects model (genotype, environment) and GxE interaction as the multiplicative effect. Analysis of the datasets indicated conflicting performance between environments, although 65% of the data (15 of the 23 environments) were common to both datasets (Table 9). The means of the 15 common environments were similar (correlation=1), with negative correlations for the first (PC1) and second principal components (PC2) on comparison of the two datasets (two and three years).

**Table 9**

**Summary of stability and adaptability analysis, via the AMMI method, for the variable grain yield (metric tons 8) of 14 common bean genotypes in value for cultivation and use (VCU) testing involving two crop years with 15 environments and three years with 23, in the wet and dry seasons in Paraná state, Brazil, considering environment-related criteria, specifically the mean and first three principal components**

| | 2 years (2014/15, 15/16) | | | | 3 years (2014/15, 2015/16, 2016/17) | | | | Pearson's correlation between 2 and 3 years of data | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Environment | Mean | PC1 | PC2 | PC3 | Mean | PC1 | PC2 | PC3 | Mean | PC1 | PC2 | PC3 |
| A1 | 3,567 | -0.2396 | 0.0601 | 0.3603 | 3,570 | 0.1731 | 0.0564 | 0.3103 | 1.000 | -0.9933 | -0.9904 | 0.5564 |
| A2 | 2,471 | 0.1441 | 0.2574 | 0.2121 | 2,471 | -0.0419 | -0.0544 | -0.1633 | | | | |
| A3 | 3,760 | -0.5078 | -0.5222 | -0.8507 | 3,760 | 0.5585 | 0.6489 | -0.3252 | | | | |
| A4 | 2,165 | -0.0805 | 0.3714 | -0.0052 | 2,165 | 0.151 | -0.1542 | -0.1776 | | | | |
| A5 | 2,750 | -0.3424 | -0.1845 | -0.2426 | 2,750 | 0.3573 | 0.3189 | -0.0356 | | | | |
| A6 | 2,836 | -0.0269 | 0.4038 | -0.0891 | 2,836 | 0.0702 | -0.1956 | -0.0826 | | | | |
| A7 | 3,383 | -0.0634 | 0.4272 | -0.035 | 3,383 | 0.116 | -0.3349 | 0.0298 | | | | |
| A8 | 3,167 | -0.3235 | -0.9259 | 0.626 | 3,167 | 0.2505 | 0.9933 | 0.2569 | | | | |
| A9 | 1,892 | -0.0565 | 0.1334 | -0.1439 | 1,892 | 0.0945 | -0.0109 | -0.0616 | | | | |
| A10 | 3,570 | 15,836 | -0.5426 | -0.1777 | 3,570 | -13,105 | 0.4923 | -0.8019 | | | | |
| A11 | 2,370 | -0.388 | -0.4165 | 0.0403 | 2,370 | 0.2725 | 0.4727 | 0.3893 | | | | |
| A12 | 3,364 | -0.1369 | 0.0021 | 0.1759 | 3,364 | 0.1208 | 0.1292 | 0.1739 | | | | |
| A13 | 2,150 | 0.093 | 0.4549 | -0.1021 | 2,150 | -0.0476 | -0.2722 | -0.0743 | | | | |
| A14 | 3,168 | 0.2691 | 0.2269 | 0.2231 | 3,168 | -0.2162 | -0.0098 | -0.0233 | | | | |
| A15 | 1,110 | 0.0757 | 0.2548 | 0.0086 | 1,110 | -0.0337 | -0.1221 | -0.0389 | | | | |
| A16 | | | | | 3,569 | 0.2548 | -0.2497 | -0.1955 | | | | |
| A17 | | | | | 2,048 | 0.0647 | -0.1246 | -0.3068 | | | | |
| A18 | | | | | 3,634 | -0.1155 | -0.1195 | 0.4764 | | | | |
| A19 | | | | | 2,735 | 0.0382 | -0.4033 | 0.1825 | | | | |
| A20 | | | | | 3,449 | 0.416 | -0.3992 | -0.2018 | | | | |
| A21 | | | | | 2,216 | 0.1272 | -0.27 | -0.0366 | | | | |
| A22 | | | | | 2,987 | -11,051 | -0.0207 | 0.8125 | | | | |
| A23 | | | | | 1,982 | -0.1947 | -0.3707 | -0.1067 | | | | |
| | | | | | | | | | | | | |
| Total | 41,721 | 0 | 0 | 0 | 64,344 | 0 | 0 | 0 | | | | |
| Mean | 2,781 | 0 | 0 | 0 | 2,798 | 0 | 0 | 0 | | | | |
| Variance | 0.559 | 0.2383 | 0.1805 | 0.1074 | 0.507 | 0.181 | 0.131 | 0.104 | | | | |
| CV (%) | 26.89 | | | | 25.46 | | | | | | | |

For both datasets, AMMI analysis with an emphasis on genotypes (Table 10) also showed contradictory results, since the means of the 14 genotypes were positively correlated (greater than 0.90), whereas PC1 and PC2 exhibited negative correlations between datasets.

**Table 10**

**Summary of stability and adaptability analysis, via the AMMI method, for the variable grain yield (metric tons 8) of 14 common bean genotypes in value for cultivation and use (VCU) testing involving two crop years with 15 environments and three years with 23, in the wet and dry seasons in Paraná state, Brazil, considering environment-related criteria, specifically the mean and first three principal components**

| | 2 years (2014/15, 15/16) | | | | 3 years (2014/15, 2015/16, 2016/17) | | | | Pearson's correlation between 2 and 3 years of data | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Genotype | Mean | PC1 | PC2 | PC3 | Mean | PC1 | PC2 | PC3 | Mean | PC1 | PC2 | PC3 |
| G1 | 2.642 | 0.692 | 0.207 | 0.503 | 2.810 | -0.876 | -0.453 | 0.302 | 0.910 | -0.924 | -0.943 | 0.595 |
| G2 | 2.249 | 0.215 | 1.281 | -0.349 | 2.419 | -0.225 | -1.328 | -0.054 | | | | |
| G3 | 2.773 | -0.595 | -0.490 | 0.001 | 2.880 | 0.381 | 0.219 | 0.622 | | | | |
| G4 | 2.784 | 0.313 | 0.006 | -0.048 | 2.794 | 0.228 | -0.141 | -0.826 | | | | |
| G5 | 2.866 | 0.325 | -0.321 | -0.622 | 2.885 | -0.135 | 0.224 | -0.598 | | | | |
| G6 | 2.825 | 0.265 | -0.260 | -0.213 | 2.866 | -0.237 | 0.128 | -0.267 | | | | |
| G7 | 2.971 | 0.264 | -0.179 | -0.355 | 2.887 | -0.220 | 0.388 | -0.388 | | | | |
| G8 | 2.935 | 0.168 | -0.254 | 0.021 | 2.896 | -0.403 | 0.406 | 0.287 | | | | |
| G9 | 2.717 | 0.021 | -0.323 | 0.391 | 2.625 | -0.109 | 0.478 | 0.049 | | | | |
| G10 | 2.856 | -1.066 | 0.233 | 0.071 | 2.818 | 1.109 | -0.076 | 0.198 | | | | |
| G11 | 2.775 | -0.880 | 0.138 | -0.162 | 2.770 | 1.103 | -0.150 | -0.090 | | | | |
| G12 | 2.728 | 0.404 | -0.103 | 0.201 | 2.696 | -0.429 | 0.179 | -0.107 | | | | |
| G13 | 2.753 | -0.112 | 0.302 | 0.586 | 2.786 | -0.012 | -0.229 | 0.511 | | | | |
| G14 | 3.066 | -0.014 | -0.236 | -0.025 | 3.033 | -0.174 | 0.355 | 0.362 | | | | |
| | | | | | | | | | | | | |
| Variance explained (%) | | 44.5 | 25.5 | 9.0 | | 38.5 | 20.3 | 12.6 | | | | |
| | | | | | | | | | | | | |
| Total | 38.940 | 0.0000 | 0.0000 | 0.0000 | 39.166 | 0.0000 | 0.0000 | 0.0000 | | | | |
| Mean | 2.781 | 0.0000 | 0.0000 | 0.0000 | 2.798 | 0.0000 | 0.0000 | 0.0000 | | | | |
| Variance | 0.036 | 0.2566 | 0.1943 | 0.1157 | 0.021 | 0.3056 | 0.2220 | 0.1752 | | | | |
| CV (%) | 6.80 | | | | 5.22 | | | | | | | |

For the GGE biplot (Tables 11 and 12), no correlations were observed for the datasets. Eigenvalues and variance that explained X obtained the highest positive correlation, while AXIS2 showed a negative correlation, especially in relation to genotypes.

**Table 11**

**Summary of stability and adaptability analysis, via the GGE biplot, for the variable grain yield (metric tons 8) of 14 common bean genotypes in value for cultivation and use (VCU) testing involving two crop years with 15 environments and three years with 23, in the wet and dry seasons in Paraná state, Brazil, considering environment-related criteria**

| | 2 years (2014/15, 15/16) | | 3 years (2014/15, 2015/16, 2016/17) | | Pearson's correlation between 2 and 3 years of data | |
|---|---|---|---|---|---|---|
| Environment | AXIS1 | AXIS2 | AXIS1 | AXIS2 | AXIS1 | AXIS2 |
| A1 | 2.642 | 0.692 | 2.810 | -0.876 | 0.910 | -0.924 |
| A2 | 2.249 | 0.215 | 2.419 | -0.225 | | |
| A3 | 2.773 | -0.595 | 2.880 | 0.381 | | |
| A4 | 2.784 | 0.313 | 2.794 | 0.228 | | |
| A5 | 2.866 | 0.325 | 2.885 | -0.135 | | |
| A6 | 2.825 | 0.265 | 2.866 | -0.237 | | |
| A7 | 2.971 | 0.264 | 2.887 | -0.220 | | |
| A8 | 2.935 | 0.168 | 2.896 | -0.403 | | |
| A9 | 2.717 | 0.021 | 2.625 | -0.109 | | |
| A10 | 2.856 | -1.066 | 2.818 | 1.109 | | |
| A11 | 2.775 | -0.880 | 2.770 | 1.103 | | |
| A12 | 2.728 | 0.404 | 2.696 | -0.429 | | |
| A13 | 2.753 | -0.112 | 2.786 | -0.012 | | |
| A14 | 3.066 | -0.014 | 3.033 | -0.174 | | |
| A15 | | | | | | |
| A16 | | 44.5 | | 38.5 | | |
| A17 | | | | | | |
| A18 | 38.940 | 0.0000 | 39.166 | 0.0000 | | |
| A19 | 2.781 | 0.0000 | 2.798 | 0.0000 | | |
| A20 | 0.036 | 0.2566 | 0.021 | 0.3056 | | |
| A21 | 6.80 | | 5.22 | | | |
| A22 | | | | | | |
| A23 | | | | | | |
| | | | | | | |
| Total | | | | | | |
| Mean | | | | | | |
| Variance | | | | | | |

**Table 12**

**Summary of stability and adaptability analysis, via the GGE biplot, for the variable grain yield (metric tons 8) of 14 common bean genotypes in value for cultivation and use (VCU) testing involving two crop years with 15 environments and three years with 23, in the wet and dry seasons in Paraná state, Brazil, considering genotype-related criteria**

| | 2 years (2014/15, 15/16) | | | 3 years (2014/15, 2015/16, 2016/17) | | | Pearson's correlation between 2 and 3 years of data | | |
|---|---|---|---|---|---|---|---|---|---|
| Genotype | Eigenvalues | AXIS1 | AXIS2 | Eigenvalues | AXIS1 | AXIS2 | Eigenvalues | AXIS1 | AXIS2 |
| G1 | 3.559 | 0.840 | 0.517 | 3.975 | 0.801 | 0.182 | 0.988 | 0.571 | -0.564 |
| G2 | 3.252 | 1.773 | -0.950 | 3.553 | 0.285 | 1.460 | | | |
| G3 | 1.538 | -0.648 | -0.442 | 2.296 | -0.364 | -0.317 | | | |
| G4 | 1.439 | 0.206 | 0.355 | 2.004 | -0.202 | 0.124 | | | |
| G5 | 1.202 | -0.104 | 0.613 | 1.663 | 0.105 | -0.291 | | | |
| G6 | 0.970 | -0.061 | 0.489 | 1.542 | 0.203 | -0.210 | | | |
| G7 | 0.874 | -0.260 | 0.592 | 1.212 | 0.180 | -0.383 | | | |
| G8 | 0.658 | -0.288 | 0.472 | 0.986 | 0.342 | -0.460 | | | |
| G9 | 0.501 | -0.039 | 0.107 | 0.896 | 0.109 | 0.023 | | | |
| G10 | 0.463 | -0.727 | -1.231 | 0.762 | -1.003 | 0.104 | | | |
| G11 | 0.401 | -0.505 | -1.066 | 0.574 | -0.991 | 0.205 | | | |
| G12 | 0.316 | 0.318 | 0.442 | 0.464 | 0.398 | 0.066 | | | |
| G13 | 0.195 | 0.133 | -0.300 | 0.443 | 0.017 | 0.146 | | | |
| G14 | 0 | -0.637 | 0.402 | 0 | 0.119 | -0.649 | | | |
| | | | | | | | | | |
| Total | 15.368 | 0.0010 | 0.0000 | 20.370 | -0.0010 | 0.0000 | | | |
| Mean | 1.098 | 0.0001 | 0.0000 | 1.455 | -0.0001 | 0.0000 | | | |
| Variance | 1.166 | 0.4451 | 0.4453 | 1.368 | 0.2516 | 0.2514 | | | |

The results of REML/BLUP analysis (Table 13) demonstrated that data collected over two or three years were equivalent, obtaining positive correlations (greater than 0.90), thus favoring genotype selection for adaptability and stability in only two years of assessment. These findings demonstrate why this method is the most widely used in breeding programs aimed at the selection of superior genotypes, making it possible to predict individual genetic values and simultaneously select for yield, stability, and adaptability.

**Table 13**
**Summary of stability and adaptability analysis, via the REML/BLUP method, for the variable grain yield (metric tons 8) of 14 common bean genotypes in value for cultivation and use (VCU) testing involving two crop years with 15 environments and three years with 23, in the wet and dry seasons in Paraná state, Brazil**

| | 2 years (2014/15, 15/16) | | | | 3 years (2014/15, 2015/16, 2016/17) | | | | Pearson's correlation between 2 and 3 years of data | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Genotype | u+g+gemm | mhvg | prvg* | mhprvg* | u+g+gem | mhvg | prvg* | mhprvg* | u+g+gem | mhvg | prvg* | mhprvg* |
| G1 | 2.654 | 2.380 | 2.649 | 2.629 | 2.809 | 2.557 | 2.808 | 2.781 | 0.910 | 0.921 | 0.909 | 0.919 |
| G2 | 2.295 | 2.037 | 2.299 | 2.242 | 2.455 | 2.228 | 2.464 | 2.413 | | | | |
| G3 | 2.773 | 2.478 | 2.766 | 2.742 | 2.872 | 2.607 | 2.865 | 2.845 | | | | |
| G4 | 2.784 | 2.473 | 2.766 | 2.757 | 2.795 | 2.519 | 2.779 | 2.759 | | | | |
| G5 | 2.859 | 2.609 | 2.868 | 2.857 | 2.876 | 2.664 | 2.888 | 2.877 | | | | |
| G6 | 2.821 | 2.541 | 2.813 | 2.806 | 2.860 | 2.625 | 2.859 | 2.851 | | | | |
| G7 | 2.955 | 2.690 | 2.961 | 2.955 | 2.879 | 2.663 | 2.890 | 2.878 | | | | |
| G8 | 2.922 | 2.592 | 2.901 | 2.895 | 2.887 | 2.606 | 2.873 | 2.859 | | | | |
| G9 | 2.723 | 2.431 | 2.714 | 2.704 | 2.641 | 2.397 | 2.634 | 2.622 | | | | |
| G10 | 2.850 | 2.590 | 2.872 | 2.828 | 2.816 | 2.589 | 2.833 | 2.792 | | | | |
| G11 | 2.776 | 2.495 | 2.779 | 2.751 | 2.773 | 2.518 | 2.772 | 2.736 | | | | |
| G12 | 2.732 | 2.486 | 2.738 | 2.724 | 2.706 | 2.492 | 2.709 | 2.697 | | | | |
| G13 | 2.756 | 2.509 | 2.763 | 2.753 | 2.787 | 2.541 | 2.781 | 2.766 | | | | |
| G14 | 3.042 | 2.775 | 3.052 | 3.045 | 3.011 | 2.767 | 3.012 | 3.003 | | | | |
| | | | | | | | | | | | | |
| Total | 38.940 | 35.085 | 38.940 | 38.687 | 39.166 | 35.771 | 39.166 | 38.879 | | | | |
| Mean | 2.781 | 2.506 | 2.781 | 2.763 | 2.798 | 2.555 | 2.798 | 2.777 | | | | |
| Variance | 0.030 | 0.029 | 0.030 | 0.034 | 0.017 | 0.017 | 0.017 | 0.019 | | | | |
| CV % | 6.22 | 6.79 | 6.26 | 6.69 | 4.73 | 5.08 | 4.70 | 5.03 | | | | |

## Conclusions

Based on the results of the present study, the methodologies proposed by Eberhart and Russell (1966), Lin and Binns (1988), Annicchiarico (1992) and Wricke (1965) and the REM/BLUP mixed model enabled the selection of genotypes with superior adaptability and stability. Choosing which of these is most appropriate depends on familiarity with the technique or unbalanced data, which prompts the need for mixed models.

All the methods used here to analyze stability and adaptability for common bean grain yield demonstrate that information obtained in two and three years of assessment were equivalent in selecting the best genotypes, except for AMMI and the GGE biplot, which showed no correlation between the two datasets.

Thus, for statistical methods that use linear regression and mixed models, the number of years analyzed did not affect result interpretation. However, in multivariate analysis, genotype behavior varied in the environments studied according to the number of years analyzed.

The results of the present study indicate that two years of assessment were sufficient to reliably indicate new cultivars with high yield potential, production stability and adaptation to different environments.

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## References

Annicchiarico, P. (1992). Cultivar adaptation and recommendation from alfalfa trials in Northern Italy. *Journal of Genetics and Plant Breeding, 46,* 269-278.

Companhia Nacional de Abastecimento (2023). *Série histórica das safras.* CONAB. https://www.conab.gov. br/info-agro/safras/serie-historica-das-safras/item/download/45942_24bab78cca84a1a5ca6086a4969e5f 6a

Cornelius, P. L., Crossa, J., Seyedsader, M.S. (1996). Statistical tests and estimators of multiplicative models for genotype-by-environment interaction. In M. S. Kang, H. G. Gauch (Eds.), *Genotype-by-environment interaction* (pp. 199-234). Boca Raton, FL.

Crossa, J., Cornelius, P. L. (1997). Sites regression and shifted multiplicative model clustering of cultivar trial sites under heterogeneity of error variances. *Crop Science, 37*(2), 406-415. doi: 10.2135/cropsci19970011183x003700020017x

Cruz, C. D. (2013). GENES - a software package for analysis in experimental statistics and quantitative genetics. *Acta Scientiarum. Agronomy, 35*(3), 271-276. doi: 10.4025/actasciagron.v35i3.21251

Domingues, L. S., Ribeiro, N. D., Minetto, C., Souza, J. F. de, Antunes, I. F. (2013). Metodologias de análise de adaptabilidade e de estabilidade para a identificação de linhagens de feijão promissoras para o cultivo no Rio Grande do Sul. *Semina: Ciências Agrárias, 34*(3), 1065-1076. doi: 10.5433/1679-0359.2013v34 n3p1065

Duarte, J. B., Vencovsky, R. (1999). *Interação genótipos x ambientes: uma introdução à análise "AMMI".* Sociedade Brasileira de Genética.

Eberhart, S. A., Russell, W. A. (1966). Stability parameters for comparing varieties 1. *Crop Science, 6*(1), 36-40. doi: 10.2135/cropsci1966.0011183x000600010011x

Food and Agriculture Organization (2020). *World food and agriculture - statistical yearbook 2020.* FAO. https://doi.org/10.4060/cb1329en

Frutos, E., Galindo, M.P., Leiva, V. (2014). An interactive biplot implementation in R for modeling genotype-by-environment interaction. *Stochastic Environmental Research and Risk Assessment, 28*(7), 1629-1641. doi: 10.1007/s00477-013-0821-z

Lin, C., Binns, M. R. (1988). A superiority measure of cultivar performance for cultivar × location data. *Canadian Journal of Plant Science, 68*(1), 193-198. doi: 10.4141/cjps88-018

Pereira, H. S., Alvares, R. C., Melo, L. C., Costa, A. F. da, Carvalho, H. W. L. de, Faria, L. C. de, Souza, T. L. P. O. de. (2016). Interação genótipos por ambientes em linhagens de feijoeiro-comum com grãos carioca, avaliadas na Região Nordeste do Brasil. *Semina: Ciências Agrárias, 37*(4), 1745-1756. doi: 10. 5433/1679-0359.2016v37n4p1745

Pontes, V. A., Jr., Melo, L. C., Pereira, H. S., Del Peloso, M. J., Faria, L. C., Wendland, A., Braz, A. J. B. P., Ferreira, S. B. (2012). Productive potential and interaction of elite bean lines with environments in the Central Cerrado of Brazil. *Crop Breeding and Applied Biotechnology, 12*(1), 8-16. doi: 10.1590/s1984-70332012000100002

Resende, M. D. V. de. (2002). *Genética biométrica e estatística no melhoramento de plantas perenes.* EMBRAPA Floresta.

Resende, M. D. V. de. (2007). *Matemática e estatística na análise de experimentos e no melhoramento genético.* EMBRAPA Florestas.

Rocha, V. P. C., Moda-Cirino, V., Destro, D., Fonseca, N. da S. Jr., Prete, C. E. C. (2010). Adaptabilidade e estabilidade da característica produtividade de grãos dos grupos comerciais carioca e preto de feijão. *Semina: Ciências Agrárias, 31*(1), 39-54. doi: 10.5433/1679-0359.

Torga, P. P., Santos Melo, P. G., Pereira, H. S., Faria, L. C. de, Del Peloso, M. J., Melo, L. C. (2013). Decomposition of the interaction of common black bean group genotypes with the environment. *Agricultural Sciences, 4*(12), 683-688. doi: 10.4236/as.2013.412092

Wricke, G. (1965). Zur berechnung der okovalenz bei sommerweizen und hafer. *Zeitschrift Fur. Pflanzenzuchtung, 52*(1), 127–138

Yan, W., Hunt, L. A., Sheng, Q., Szlavnics, Z. (2000). Cultivar evaluation and mega-environment investigation based on the GGE Biplot. *Crop Science, 40*(3), 597-605. doi: 10.2135/cropsci2000.403597x

Zobel, R. W., Wright, M. J., Gauch, H. G. (1988). Statistical analysis of a yield trial. *Agronomy Journal, 80*(3), 388-393. doi: 10.2134/agronj1988.00021962008000030002x