

Genetic parameters and simultaneous selection for root yield, adaptability and stability of cassava genotypes

João Tomé de Farias Neto⁽¹⁾, Elisa Ferreira Moura⁽¹⁾, Marcos Deon Vilela de Resende⁽²⁾,
Pedro Celestino Filho⁽³⁾ and Sebastião Geraldo Augusto⁽⁴⁾

⁽¹⁾Embrapa Amazônia Oriental, Travessa Dr. Enéas Pinheiro, s/nº, CEP 66095100 Belém, PA, Brazil. Email: joao.farias@embrapa.br, elisa.moura@embrapa.br ⁽²⁾Embrapa Florestas, Estrada da Ribeira, Km 111, Caixa Postal 319, CEP 83411000 Colombo, PR, Brazil. Email: marcos.resende@embrapa.br ⁽³⁾Embrapa Amazônia Oriental, Núcleo de Apoio à Pesquisa e Transferência de Tecnologia, Transamazônica, Travessa Comandante Castilho, nº 190, Centro, CEP 68371150 Altamira, PA, Brazil. Email: pedro.celestino@embrapa.br ⁽⁴⁾Universidade Federal do Pará, Campus Universitário de Altamira, Avenida Coronel José Porfírio, s/nº, São Sebastião, CEP 68370000 Altamira, PA, Brazil. Email: saugusto@ufpa.br

Abstract – The objective of this work was to estimate genetic parameters and to evaluate simultaneous selection for root yield and for adaptability and stability of cassava genotypes. The effects of genotypes were assumed as fixed and random, and the mixed model methodology (REML/Blup) was used to estimate genetic parameters and the harmonic mean of the relative performance of genotypic values (HMRPGV), for simultaneous selection purposes. Ten genotypes were analyzed in a complete randomized block design, with four replicates. The experiment was carried out in the municipalities of Altamira, Santarém, and Santa Luzia do Pará in the state of Pará, Brazil, in the growing seasons of 2009/2010, 2010/2011, and 2011/2012. Roots were harvested 12 months after planting, in all tested locations. Root yield had low coefficients of genotypic variation (4.25%) and broad-sense heritability of individual plots (0.0424), which resulted in low genetic gain. Due to the low genotypic correlation (0.15), genotype classification as to root yield varied according to the environment. Genotypes CPATU 060, CPATU 229, and CPATU 404 stood out as to their yield, adaptability, and stability.

Index terms: *Manihot esculenta*, genotype x environment interaction, HMRPGV, REML/Blup.

Parâmetros genéticos e seleção simultânea quanto à produtividade de raízes, adaptabilidade e estabilidade de genótipos de mandioca

Resumo – O objetivo deste trabalho foi estimar parâmetros genéticos e avaliar a seleção simultânea quanto à produtividade de raízes e à adaptabilidade e estabilidade de genótipos de mandioca. Os efeitos dos genótipos foram considerados como fixos e aleatórios, e a metodologia de modelos mistos (REML/Blup) foi utilizada para estimar os parâmetros genéticos e a média harmônica do desempenho relativo dos valores genotípicos (MHPRVG), para seleção simultânea. Dez genótipos foram avaliados em delineamento de blocos ao acaso, com quatro repetições. O experimento foi realizado nos municípios de Altamira, Santarém e Santa Luzia do Pará, PA, nos anos agrícolas de 2009/2010, 2010/2011 e 2011/2012. As raízes foram colhidas 12 meses após o plantio, em todos os locais testados. A produtividade de raízes apresentou baixo coeficiente de variação genotípica (4,25%) e herdabilidade de parcelas individuais no sentido amplo (0,0424), o que resultou em baixo ganho genético. Em razão da baixa correlação genotípica (0,15), a classificação dos genótipos quanto à produtividade de raízes variou de acordo com o ambiente. Os genótipos CPATU 060, CPATU 229 e CPATU 404 destacaram-se quanto à produtividade, adaptabilidade e estabilidade.

Termos para indexação: *Manihot esculenta*, interação genótipo x ambiente, MHPRVG, REML/Blup.

Introduction

Cassava (*Manihot esculenta* Crantz) is a major source of carbohydrates for more than 800 million people, in several tropical countries (Save and grow, 2013). In 2012, Brazil was the second main world producer of cassava, with 25,744,829 tons of roots. The state of Pará is the main producer, with 17.92%

of the national production in that same year (Instituto Brasileiro de Geografia e Estatística, 2013).

In genetic breeding programs, a great number of promising genotypes and clones are tested in different environments. Although studies on genotype x environment interaction are of great value for genotype selection in different climatic conditions, they do not provide detailed information on the individual

performance of the genotypes in each environment. Adaptability and stability studies are needed for that (Cruz & Regazzi, 1994).

Vidigal Filho et al. (2007) reported that the methodologies proposed by Lin & Binns (1988) and Annicchiarico (1992) were similar for selecting more stable cassava genotypes. According to Kvitschal et al. (2009), the methodologies recommended by Eskridge (1990), Annicchiarico (1992), and Lin & Binns (1988) are more suitable for situations of low genotype x environment interaction, whereas the additive main effect and multiplicative interaction (AMMI) methodology and the one of Toler & Burrows (1998) provide better details for specific adaptations of genotypes to environments.

The harmonic mean of the relative performance of genotypic values (HMRPGV), presented by Resende (2002), allows selecting simultaneously for yield, adaptability, and stability, and can be performed using the same Blup predictors and mixed model equations. Colombari Filho et al. (2013) used this methodology to perform a global analysis of 26 years of rice genetic breeding in Brazil. It has been used also for other species, such as sugarcane (Zeni-Neto et al., 2008), rubber tree (Arantes et al., 2013), rice (Reginato Neto et al., 2013), and common bean (Carbonell et al., 2007). For cassava, there are no known reports on the use of HMRPGV.

The objective of this work was to estimate genetic parameters and to evaluate simultaneous selection for root yield and for adaptability and stability of cassava genotypes.

Materials and Methods

Ten cassava genotypes (Table 1) were used in trials established in the municipalities of Santa Luzia do Pará (01°27'06"S, 46°57'35"W), Santarém (2°24'54"S, 54°24'36"), and Altamira (3°12'12"S, 52°12'13"W), in the state of Pará, Brazil. The trials were carried out in the growing seasons of 2009/2010, 2010/2011, and 2011/2012. Santarém has an Am climate type, according to Köppen's classification, with humid and hot weather and an average temperature of 27°C. The average rainfall is about 2,000 mm, with two distinct periods of rain and most rainy days concentrated from December to June. Altamira has both Am and Aw climate types. The average temperature is of 27°C and precipitation is of 2,100 mm, concentrated mostly from

February to April. Santa Luzia do Pará has a hot and humid weather, with an average rainfall of 2,300 mm per year and an average temperature of 28°C.

All trials were established in a randomized complete block design, with four replicates. The plots had 25 plants each, distributed in five lines of five plants. Roots were harvested from nine plants located within the central lines. The soil was tilled and planting was done with a 1.0x1.0 m spacing. One single application of the NPK 10-28-20 was done, 35 days after the planting of the stakes, using 40 g of fertilizer per planting spot. No irrigation was performed.

Evaluations were done 12 months after sowing. Root yield of each replicate was corrected using the covariance method (Vencovsky & Barriga, 1992), according to the final stand, considering nine plants. Root yield was evaluated in kg ha⁻¹. The evaluated genotypes belong to the Germplasm Bank of Embrapa Amazônia Oriental, located at Belém, state of Pará, Brazil: CPATU 444, CPATU 404, CPATU 060, CPATU 229, CPATU 013, CPATU 402, CPATU 302, CPATU 058, BRS Poti, and BRS Kiriris. The two last ones are commercial cultivars tolerant to root rot, a disease caused by *Phytophthora* sp. and *Fusarium* sp.

The matrix form of this model, considering one observation per plot, is represented by:

$y = Xb + Zg + Wc + \varepsilon$, in which: y , b , g , c , and ε are, respectively, vectors of data, fixed effects of blocks over the locations, genotypic effects of genotypes (random), effect of genotype x environment effects

Table 1. Description of the cassava (*Manihot esculenta*) accessions from the Germplasm Bank of Embrapa Amazônia Oriental, Brazil.

| Accession | Sampling location in Brazil | Year | Main traits |
|-------------|-----------------------------|------|--|
| CPATU 013 | Belém, PA | 1947 | |
| CPATU 058 | Unknown | 1970 | |
| CPATU 060 | Unknown | 1970 | |
| CPATU 229 | Nova Timboteua, PA | 1998 | Used for tapioca flour ⁽¹⁾ |
| CPATU 302 | Castanhal, PA | 2000 | |
| CPATU 402 | Castanhal, PA | 2005 | Used for tapioca flour ⁽¹⁾ |
| CPATU 404 | Santa Maria do Pará, PA | 2005 | |
| CPATU 444 | Terra Alta, PA | 2008 | Yellow pulp root |
| BRS Kiriris | - | 2006 | Tolerant to root rot, low hydrogen cyanide content |
| BRS Poti | - | 2007 | Tolerant to root rot, erect growing |

⁽¹⁾According to information given by producers at the sampling location.

(random), and random errors; and X, Z, and W are the matrices of incidence of b, g, and ge, respectively, as described by Resende (2007a). The authors have shown statistically that, when using mixed models, the medium quadratic error is minimized in the prediction of true genetic values if the effects of genotypes are considered random and the number of treatments is ten or more.

The distribution and structure of means and variances are the following:

$$E \begin{bmatrix} y \\ g \\ ge \\ e \end{bmatrix} = \begin{bmatrix} Xb \\ 0 \\ 0 \\ 0 \end{bmatrix}; \quad \text{Var} \begin{bmatrix} g \\ ge \\ e \end{bmatrix} = \begin{bmatrix} I\sigma_g^2 & 0 & 0 \\ 0 & I\sigma_{ge}^2 & 0 \\ 0 & 0 & I\sigma_e^2 \end{bmatrix}$$

The equations of mixed models are:

$$\begin{bmatrix} X'X & X'Z & X'W \\ Z'X & Z'Z + I\lambda_1 & Z'W \\ W'X & W'Z & W'W + I\lambda_2 \end{bmatrix} \begin{bmatrix} \hat{b} \\ \hat{g} \\ \hat{ge} \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \\ W'y \end{bmatrix}$$

in which:

$$\lambda_1 = \frac{\sigma_e^2}{\sigma_g^2} = \frac{1 - h_g^2 - c_{ge}^2}{h_g^2}; \quad \lambda_2 = \frac{\sigma_e^2}{\sigma_{ge}^2} = \frac{1 - h_g^2 - c_{ge}^2}{c_{ge}^2}.$$

In this case, $h_g^2 = \frac{\sigma_g^2}{\sigma_g^2 + \sigma_{ge}^2 + \sigma_e^2}$ is the broad-sense heritability at the individual plot level in the block;

$c_{ge}^2 = \frac{\sigma_{ge}^2}{\sigma_g^2 + \sigma_{ge}^2 + \sigma_e^2}$ is the determination coefficient

of effects of genotype x environment interaction;

σ_g^2 is the genotypic variance among genotypes;

σ_{ge}^2 is the variance of genotype x environment interaction;

σ_e^2 is the residual variance among plots; and

$$r_{gloc} = \frac{\sigma_e^2}{\sigma_g^2 + \sigma_{ge}^2} = \frac{h_g^2}{h_g^2 + c_{ge}^2} \text{ is the genotypic}$$

correlation of genotypes among environments.

The estimators of components of variance using REML, with the EM algorithm, are:

$$\hat{\sigma}_e^2 = [y'y - \hat{b}'y - \hat{g}'Z'y - \hat{c}'W'y]/[N - r(x)],$$

$$\hat{\sigma}_g^2 = [\hat{g}'\hat{g} + \hat{\sigma}_e^2 \text{tr} C^{22}]/q, \text{ and}$$

$$\hat{\sigma}_{ge}^2 = [\hat{g}\hat{e}' + \hat{\sigma}_e^2 \text{tr} C^{33}]/s,$$

in which, C^{22} and C^{33} come from,

$$C^{-1} = \begin{bmatrix} C_{11} & C_{12} & C_{13} \\ C_{21} & C_{22} & C_{23} \\ C_{31} & C_{32} & C_{33} \end{bmatrix}^{-1} = \begin{bmatrix} C^{11} & C^{12} & C^{13} \\ C^{21} & C^{22} & C^{23} \\ C^{31} & C^{32} & C^{33} \end{bmatrix},$$

in which: C is the coefficient matrix of the mixed model equations; tr is the trace operator matrix; r(x) is the rank of the matrix X; N, q, and s are the total number of data, number of genotypes, and number of genotype x environment combinations, respectively.

In this model, the predicted genotypic values free of interaction, considering all locations, are measured by $\mu + g$, in which μ is the mean of all locations. For each j location, genotypic values are predicted by $\mu_j + g + ge$, in which μ_j is the mean for location j.

In the model in which genotypic effects were considered fixed, the g vector was adjusted as a fixed effect and the b vector was adjusted as a random effect.

The estimates of components of variance and genetic parameters were obtained with the linear mixed model methodology, in the statistical genetics software SelegenREML/Blup (Resende, 2007b).

The analysis of stability and adaptability was carried out with the HMRPGV method, calculated as:

$$\text{HMRPGV} = n / \sum_{j=1}^n \frac{V\bar{G}_j}{VG_{ij}},$$

in which: n is the number of locations; $V\bar{G}_{ij} = u_j + g_i + ge_{ij}$ represents the genotypic value of genotype i in the specific location j, in which the mean for location j and g_i and ge_{ij} are the Blups of genotype i and of the interaction between genotype i and location j, respectively; and $V\bar{G}_j$ is the mean for $V\bar{G}_{ij}$ in location j.

Results and Discussion

The effects of genotypes, free of interaction, were not significant, which is normal in joint analyses considering contrasting environments. However, the effects of interaction were highly significant, and a study of genotype stability and adaptability is needed for selection (Table 2).

Root yield showed low levels of genotypic variation (4.25%). The broad-sense individual heritability, related to genotypic effects, free of the interaction with environments, was 0.0424 (Table 3), configuring a genetic gain of low magnitude (Resende, 2002). Average root yield in each location was: 28.21 Mg ha⁻¹ in Altamira, 17.59 Mg ha⁻¹ in Santarém, 19.25 Mg

ha⁻¹ in Santa Luzia do Pará; and the general mean was 23.32 Mg ha⁻¹ (Table 4). These results agree with the quantitative and polygenic nature of this trait and are similar to the estimates obtained by Barreto & Resende (2010).

The square root of heritability resulted in a selective accuracy of moderate magnitude (52.55%), which guarantees security in the selection of superior genotypes (Resende, 2004). However, the adoption of

an adequate number of replicates is essential in trials aiming for efficient and high accuracy selection. With a heritability of 20%, the use of five replicates leads to a selective accuracy of 74.56%, which is adequate. The coefficient of variation showed a moderate value of 20.93%, confirming the good precision of the trials. The genotype x environment interaction was high, and the genotypic correlation for the behavior in different environments (genotypic correlation of genotypes

Table 2. Analysis of deviance for cassava (*Manihot esculenta*) root production.

| Effect | Deviance ⁽¹⁾ | LRT (Chi-square) |
|------------------------------------|-------------------------|---------------------|
| Genotypes | 1,310.66 | 0.28 ^{ns} |
| Genotype x environment interaction | 1,331.4 | 21.02 ^{**} |
| Residual | - | - |
| Complete model | 1,310.38 | - |

⁽¹⁾Deviance of adjusted model without the cited effects; distribution for 1 degree of freedom. LRT, likelihood; chi-square, 3.84 and 6.63 at 5 and 1% probability, respectively.

Table 3. Estimate of components of means and variance for root yield (Mg ha⁻¹) of cassava (*Manihot esculenta*) genotypes⁽¹⁾.

| Genotypes | Genotypic effect | $\mu + g$ | Genetic gain | New mean | $\mu + g + ge$ |
|---|------------------|-----------|--------------|----------|----------------|
| CPATU 404 | 0.5917 | 23.912 | 0.5917 | 23.9118 | 25.0136 |
| CPATU 060 | 0.5473 | 23.867 | 0.5695 | 23.8896 | 24.8867 |
| CPATU 229 | 0.4558 | 23.776 | 0.5316 | 23.8517 | 24.6248 |
| CPATU 013 | 0.4389 | 23.759 | 0.5084 | 23.8286 | 24.5763 |
| CPATU 402 | 0.1685 | 23.488 | 0.4404 | 23.7606 | 23.8024 |
| CPATU 302 | 0.0204 | 23.299 | 0.3636 | 23.6838 | 23.2618 |
| BRS Kiriris | 0.3271 | 22.993 | 0.2650 | 23.5851 | 22.3840 |
| CPATU 444 | 0.5053 | 22.815 | 0.1687 | 23.4888 | 21.8739 |
| CPATU 058 | 0.5239 | 22.796 | 0.0917 | 23.4119 | 21.8205 |
| BRS Poti | 0.8256 | 22.495 | 0.0000 | 23.3201 | 20.9572 |
| Genotypic variance | | | | | 0.9815 |
| Variance of genotype x environment interaction | | | | | 5.4835 |
| Residual variance | | | | | 23.8238 |
| Phenotypic variance | | | | | 30.2889 |
| Broad-sense individual heritability free of interaction | | | | | 0.0424 |
| Average heritability | | | | | 0.2762 |
| Selective accuracy | | | | | 52.55% |
| R ² of genotype x environment interaction | | | | | 0.1811 |
| Genotypic correlation of behavior in different environments | | | | | 0.1518 |
| Coefficient of genotypic variation (%) | | | | | 4.2484 |
| Coefficient of residual variation (%) | | | | | 20.9303 |
| General mean (Mg ha ⁻¹) | | | | | 23.32 |

$\mu + g$, predicted genotypic values (free of interaction); $\mu + g + ge$, average genotypic value in the environments.

Table 4. Estimate of predicted genetic gain for cassava (*Manihot esculenta*) root yield (Mg ha⁻¹) in three locations in the state of Pará, Brazil.

| Genotype | g + ge | $\mu + g + ge$ | Genetic gain | | |
|---------------------|--------|----------------|---------------------------|--------------|----------|
| | | | Genetic values | Genetic gain | New mean |
| Altamira | | | | | |
| CPATU 404 | 5.2957 | 33.5101 | 29.4774 | 5.2957 | 33.5101 |
| CPATU 013 | 3.3707 | 31.5851 | 27.5309 | 4.3332 | 32.5476 |
| CPATU 060 | 2.5484 | 30.7629 | 26.8235 | 3.7383 | 31.9527 |
| CPATU 229 | 1.8113 | 30.0257 | 26.0546 | 3.2565 | 31.4709 |
| CPATU 402 | 1.5533 | 29.7677 | 25.6031 | 2.9159 | 31.1303 |
| CPATU 302 | 0.4562 | 28.6706 | 24.4210 | 2.5059 | 30.7204 |
| CPATU 444 | 3.0979 | 25.1165 | 20.6824 | 1.7054 | 29.9198 |
| BRS Kiriris | 3.1434 | 25.0710 | 20.7663 | 1.0993 | 29.3137 |
| CPATU 058 | 3.3423 | 24.8722 | 20.4359 | 0.6058 | 28.8202 |
| BRS Poti | 5.4519 | 22.7625 | 18.2069 | 0.0000 | 28.2144 |
| Mean | | | 28.21 Mg ha ⁻¹ | | |
| Santarém | | | | | |
| CPATU 060 | 1.6141 | 19.2081 | 24.7283 | 1.6141 | 19.2081 |
| CPATU 229 | 1.2498 | 18.8438 | 24.2353 | 1.4320 | 19.0260 |
| CPATU 404 | 0.7630 | 18.3570 | 24.0591 | 1.2090 | 18.8030 |
| BRS Kiriris | 0.3748 | 17.9688 | 22.5071 | 1.0004 | 18.5944 |
| BRS Poti | 0.2381 | 17.3559 | 21.4132 | 0.7527 | 18.3467 |
| CPATU 444 | 0.2631 | 17.3309 | 21.7379 | 0.5834 | 18.1774 |
| CPATU 402 | 0.3240 | 17.2700 | 22.3890 | 0.4538 | 18.0478 |
| CPATU 013 | 0.6598 | 16.9342 | 22.3152 | 0.3146 | 17.9086 |
| CPATU 302 | 0.9835 | 16.6105 | 21.5026 | 0.1704 | 17.7644 |
| CPATU 058 | 1.5333 | 16.0607 | 20.35744 | 0.0000 | 17.5940 |
| Mean | | | 17.59 Mg ha ⁻¹ | | |
| Santa Luzia do Pará | | | | | |
| CPATU 013 | 1.0568 | 20.3144 | 24.3731 | 4.0568 | 20.3144 |
| CPATU 229 | 0.8521 | 20.1098 | 24.0432 | 0.9545 | 20.2121 |
| CPATU 060 | 0.5360 | 19.7936 | 23.8122 | 0.8150 | 20.0726 |
| CPATU 058 | 0.3777 | 19.6353 | 22.6222 | 0.7057 | 19.9633 |
| CPATU 302 | 0.3524 | 19.6100 | 23.1553 | 0.6350 | 19.8926 |
| CPATU 402 | 0.2172 | 19.4748 | 23.1961 | 0.5654 | 19.8230 |
| BRS Kiriris | 0.0390 | 19.2186 | 22.2979 | 0.4790 | 19.7367 |
| CPATU 444 | 0.9766 | 18.2810 | 21.2097 | 0.2971 | 19.5547 |
| CPATU 404 | 0.9794 | 18.2782 | 22.4361 | 0.1552 | 19.4129 |
| BRS Poti | 1.3972 | 17.8604 | 20.4108 | 0.0000 | 19.2576 |
| Mean | | | 19.25 Mg ha ⁻¹ | | |

g + ge, genotypic effect per environment; $\mu + g + ge$, predicted genotypic value capitalizing the interaction with the environments.

with locations) was low (0.1518). This indicates that this interaction is complex, resulting in changes in genotype classification (productivity rank) between locations.

The genotypic values free of interaction ($\mu + g$) for the average location indicate that the three best genotypes were: CPATU 404, CPATU 060, and CPATU 229. In this case, the average genetic gain obtained with the selection of the three genotypes was 2.28%. The estimate of genotypic values, considering the average interaction among genotypes and environments ($\mu + g + ge$), indicated the same genotypes previously selected for use in areas with similar patterns of genotype x environment interaction. Although both methodologies selected the same genotypes, the predictions of genotypic values in the second case ($\mu + g + ge$) were superior. Bastos et al. (2007) found that the prediction of genotypic values, considering interaction, can only be superior when the selected genotypes are grown in a location with the same pattern of genotype x environment interaction, as the one where the original trials were executed. However, inferences on genotypic means based on the first case are more secure (Table 3).

The statistics of the genetic mean per location ($\mu + g + ge$) showed that the three best genotypes in each location were: CPATU 404, CPATU 013, and CPATU 060 in Altamira; CPATU 060, CPATU 229, and CPATU 404 in Santarém; and CPATU 013, CPATU 229, and CPATU 060 in Santa Luzia do Pará (Table 4). The genetic gain with the selection of the three most productive genotypes was more expressive in Altamira (13.36%), followed by Santa Luzia do Pará

(5.82%), and Santarém (4.25%). The genetic gains in each environment (Table 4) were superior to the other estimates, considering the average of environments based on the selection according to average (Table 3). This genetic mean is the parameter that least affects the predicted genotypic values, since it considers the effects of the interaction of each environment in the selection per environment, compared with the selection for all environments based on genetic value (Rosado et al., 2012).

The negative values of $g + ge$ show that the genotypes CPATU 302, BRS Kiriris, CPATU 444, CPATU 058, and BRS Poti are above the general mean (23.32 Mg ha⁻¹) (Table 4). The genotypes CPATU 444, BRS Kiriris, CPATU 058, and BRS Poti were the least productive in all locations. Thus, since the selection carried out in this study considered root yield alone, these genotypes should be discarded. The genotypes CPATU 060 and CPATU 229 were among the most productive, in all locations. Therefore, these genotypes did not interact significantly with the environment.

The expected reduction or increase in root yield varied according to genotype performance related to stability (HMGV), adaptability (RPGV), and both simultaneously (HMRPGV) for all environments (Table 5). There was total agreement between the three most productive genotypes based on HMGV, RPGV, HMRPGV, and average yield. These results indicate that secure predictions about genetic values can be made based on a single standard contemplating yield, stability, and adaptability (Verardi et al., 2009).

The HMRPGV method selects genotypes based on their adaptability and stability, which is important

Table 5. Stability of genotypic values (HMGV), adaptability of genotypic values (RPGV), and stability and adaptability of genotypic values (HMRPGV) for cassava (*Manihot esculenta*) genotypes root yield.

| Genotype ⁽¹⁾ | HMGV | Genotype | RPGV | RPGV × GM ⁽²⁾ | Genotype | HMRPGV | HMRPGV × GM |
|-------------------------|---------|----------|--------|--------------------------|----------|--------|-------------|
| 08 | 22.2075 | 08 | 1.0701 | 24.9518 | 08 | 1.0691 | 24.9320 |
| 02 | 22.0427 | 10 | 1.0601 | 24.7209 | 02 | 1.0597 | 24.7124 |
| 10 | 21.5786 | 02 | 1.0598 | 24.7153 | 10 | 1.0512 | 24.5132 |
| 05 | 21.4380 | 05 | 1.0456 | 24.3838 | 05 | 1.0416 | 24.2899 |
| 01 | 21.0017 | 01 | 1.0160 | 23.6926 | 01 | 1.0151 | 23.6718 |
| 06 | 20.5373 | 06 | 0.9929 | 23.1535 | 06 | 0.9916 | 23.1249 |
| 03 | 20.3291 | 03 | 0.9693 | 22.6039 | 03 | 0.9657 | 22.5203 |
| 07 | 19.7088 | 07 | 0.9415 | 21.9562 | 07 | 0.9399 | 21.9178 |
| 09 | 19.5570 | 09 | 0.9380 | 21.8743 | 09 | 0.9344 | 21.7904 |
| 04 | 19.0429 | 04 | 0.9069 | 21.1489 | 04 | 0.9005 | 20.9999 |

⁽¹⁾01, CPATU 402; 02, CPATU 229; 03, BRS Kiriris; 04, BRS Poti; 05, CPATU 013; 06, CPATU 302; 07, CPATU 444; 08, CPATU 060; 09, CPATU 058; 10, CPATU 404. ⁽²⁾GM, general mean.

to direct controlled crossings in evaluation phases of genetic breeding programs and to recommend superior genotypes for commercial use. Generally, a univariate model of repeatability, considering all locations simultaneously, is suitable for selection, focusing on the average yield in all locations. However, a more complete model may allow additional inferences, such as specific genotypes for each location, selection of stable genotypes, selection of responsive genotypes (high adaptability) to environmental improvements, and selection considering the three aspects simultaneously (Sturion & Resende, 2005). Resende (2004) demonstrated that the simultaneous selection for yield, stability, and adaptability using mixed models can be done by the HMRPGV method. In the present work, the three best genotypes based on RPGV, HMGV, and HMRPGV were the same as the best ones based on average yield. The best genotypes to be selected based on HMRPGV were: CPATU 060, CPATU 229, and CPATU 404. This selection would generate a genetic gain of 6.0% over the general mean.

The method also contemplates the specific adaptation of a genotype to an environment, using $y_{ij} = u_j + g_i + ge_{ij}$, which is the genotypic value of genotype i in the specific location j . Groups of varieties can be formed according to the specific adaptability to each environment, using the magnitude and signal of the estimate of interactions. The genotypes CPATU 404, CPATU 013, and CPATU 060 showed higher synergy with Altamira (Table 4).

Conclusions

1. Cassava genotypes highly interact with the environment as to root yield, which results in low genotypic correlation between environments.

2. The selected genotypes do not vary when genetic effects are used as random or fixed.

3. The genotypes CPATU 060, CPATU 229, and CPATU 404 stood out with the best yield, adaptability, and stability, and should be recommended for breeding programs.

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