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

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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 know 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 Ami 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:

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

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

$c_{ge}^2 = \dfrac{\sigma_{ge}^2}{\sigma_g^2 + \sigma_{ge}^2 + \sigma_e^2}$ 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

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

correlation of genotypes among environments.

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

$$\hat{\sigma}_e^2 = [y'y - \hat{b}'y - \hat{g}'Z'y - \hat{c}'W'y]/[N - r(x)],$$
$$\hat{\sigma}_g^2 = [\hat{g}'\hat{g} + \hat{\sigma}_e^2 \, tr \, C^{22}]/q, \text{ and}$$
$$\hat{\sigma}_{ge}^2 = [g\hat{e}'g\hat{e} + \hat{\sigma}_e^2 \, tr \, C^{33}]/s,$$

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 statisticalgenetics software SelegenREML/Blup (Resende, 2007b).

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

$$HMPRVG = n/\sum_{j=1}^{n} \frac{\overline{VG}_{.j}}{VG_{ij}},$$

in which: n is the number of locations; $VG_{ij} = u_j + g_i + ge_{ij}$ 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 $\overline{VG}_{.j}$ is the mean for VG_{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 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	0.000	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	0.000	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	0.000	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 $= u_j + g_i + ge_{ij}$, 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 no 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.

Acknowledgements

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