# Black bean genotypes for adaptability, stability, and productivity via mixed models for the state of Rio de Janeiro, Brazil

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**ABSTRACT**: The study of adaptability, stability, and productivity is essential for selecting and recommending superior genotypes. This fact is particularly the case for the introduction of common bean cultivars in Rio de Janeiro, Brazil, whose production is negligible and does not meet the internal demand. Thus, this study estimated genetic parameters and selection gains and undertake a simultaneous selection for adaptability, stability, and productivity in black bean genotypes via mixed models. The investigation was carried out in three municipalities in the state of Rio de Janeiro during three crop years. The trials were set up in a randomized block design with 11 genotypes and three replications. High mean heritability (81%) and selection accuracy (90%), as well as good selection prospects, were observed. Gains between 1.03 and 9.49% were achieved for grain yield. Simultaneous selection was efficient, indicating two black bean lines (CNFP 15290 and CNFP 15361) as the most productive, adaptable, and stable. As such, these lines have the potential to be released as new black bean cultivars for the state of Rio de Janeiro.
**Key words**: genetic gain, genetic parameters, HMRPGV, *Phaseolus vulgaris*, REML/BLUP.

## Genótipos de feijão preto para adaptabilidade, estabilidade e produtividade via modelos mistos para o estado do Rio de Janeiro, Brasil

**RESUMO**: O estudo de adaptabilidade, estabilidade e produtividade é importante para selecionar e recomendar genótipos superiores. Esse fato é particularmente válido para a introdução de cultivares de feijão comum no Rio de Janeiro, Brasil, cuja produção é ínfima e não atende a demanda interna. Assim, este trabalho teve como objetivo estimar parâmetros genéticos e ganhos de seleção e realizar uma seleção simultânea para adaptabilidade, estabilidade e produtividade de genótipos de feijão preto através de modelos mistos. O estudo foi realizado em três municípios do estado do Rio de Janeiro e em três anos agrícolas. Os ensaios foram instalados em delineamento de blocos casualizados com 11 genótipos e três repetições. Observou-se alta herdabilidade média (81%), acurácia seletiva (90%) e boas perspectivas de seleção. Também foram observados ganhos satisfatórios para a característica entre 1,03 e 9,49%. A seleção simultânea foi eficiente e permitiu selecionar duas linhagens de feijão preto CNFP (15290 e 15361) como sendo as mais produtivas, adaptáveis e estáveis e, portanto, têm potencial para serem lançadas como novas cultivares de feijão preto para o estado do Rio de Janeiro.
**Palavras-chave**: ganho genético, parâmetros genéticos, HMRPGV, *Phaseolus vulgaris*, REML/BLUP.

## INTRODUCTION

The common bean (*Phaseolus vulgaris* L.) holds significant importance as a staple in human nutrition, offering substantial nutritional value and contributing to the income of producers. It is cultivated across all Brazilian states, some of which even support the potential for three annual harvests. In this context, according to the National Supply Company (CONAB, 2023), the total production of common bean in Brazil amounted to approximately 3 million tons in the 2021/22 harvest. Of this total, the output of black bean variants stood at roughly 576 thousand tons. In the 2021/22 harvest, the state of Rio de Janeiro produced 1300 t from an area of 1000 ha.

It is also worth noting that the reduction in the area used for cultivation in the last 30 years is the main reason why Rio de Janeiro does not produce enough black beans (CONAB, 2023). This may have resulted in an intense and irreversible loss of variety diversity since common bean varieties are sparsely preserved at the national germplasm bank (CAVALCANTI et al., 2021). Currently, the demand for common bean in the state is at 245 thousand tons, a significant disparity in comparison to the amount produced. Consequently, the state finds itself

compelled to import nearly 99% of its common bean needs from other regions and countries.

The use of genotypes adapted to different regions emerges as a central strategy to boost the productivity of Brazilian beans, thereby reducing the need for imports (PEREIRA et al., 2017; SOUZA et al., 2018). Therefore, for a genetic breeding program to achieve its objective and develop cultivars suited to the different producing regions of the country, genotypes must be subjected to many environments that mimic the conditions these cultivars will face. However, the genotype x environment interaction influences selection gains, directly impacting genotype performance. This underscores the necessity to quantify the intensity and nature of this interaction, indicating the real impact of selection and ensuring a high degree of reliability in recommending genotypes for a given environment or set of environments (ROSADO et al., 2012).

In this respect, the restricted maximum likelihood/best linear unbiased predictor (REML/BLUP) methodology proves to be especially adept at managing imbalanced data, leading to more precise estimations and predictions of variance components and genetic values (RESENDE, 2007). REML is an efficient tool to examine the various sources of variation inherent to the evaluation of field experiments. It achieves this by decomposing phenotypic variation into its various genetic and environmental components and genotype x environment interaction. Key practical advantages of the REML/BLUP approach include: (i) allowing for comparisons of individuals or varieties across different timeframes (generations, years) and spaces (locations, blocks); (ii) enabling simultaneous correction for environmental influences, estimation of variance components, and prediction of genetic values; (iii) handling complex data structures such as repeated measures, multiple years, locations, and experimental designs; and (iv) applicability to unbalanced data and non-orthogonal designs (CARVALHO et al., 2022; SANTOS et al., 2019).

Thus, the REML/BLUP methodology stands out for its interpretational clarity in results and precision in the selection of common bean genotypes (SANTOS et al., 2018). This selection process can be effectively executed using the method called "harmonic mean of the relative performance of predicted genotypic values" (HMRPGV) (ROSADO et al., 2012). The HMRPGV approach allows for selection based on predicted genetic values, considering the average performance across all environments (without interaction effects), individual

performance in each environment (considering interaction effects), and simultaneous selection for yield, adaptability, and stability. This multi-faceted approach, within the framework of mixed models (REML/BLUP), has been applied to various crops including eucalyptus (ROSADO et al., 2012), carioca and black beans (SOUZA et al., 2018; SANTOS et al., 2018; 2019; ROCHA et al., 2020; SOUZA et al., 2023), cowpea (ROCHA et al., 2017; SOUSA et al., 2019), and soybean (GONÇALVES et al., 2020; EVANGELISTA et al., 2021).

With these considerations, the objectives of this study were: (i) to estimate genetic parameters for grain yield, (ii) to attain genetic gains through the mixed model methodology (REML/BLUP), and (iii) to select superior black bean genotypes enhancing grain yield in the state of Rio de Janeiro.

## MATERIALS AND METHODS

*Description of the genotypes and experimental conduct*

The balanced data employed in this study originated from Value for Cultivation and Use (VCU) trials involving 11 distinct genotypes of black beans derived from the Breeding Program of Embrapa Rice and Beans. These genotypes comprised three cultivars, namely, BRS Campeiro, BRS Esplendor, and IPR Uirapurú, alongside eight lines: CNFP 15289, CNFP 15290, CNFP 15292, CNFP 15302, CNFP 15304, CNFP 15310, CNFP 15359, and CNFP 15361. These three cultivars, considered as reference (control group), stand out in national cultivation due to characteristics such as resistance to major diseases, high grain yield, and superior grain quality.

These trials, conducted in different regions of the state of Rio de Janeiro – RJ, were carried out during the drought season in the years 2013/14, 2014/15, and 2015/16, between the parallels and meridians of 22º75' S, 42º25' W, and 39 m (Araruama); 21º71' S, 41º34' W, and 17 m (Campos dos Goytacazes); and 22°17' S, 41°51' W, and 11 m (Macaé), totaling nine growing environments. The respective soils were classified as dystric Red-Yellow Podzolic, alic Yellow Podzolic, and alic Red-Yellow Latosol. In accordance with the Köppen classification, the regional climate is designated as Aw, characterized by a rainy summer and a dry winter (KOTTEK et al., 2006), with an average annual temperature of approximately 24 ºC and minimal fluctuations in thermal amplitude (INMET, 2022).

The experimental layout employed a randomized block design, incorporating 11 genotypes

and three replications. Each plot consisted of four 4-m rows spaced 0.50 m apart. Data collection was conducted within the central two rows, while a border area of 0.50 m from each end was excluded. All sowing activities were carried out manually, ensuring an even distribution of 15 seeds per linear meter. The crop management protocols strictly adhered to the established requirements for this crop.

As the crops reached maturity, indicated by the final phase of the reproductive period (developmental stage R9), the plants experienced complete water stress, resulting in a 15% reduction in seed moisture content during harvest. The characteristic evaluated in this study was grain productivity, quantified within the plot area. This measurement accounts for the grain yield of plants after harvest and processing, adjusting the grain weight to a moisture content of 13% and extrapolating the value to kg ha$^{-1}$.

*Data analysis*

Following the model proposed by VIANA & RESENDE (2014), analysis of deviance was formulated as:

$D = -2In(L)$

$\ln(L) = -1/2\ln|X'V - 1X| -$

$1/2\ln|V| - 1/2(y - Xm)`V - 1(y - Xm)$ ,

where *ln (L)* is the maximum point of the logarithmic function of the restricted maximum likelihood (REML) (PATTERSON & THOMPSON, 1971); *y* is the vector of the analyzed variable; *m* is the vector of measurement effects, assumed to be fixed and added to all means; *X* is the incidence matrix for the fixed effects; and *V* is the variance and covariance matrix of *y*.

Analysis of deviance, estimation of genetic parameters, and prediction of gains, adaptability, and stability of genotypes were conducted in this study.

The likelihood ratio test (LRT) was used to test the significance of the effects, and it was calculated using the following formula:

$LRT: | -2\ln(Lse) + 2\ln(Lfm)$ ,

where Lse is the maximum point of the maximum likelihood function for the reduced model (without the effects); and Lfm is the maximum point of the maximum likelihood function for the full model.

Variance components were estimated and the effects of genotypes and genotype x environment interaction were predicted by REML/BLUP through the following model:

$y = Xf + Zg + Qa + Ti + Wt + e$ ,

where *y* is the data vector; *f* is the vector of the effects of replication-location-year combinations (fixed) added to the overall mean; *g* is the vector of

the genotypic effects (random); *a* is the vector of genotype x year interaction effects (random); *i* is the vector of genotype x location interaction effects (random); *t* is the vector of genotype x location x year triple interaction effects (random); *e* is the vector of errors or residuals (random); and *X*, *Z*, *Q*, *T*, and *W* represent the incidence matrices for those effects. The effects of years, locations, and block/years/locations are grouped into effect *f*, as they are purely environmental effects.

This model is suitable for evaluating genotypes across various environments and cultivation years. This approach allowed us to estimate variance components using restricted maximum likelihood (REML) and individual genotypic values employing the best linear unbiased predictors (BLUP). The quantitative variable was analyzed using Selegen-REML/BLUP software (RESENDE, 2016)

The significance of model effects was evaluated by analysis of deviance, following the recommendations of RESENDE (2007). Deviations were calculated with and without genotypic effects. The resulting deviation without the genotypic effect was subtracted from each deviation in the full model, and the differences were compared against the chi-square value with one degree of freedom at probability levels (P < 0.01 and P < 0.05).

*Variance components estimates*

The following parameters were estimated: genotypic variance (Vg); variance of the genotype x year interaction (Vgy); variance of the genotype x location interaction (Vgl); variance of the genotype x location x year interaction (Vgly); environmental or residual variance (Ve); phenotypic variance (Vp); single plots broad-sense heritability ($h^2_g$); heritability at genotype-mean level ($h^2_{mg}$); coefficient of determination of the genotype x year interaction effects ($c^2gy = c2$); coefficient of determination of the genotype x location interaction effects ($c^2gl = c21$); coefficient of determination of the genotype x location x year interaction effects ($c^2gly = c22$); genotypic correlation across locations, valid for any year (rgl); genotypic correlation over the years, valid for any location (rgy); genotypic correlation across locations, in a given year (rgl_y); genotypic correlation over the years, in a given location (rgy_l); genotypic correlation across locations, for the mean for all years (rgl_my); genotypic correlation over the years, for the mean of all locations (rgy_ml); genotypic correlation across locations and years (rgly); selection ($\hat{r}_{gg}$); coefficient of genetic variation of all environments (CVgy); and relative coefficient

of variation, calculated as $CV_g/CV_e$, where $CV_g$ and $CV_e$ are the coefficients of genetic and environmental variation, respectively.

*Productivity, stability, and adaptability estimates*

The parameters of harmonic mean of genotypic values (HMGV), relative performance of genotypic values (RPGV), and harmonic mean of the relative performance of genetic values (HMRPGV) were obtained as described next. Stability was estimated by the HMGV method, given by:

$$HMGV = \frac{n}{\sum_{j=1}^{n} \left(\frac{1}{Vg_{ij}}\right)}$$

where $n$ is the number of environments (n=nine) in which genotype $i$ was evaluated; and $Vg_{ij}$ is the genotypic value of genotype $i$ in environment $j$. Adaptability was measured by the RPGV values, according to the expression:

$$RPGV = \frac{1}{n} * \left(\sum_{j=1}^{n} \frac{Vg_{ij}}{M_j}\right)$$

where $M_j$ represents the average grain yield in environment $j$. The simultaneous selection for yield, stability, and adaptability given by HMRPGV is calculated by the equation below:

$$HMRPGV = \frac{1}{\frac{1}{n} * \left(\sum_{j=1}^{n} \frac{Vg_{ij}}{M_j}\right)}$$

The obtained data were analyzed statistically via mixed models, according to the statistical model already presented. Differences between deviance means were identified using the likelihood ratio test (LRT) at the 5% and 1% probability levels. These analyses were conducted employing Selegen-REML/BLUP software (RESENDE, 2016).

## RESULTS AND DISCUSSION

There was a significant effect of genotypes (Table 1), indicating some heterogeneity between the evaluated genotypes. This highlights the presence of genetic variability, enabling a successful selection of superior genotypes and precise estimates of variance components. Furthermore, the interactions of genotypes with years, locations, and years x locations show significance at a higher level (P < 0.01) (Table 1), indicating differential genotypic behavior across varying environments and evaluation years and evidencing the distinct responses of genotypes to different growing periods and locations.

Therefore, the genotype x environment interaction plays a fundamental role in genotype

evaluation trials, influencing the selection of superior genotypes and bolstering the recommendation of new cultivars by the breeder. In line with this context, studies by DELFINI et al. (2018), MELO et al. (2018), SANTOS et al. (2018; 2019), and ROCHA et al. (2020) also found significant interaction effects when investigating common bean genotypes.

The variance components, indicative of variances associated with random effects in the statistical model, revealed the contribution of genotypic variance to phenotypic expression, constituting approximately 21% (Table 2). This underscores the significance of mixed models, which prioritize genetic value over environmental factors, leading to a more accurate selection of superior genotypes.

In the estimation of individual broad-sense heritability ($h^2_{mg}$), the value found was of medium magnitude, estimated at 0.21 (Table 2). This estimation encompasses pure genotypic effects for the trait, disregarding interactions with years and locations. As outlined by RESENDE (2002), heritability is classified as low (h < 0.15), moderate (0.15 < h < 0.50), or high (h > 0.50). Hence, the observed $h^2_{mg}$ suggests moderate genetic variability between the evaluated bean genotypes, further evidenced by a low coefficient of genetic variation (CVg = 8.20%), indicating the proportion of genetic variance available for selection.

As ALLARD (1999) asserts, many economically and agronomically significant traits in plant species are inherently quantitative, leading to lower heritability values due to their polygenic nature. As described by PREISIGKE et al. (2020), low heritability estimates may be related to several factors, e.g. the polygenic nature of the trait, which is highly influenced by the environment.

Quantitative traits, such as grain yield, generally exhibit low heritability but lead to mean genotype heritability coefficients of moderate magnitude (RESENDE, 2002). Estimating heritability at the genotype-mean level ($h^2_{mg}$), a high value of 0.81 was obtained (Table 2). This result substantially minimizes environmental effects and enables a very high selection accuracy ($\hat{r}_{gg}$) (RESENDE & DUARTE, 2007), which reached 90% for genotypes across different environments.

The high accuracy of selection reflects robust experimental precision, enhancing reliability and confidence in the selection of promising genotypes. DELFINI et al. (2018), SANTOS et al. (2018), and SOUZA et al. (2018) reported similar outcomes also in studies involving common bean. The observed coefficient of environmental variation (CVe) stands at

Table 1 - Analysis of deviance for grain yield (kg ha$^{-1}$) involving 11 black bean genotypes evaluated in nine environments.

| Effect | -------------------Deviance------------------- | -------------------LRT ($X^2$)------------------- |
|---|---|---|
| Genotypes (g) | 3345 | 5.78[*] |
| Genotypes x years (gy) | 3348 | 9.33[**] |
| Genotypes x locations (gl) | 3350 | 11.01[**] |
| Genotypes x locations x years (gly) | 3359 | 19.93[**] |
| Full model | 3339 | |

[**] and [*]: significant at 1% (6.63) and 5% (3.84) probability, respectively, by the chi-square test (X2) with 1 degree of freedom.

11.88% (Table 2), a medium and satisfactory value for grain yield traits in black bean (OLIVEIRA et al., 2009), yet lower than values described by PEREIRA et al. (2017) and MELO et al. (2018). Conversely, the relative coefficient of variation ($CV_r$) was estimated at 0.69, attributing a substantial portion of phenotypic variation to environmental factors.

Given the considerable contribution of the GxLxY interaction variance, the correlation between genotype rankings across environments and years is diminished, as evidenced by the low genotypic correlation value between locations and years (rgly) of the order of 0.37, reinforcing the consistency of genotype rankings within the studied environments.

Notably, there was a change in the ranking of genotypes due to the presence of a complex interaction (Tables 3 and 4). These aspects highlight the importance of studying the adaptability and stability of genotypes.

These results suggested that, despite the substantial contribution of environmental variance, considerable genetic gains can be achieved. To this end, three distinct selection strategies were employed (Tables 3, 4, and 5). The first strategy, centered on the mean genotype performance across all environments while neutralizing interaction effects, identified two superior genotypes CNFP 15290 and CNFP 15361 outperforming the three control genotypes with new means of 9.49% and 8.18%, respectively

Table 2 - Variance component estimates (individual REML) for grain yield in 11 black bean genotypes evaluated in nine environments.

| -----------------------------------------------------Variance component (individual REML)----------------------------------------------------- | | | |
|---|---|---|---|
| Vg | 20902 | rgy | 0.77 |
| Vgy | 6106 | rgl_y | 0.77 |
| Vgl | 7892 | rgy_l | 0.82 |
| Vgly | 20891 | rgl_my | 0.79 |
| Ve | 43867 | rgy_ml | 0.83 |
| Vp | 99660 | rgly | 0.37 |
| $h^2_g$ | $0.21 \pm 0.07$ | $\hat{r}_{gg}$ | 0.90 |
| $h^2_{mg}$ | 0.81 | CVge | 0.49 |
| $c^2_{gy}$ | 0.06 | $CV_g$ (%) | 8.20 |
| $c^2_{gl}$ | 0.07 | $CV_e$ (%) | 11.88 |
| $c^2_{gly}$ | 0.20 | $CV_r$ (%) | 0.69 |
| rgl | 0.72 | μ (kg ha$^{-1}$) | 1762 |

Vg: genotypic variance, Vgy: variance of the genotype x year interaction, Vgl: variance of the genotype x location interaction, Vgly: variance of the genotype x location x year interaction, Ve: environmental or residual variance, Vp: phenotypic variance, $h^2_g$: single plots broad-sense heritability (free from interaction), $h^2_{mg}$: heritability at genotype-mean level, $c^2_{gy}$: coefficient of determination of the genotype x year interaction effects, $c^2_{gl}$: coefficient of determination of the genotype x location interaction effects, $c^2_{gly}$: coefficient of determination of the genotype x location x year interaction effects, rgl: genotypic correlation across locations, valid for any year, rgy: genotypic correlation over the years, valid for any location, rgl_y: genotypic correlation across locations, in a given year, rgy_l: genotypic correlation over the years, in a given location, rgl_my: genotypic correlation across locations, for the mean of all years, rgy_ml: genotypic correlation over the years, for the mean of all locations, rgly: genotypic correlation across locations and years, $\hat{r}_{gg}$: accuracy of selection, CVge: coefficient of genetic variation of all environments, CVg (%): coefficient of genetic variation, CVe (%): coefficient of environmental variation, CVr (%): relative coefficient of variation, μ = overall mean.

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Table 3 - New predicted mean and genetic gain estimated via REML/BLUP for grain yield in 11 black bean genotypes, considering the average performance of genotypes cultivated in Araruama, Campos dos Goytacazes, and Macaé, in the state of Rio de Janeiro, in the 2013/14, 2014/15, and 2015/16 harvests.

| Order | --------Genotype--------- | ------Gain (kg ha$^{-1}$)------ | --------Gain (%)--------- | --------New mean-------- |
|---|---|---|---|---|
| 1 | CNFP 15290 | 167 | 9.49 | 1929 |
| 2 | CNFP 15361 | 144 | 8.18 | 1906 |
| 3 | BRS Campeiro | 126 | 7.20 | 1889 |
| 4 | CNFP 15310 | 117 | 6.65 | 1879 |
| 5 | CNFP 15289 | 104 | 5.92 | 1866 |
| 6 | BRS Esplendor | 90 | 5.14 | 1852 |
| 7 | CNFP 15304 | 80 | 4.58 | 1842 |
| 8 | CNFP 15292 | 59 | 3.35 | 1821 |
| 9 | CNFP 15302 | 39 | 2.24 | 1801 |
| 10 | CNFP 15359 | 18 | 1.03 | 1780 |
| 11 | IPR Uirapurú | 0 | 0.00 | 1762 |

(Table 3). These genotypic values hold potential for recommendation, especially in environments featuring a genotype x environment interaction pattern similar to that of this study. Encouragingly, predicted genetic gains ranged from 9.49% to 1.03%.

From the pool of evaluated genotypes, 90.90% displayed new mean performances surpassing the overall mean. Notably, among these genotypes are BRS Campeiro and BRS Esplendor cultivars, maintaining their superiority over the assessed black bean lines. They achieved the third and sixth highest genetic predictions, respectively. According to RESENDE (2007), the REML/BLUP methodology facilitates the ranking of potential genotypes for selection by comprehensively exploring genotypic variations for each analyzed variable.

The difference between the highest and lowest new mean of the genotypes within the ranking was narrow in amplitude. This phenomenon can be attributed to the constriction of predicted means through REML/BLUP, which leads to the reduction of differences between genotypes. These differences are primarily attributed to genetic factors rather than environmental influences (RESENDE, 2002).

SANTOS et al. (2018) achieved genetic gains surpassing those obtained in this study. The

Table 4 - Predicted genetic gain estimates and new mean of genotypes for grain yield in 11 black bean genotypes, considering the average performance of genotypes cultivated in Araruama (Location I), Campos dos Goytacazes (Location II), and Macaé (Location III), in the state of Rio de Janeiro, in the 2013/14, 2014/15, and 2015/16 harvests.

| --------------------Location I-------------------- | | | --------------------Location II-------------------- | | | -----------------Location III------------------ | | |
|---|---|---|---|---|---|---|---|---|
| Genotype | Gain | New mean | Genotype | Gain | New mean | Genotype | Gain | New mean |
| CNFP 15290 | 188 | 1801 | CNFP 15361 | 151 | 1740 | CNFP 15290 | 226 | 2310 |
| CNFP 15310 | 154 | 1767 | CNFP 15290 | 151 | 1740 | CNFP 15289 | 203 | 2287 |
| CNFP 15361 | 140 | 1753 | BRS Campeiro | 138 | 1727 | BRS Campeiro | 187 | 2271 |
| BRS Campeiro | 117 | 1730 | BRS Esplendor | 126 | 1715 | CNFP 15361 | 176 | 2260 |
| CNFP 15289 | 99 | 1712 | CNFP 15310 | 118 | 1707 | CNFP 15310 | 159 | 2242 |
| BRS Esplendor | 83 | 1696 | CNFP 15304 | 100 | 1688 | CNFP 15304 | 144 | 2227 |
| CNFP 15304 | 71 | 1684 | CNFP 15289 | 81 | 1670 | BRS Esplendor | 120 | 2204 |
| CNFP 15292 | 52 | 1665 | CNFP 15292 | 59 | 1648 | CNFP 15292 | 88 | 2172 |
| CNFP 15302 | 36 | 1649 | CNFP 15302 | 39 | 1628 | CNFP 15302 | 58 | 2141 |
| CNFP 15359 | 18 | 1631 | CNFP 15359 | 20 | 1608 | IPR Uirapurú | 28 | 2112 |
| IPR Uirapurú | 0 | 1613 | IPR Uirapurú | 0 | 1589 | CNFP 15359 | 0 | 2084 |
| Mean | | 1700 | | | 1678 | | | 2210 |

Table 5 - Stability (HMGV), adaptability (RPGV and RPGVμ), and stability and adaptability of genetic values (HMRPGV and HMRPGVμ) for grain yield (kg ha$^{-1}$) in 11 black bean genotypes predicted by BLUP analysis.

| Genotype | -------HMGV------ | -------RPGV------- | -------RPGVμ------ | -----HMRPGV----- | ----HMRPGVμ---- |
|---|---|---|---|---|---|
| CNFP 15290 | 1919 | 1.11 | 1950 | 1.11 | 1949 |
| CNFP 15361 | 1872 | 1.07 | 1900 | 1.07 | 1899 |
| BRS Campeiro | 1832 | 1.06 | 1864 | 1.06 | 1863 |
| CNFP 15310 | 1836 | 1.06 | 1863 | 1.06 | 1862 |
| CNFP 15289 | 1772 | 1.03 | 1812 | 1.03 | 1809 |
| BRS Esplendor | 1766 | 1.02 | 1791 | 1.02 | 1790 |
| CNFP 15304 | 1751 | 1.01 | 1782 | 1.01 | 1782 |
| CNFP 15292 | 1635 | 0.94 | 1659 | 0.94 | 1659 |
| CNFP 15302 | 1609 | 0.93 | 1632 | 0.93 | 1632 |
| CNFP 15359 | 1550 | 0.89 | 1571 | 0.89 | 1570 |
| IPR Uirapurú | 1532 | 0.88 | 1556 | 0.88 | 1556 |

RPGVμ: adaptability multiplied by the overall mean of all environments, HMRPGVμ: adaptability and stability multiplied by the overall mean of all environments.

authors evaluated 11 genotypes of black beans cultivated in the municipalities of Arcoverde and Caruaru, semi-arid regions, in the state of Pernambuco, Brazil. The CNFP 15684 line exhibited the highest genetic gain, of 629 (32.33%), and cultivar IPR Uirapurú also stood out with a genetic gain of 174 (8.97%).

In the second selection strategy, the performance of selected genotypes was contextualized within specific environments. Genotype CNFP 15290 maintained its superiority in Araruama and Macaé, while also ranking among the top two genotypes selected in Campos dos Goytacazes (Table 4). This trend mirrored the selection based on average performance across all environments and genotypic values unaffected by interactions (Table 3).

Examining environment means, Macaé boasted the highest yield mean at 2210 kg ha$^{-1}$, followed by Araruama with 1700 kg ha$^{-1}$, and Campos dos Goytacazes with 1678 kg ha$^{-1}$ (Table 4). Macaé's distinct climatic conditions, characterized by mild temperatures and regular rainfall, contribute to its conducive environment for robust crop development. Although, Campos dos Goytacazes exhibited lower productivity, it still offers favorable conditions for black bean cultivation.

In support of this, SOUZA et al. (2023) conducted a similar assessment of the same genotypes and environments, but u,sing GGE biplot analysis. They found that Macaé stood out as the ideal location for testing, showing high yield, adaptability, and performance stability for the genotype CNFP 15290, considered an ideotype.

These results suggestes its viability for grain production in the state of Rio de Janeiro.

In line with this, PEREIRA et al. (2018a; 2018b) evaluated two black bean cultivars developed by the Common Bean Breeding Program at Universidade Estadual do Norte Fluminense Darcy Ribeiro (UENF), tailored for the north and northwest regions of Rio de Janeiro: UENF 2014 and UENF Rio Paraíba. These cultivars demonstrated impressive performance, stability, broad adaptability, and, notably, high grain yield compared to the control cultivars Xamego, BR1-Xodó, and BR3-Ipanema, recommended for cultivation in the state. This shows that, compared to genotypes selected specifically for certain environments (Table 4), these tested and registered cultivars for Rio de Janeiro outperformed the average yield of each environment in this study.

When encompassing the best selected genotypes across all environments, we anticipated the preservation of the superiority hierarchy (Table 4) for values like Vgly (20891) and $C^2_{gly}$ (0.20) (Table 2), reflecting GxLxY interaction. ROSADO et al. (2012) asserted the possibility of extrapolating cultivation across various environments for selected genotypes by analyzing the pattern of experimental network interactions.

The third strategy employed the harmonic mean of genotypic values (HMGV) to define stability and grain yield; adaptability analysis to assess genotype responses to environmental stimuli, predicted through the relative performance of genotypic values (RPGV) across environments;

and the harmonic mean-based value prediction (HMRPGV), which facilitated simultaneous selection for yield, adaptability, and stability (RESENDE, 2004).

The adaptability and stability assessment via HMRPGV revealed that genotypes CNFP 15290, CNFP 15361, BRS Campeiro, CNFP 15310, CNFP 15289, BRS Esplendor, and CNFP 15304 can be considered promising, yielding between 1782 and 1949 kg ha$^{-1}$ (Table 5). These genotypes showcase high yield, predictability, and broad adaptability, performing well in favorable conditions while maintaining their yield under adverse environmental conditions.

Among the evaluated methods, HMRPGV is the one that least penalizes the predicted genotypic values, as it takes into account the genotype x environment interaction effects in each environment (ROSADO et al., 2012). Thus, according to RESENDE (2007), the HMGV, RPGV, and HMRPGV methods align in the prioritization of genetic materials. Their incorporation as selection criteria enhances the refinement of selection and the accuracy of genetic value predictions simultaneously for productivity, stability, and adaptability. Therefore, the lines selected by this method are productive, stable across different environments, and respond positively to environmental stimuli; i.e., when combined, they enable the release of a new cultivar.

## CONCLUSION

The high estimates of heritability at genotype-mean level and the selection obtained for the grain yield trait enabled the selection of superior common black bean genotypes.

HMRPGV analysis, which encompasses productivity, adaptability, and stability simultaneously, was efficient and indicated two lines CNFP 15290 and CNFP 15361 as the most productive, adaptable, and stable in different environments, exhibiting greater genetic gains. Therefore, the selected genotypes have the potential to be released as new black bean cultivars for the state of Rio de Janeiro.

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## DECLARATION OF CONFLICT OF INTEREST

We have no conflict of interest to declare.

## AUTHORS' CONTRIBUTIONS

All authors contributed equally to the conception and writing of the manuscript. All authors critically revised the manuscript and approved the final version.

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