








ARTIGO ORIGINAL

Biometric analysis of cassava clones

Análise biométrica de clones de mandioca

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ABSTRACT: In the last ten years cassava roots represented the fourth most produced commodity in Brazil. Given its commercial importance, higher yields are constantly sought in breeding programs. This study was aimed at conducting a biometric analysis of cassava clones based on the estimation/prediction of genetic parameters and correlated genetic gain using mixed models and path analysis, respectively. Forty-eight clones were evaluated in a randomized block design with two replicates. The experiment was carried out in northern Minas Gerais in 2010. The agronomic characteristics evaluated were plant height (PH), fresh weight of aerial parts (FWAP), fresh root weight (FRW), fresh weight of commercial roots (FWCR), root length (RL), and root diameter (RD). These traits were evaluated at six and twelve months after planting. All traits examined were significantly affected by genotype. FWAP, RL and RD changed according the time of harvesting and RL was superior at six months. Accuracy was highest for PH (0.90) and lowest for FRW and FWCR (0.64). UFLA 42 was the most commercially productive. The trait RL exhibited the highest gain via correlated response to FWCR at twelve months after planting. At six months after planting, no traits were suitable for indirect selection. The traits PH and FWAP had little relevance as secondary components in path analysis.

RESUMO: Nos últimos dez anos a mandioca foi a quarta commodity mais produzida no Brasil. Dada sua importância econômica, constantemente, busca-se ganhos em produção em programas de melhoramento genético. O objetivo deste trabalho foi estimar/predizer os parâmetros genéticos e o ganho genético correlacionado usando modelos mistos e a análise de trilha, respectivamente. Quarenta e oito clones foram avaliados no delineamento em blocos ao acaso, com duas repetições. O experimento foi realizado na região norte do estado de Minas Gerais, no ano de 2010. As características agronômicas avaliadas foram altura de planta (AP), massa fresca da parte aérea (MFPA), massa fresca da raiz (MFR), massa fresca das raízes comerciais (MFRCO), comprimento de raiz (COR) e diâmetro de raiz (DIR). Os clones foram avaliados aos seis e doze meses de colheita. Todos os caracteres apresentaram significância para o efeito de genótipo. Somente MFPA, COR e DIR variaram para época de colheita, sendo que apenas COR foi superior aos seis meses. AP apresentou a maior acurácia seletiva (0,90) e MFR e MFRCO a menor (0,64). O clone UFLA 42 se destacou por ser o mais produtivo comercialmente. A característica COR mostrou-se superior para ganhos via resposta correlacionada em MFRCO aos doze meses de colheita, e aos seis nenhuma característica apresentou-se adequada para a seleção indireta. As características AP e MFPA não apresentaram relevância como componentes de produção secundários para a análise de trilha.

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1 Introduction

Cassava is one of the most important sources of carbohydrates for more than 800 million people in several tropical countries (FAO, 2013). Brazil is the fifth largest world producer of cassava and it represents the fifth most produced commodity in the country (FAO, 2017).

According to Piepho et al. (2007), the estimation of genotypic values is the central point of any crop breeding effort, as they are indicators of the best genotypes to be selected in segregating populations. In the estimation or prediction of genotypic values, the choice of the method of estimation/prediction is essential.

A method with great power of estimation/prediction in plant breeding is REML/BLUP (*restricted maximum likelihood/best linear unbiased prediction*). The estimates of variance components and prediction of genetic values by REML/BLUP are superior compared to least squares procedures and multi-effect index, respectively, when data are unbalanced (Resende & Fernandes, 1999), but equally adequate for balanced data.

Knowledge on the correlations among traits is also important, especially when there is an interest in indirect or even simultaneous gains in different traits. The efficiency of the selection of a trait can be increased when this information is known, particularly when the main trait is difficult to be selected because of low heritability (Cruz et al., 2014). This is usually the case for production traits that are by nature polygenic and highly influenced by the environment.

This study was aimed at conducting a biometric analysis of cassava clones based on the estimation/prediction of genetic parameters and correlated genetic gain using mixed models and path analysis, respectively.

2 Material and Methods

The study was conducted in an area of the Jaíba Project, northern Minas Gerais. Forty-eight cassava genotypes from the collection maintained by Empresa de Pesquisa Agropecuária de Minas Gerais (Epamig) were used. Planting was carried out in November 2010 and plants were harvested at six and twelve months in order to evaluate the influence of different harvest times on the agronomic traits.

The assay was carried out with experimental plots consisted of three rows of 1.0 m x 0.6 m with two replicates, and to calculate the mean value of each replicate, five plants were measured. The manioc, with two buds, were planted in furrows with depth of 10 cm and soil fertilization was performed according to soil analysis. The agronomic traits evaluated were: plant height (PH), fresh weight of aerial parts (FWAP), fresh root weight (FRW), fresh weight of commercial roots (FWCR), root length (RL), and root diameter (RD).

The statistic model used to analyze the clones, number 23 at Selegen, was the randomized block design, with one observation per plot and at different harvest times, as follows: $y = Xb + Zg + Wc + e$, where y , b , g , c , e = data vectors of fixed effects (mean of blocks at harvest times), genotypic effects of clones (random), effects of the interaction between genotype and harvest time (random) and random errors, respectively; and X , Z and W = incidence matrices for b , g and c , respectively.

The genotypic effects were considered random as defined by Resende & Duarte (2007) that suggested treating genotypic

effects as random when the number of treatments is equal or over 10.

The distributions and structures of means and variances are as follows:

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

The equations of the mixed model are:

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

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

where

$$h_g^2 = \frac{\sigma_g^2}{\sigma_g^2 + \sigma_{ge}^2 + \sigma_e^2}$$

is the individual broad-sense heritability of the block;

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

is the coefficient of determination of the effects of the interaction between genotype and harvest time; σ_g^2 is the genotypic variance among genotypes; σ_{ge}^2 is the variance of the interaction between genotype and harvest time; σ_e^2 is the residual variance among plots. The REML estimates of the variance components obtained with the algorithm EM are as follows:

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

$$\sigma_g^2 = [\hat{g}'\hat{g} + \sigma_e^2 \text{tr } C^{22}] / q \text{ and}$$

$$\sigma_{ge}^2 = [\hat{ge}'\hat{ge} + \sigma_e^2] / s,$$

C^{22} e C^{33} are:

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

where C is the coefficient matrix of the mixed model equations; tr = trace of the matrix; $r(x)$ = rank of the X matrix; N, q, s = total number of data, number of clones, and number of combinations between genotype and harvest time, respectively. The mixed model analysis was carried out using the software Selegen-REML/BLUP (Resende, 2007).

For the path analysis, a path diagram was drawn in which variables were divided into two groups: primary and secondary components. The primary component group was composed of the primary variables root length and root diameter. The secondary component group consisted of the secondary variables plant height and fresh weight of aerial parts. Fresh weight of commercial roots

was defined as the base variable instead of fresh root weight because of the commercial value of the product. The analysis was carried out with the software Genes (Cruz, 2013).

3 Results and Discussion

All traits examined were significant for genotype, and interactions between genotype and harvest time were not observed (Table 1). Thus, the better-performing genotypes harvested at six months were the same at twelve months. This is a desirable characteristic, as it allows the early selection of the most promising clones at six months, accelerating the breeding process.

Table 1. Deviance analysis for the six¹ components of cassava production

Tabela 1. Análise de *deviance* para os seis¹ componentes da produção de mandioca

PH				FWAP			
Effect	Deviance	LRT	C.V. ²	Effect	Deviance	LRT	C.V.
Genotype	-129.79	32.18*	0,10*	Genotype	332.82	7.04*	0.60*
Interaction ³	-161.96	0.01	0,001	Interaction	329.59	3.81	0.38
Residue	-	-	0,09	Residue	-	-	1.24
Complete Mod. ⁴	-161.97			Complete Mod.	325.78		
Broad-sense heritability			0.53	Broad-sense heritability			0.27
Selection accuracy			0.90	Selection accuracy			0.74
Genotypic correlation between harvests			0.99	Genotypic correlation between harvests			0.61
Genotypic Coef. Var. ⁵ (%)			12.79	Genotypic Coef. Var. (%)			28.14
Residual Coef. Var. (%)			12.07	Residual Coef. Var. (%)			40.55
Mean			2.52	Mean			2.74
FRW				FWCR			
Effect	Deviance	LRT	C.V.	Effect	Deviance	LRT	C.V.
Genotype	325.40	5.81*	0.29*	Genotype	243.54	5.98*	0.19*
Interaction	319.60	0.01	0.07	Interaction	237.56	0.00	0.04
Residue	-	-	1.57	Residue	-	-	1.01
Complete Mod.	319.59			Complete Mod.	237.56		
Broad-sense heritability			0.15	Broad-sense heritability			0.15
Selection accuracy			0.64	Selection accuracy			0.64
Genotypic correlation between harvests			0.82	Genotypic correlation between harvests			0.82
Genotypic Coef. Var. (%)			23.27	Genotypic Coef. Var. (%)			23.94
Residual Coef. Var. (%)			53.81	Residual Coef. Var. (%)			54.90
Mean			2.33	Mean			1.83
RL				RD			
Effect	Deviance	LRT	C.V.	Effect	Deviance	LRT	C.V.
Genotype	840.86	11.41*	9.40*	Genotype	67.11	7.42*	0.10*
Interaction	829.49	0.04	0.041	Interaction	59.70	0.01	0.003
Residue	-	-	21.40	Residue	-	-	0.39
Complete Mod.	829.45			Complete Mod.	59.69		
Broad-sense heritability			0.63	Broad-sense heritability			0.20
Selection accuracy			0.79	Selection accuracy			0.71
Genotypic correlation between harvests			0.96	Genotypic correlation between harvests			0.96
Genotypic Coef. Var. (%)			9.71	Genotypic Coef. Var. (%)			6.90
Residual Coef. Var. (%)			14.66	Residual Coef. Var. (%)			13.56
Mean			31.55	Mean			4.59

¹PH = plant height, FWAP = fresh weight of aerial parts, FRW = fresh root weight, FWCR = fresh weight of commercial roots, RL = root length, RD = root diameter.

²C.V. = variance component.

³Interaction between Genotype and Harvest time.

⁴Complete Mod. = complete model.

⁵Coef. Var. = coefficient of variation.

*Significant at 5% with the chi-square test.

In a second analysis, deviance values for fresh weight of aerial parts (FWAP), root length (RL), and root diameter (RD) were significantly different between harvest times (Table 2). Of these, a higher value at six months was observed only for RL.

Heritability was highest for plant height (PH) and root length (RL), and lowest for fresh root weight (FRW) and fresh weight of commercial roots (FWCR) (Table 1). Despite the low heritability of FRW and FWCR, this is agreement with the quantitative and polygenic nature of traits highly influenced by the environment (Vencovsky, 1987). The highest genotypic coefficients of variation (CVg) were observed for FRW, FWCR, and FWAP. Values above 10% indicate genetic variability with potential for selection, as reported by Oliveira et al. (2011). The residual coefficient of variation (CVe) was lowest for PH, RL and RD, indicating greater experimental accuracy for these traits, and highest for FRW, FWAP and FWCR, respectively (Table 1). Cavalcante et al. (2006) reported that CVe values like these are common when the traits being analyzed are underground structures, where environmental control is more difficult. According to Cavalcante et al. (2003, 2006), crops such as carrot (*Daucus carota* L.), cassava (*Manihot esculenta* Crantz), and potato (*Solanum tuberosum* L.) have similar CVe values.

When the CVg/CVe ratio (relative coefficient of variation – CVr) is equal or higher than the experimental unit, conditions are more favorable for selection (Vencovsky, 1987). In our study, this was observed only for PH (Table 1). Resende & Duarte (2007), on the other hand, associated CVr with number of repetitions to obtain greater accuracy, where for experiments with two repetitions, these values should range between 0.70 and 1.25. Although the accuracy values were higher than those reported by these authors, the relationship between CVr and accuracy was maintained. Accuracy was highest for PH and lowest for FRW and FWCR, which also had the lowest CVr values (Table 1). Henderson (1984) reported that selection accuracy is the most important parameter in a genotypic analysis. This parameter is a correlation between true genotypic value of the genetic treatment and the estimated or predicted value based on experiments. Thus, the higher the value, the more possibilities of genetic gains with selection (Resende & Duarte, 2007). Although accuracy levels were lowest for FRW and FWCR, these values were moderate, suggesting possible gains with the selection of superior genotypes.

No effects of interaction between genotype and harvest time were observed. Consequently, the genotypic correlation between harvest times that associated the best genotypes at six and twelve months was high (above 0.70) for nearly all traits, except FWAP with a moderate correlation value (0.64). It should be pointed out that the genetic parameters observed for FRW and FWCR

were approximate values, reflecting a high level relationship between these traits.

Of the forty-eight clones evaluated, only the best ten were classified based on the predicted genotypic values ($u + g$) for each trait (Table 3). The three most promising clones based on PH were Paraguaia, Rosa and Maragogipe; on FWAP, UFLA 42, Rosa Branca and Gema de ovo; on RL, 347, Saracura and Barro Vermelho; and on RD, Mantiqueira, Saracura and UFLA 42. An interesting relationship was observed between FRW and FWCR, with a coincidence of 60% among the ten best clones. The highest predicted genotypic value of FRW was observed for clone 266, however, when including only commercial roots, it was not among the first ten. The same was observed for the clones 1418, 354 and Dona Rosa. On the other hand, the clones Manteiga, Barro Vermelho, Gema de ovo and Maragogipe were not among the most promising ones for MRF but had the highest values for FWCR. The most commercially productive clones were UFLA 42, UFLA 10 and Saracura. The clone UFLA 42 was among the first ten for all traits and with the highest predicted genotypic value for commercial production (FWCR).

The highest genetic gains obtained by selecting the ten most promising clones were 43% for FWAP and 30% for FWCR, which was reflected in the CVg values, indicating that the more heterogeneous the population for one trait, the highest the selection differential, and consequently the genetic gain, as BLUP uses genotypic values.

The path analysis was carried out using FWCR as the variable base, because of its high correlation with FRW (0.73) and commercial relevance. Collinearity was low among the components, and as a result, all components were maintained in the analysis. The primary components were affected by harvest time (Table 4). The trait with the strongest effect, direct and indirect, on FWCR at six months after planting was RD (0.39), and also the one with the strongest direct effect (0.37). Conversely at twelve months after planting, RL was the trait with the strongest total effect (0.57) as well as direct effect (0.53). Gomes et al. (2007) examined the correlation between the primary component root length and production of cassava roots and observed similar values (0.50). Pinho et al. (1995) suggested that root length is the trait most closely correlated with productivity. Therefore, in an indirect selection process for gains in fresh weight of commercial roots, the variable RL can be considered at twelve months after planting, as it maintains a moderate correlation with the variable of interest and heritability and selection accuracy of 0.63 and 0.79, respectively. At six months after planting, no components were suitable due to the low correlation with FWCR.

Table 2. Analysis of deviance of harvest time with six¹ components of cassava production

Tabela 2. Análise de deviance do tempo de colheita com seis¹ componentes da produção de mandioca

Effect	PH		FWAP		FRW	
	Deviance	LRT	Deviance	LRT	Deviance	LRT
Harvest Time	-1.69	3.69 ^{NS}	-2.63	5.60*	-0.08	2.14 ^{NS}
Complete Model	-5.38		-8.23		-2.22	
Effect	FWCR		RL		RD	
	Deviance	LRT	Deviance	LRT	Deviance	LRT
Harvest Time	0.58	0.02 ^{NS}	2.94	4.36*	2.26	4.26*
Complete Model	-0.60		-1.42		-2.00	

¹PH = plant height, FWAP = fresh weight of aerial parts, FRW = fresh root weight, FWCR = fresh weight of commercial roots, RL = root length, RD = root diameter.

^{NS}: *Not significant and significant at 5% with the chi-square test.

Table 3. Components of mean and predicted genotypic values of the ten best clones for six¹ components of cassava production**Tabela 3.** Componentes dos valores genotípicos médios e preditos dos dez melhores clones para seis¹ componentes da produção de mandioca

PH					FWAP				
Clone	g ²	u + g ³	G. G. ⁴	N. M ⁵	Clone	g	u + g	G. G.	N. M.
Paraguaia	0.73	3.26	0.73	3.26	UFLA 42	1.79	4.53	1.79	4.53
Rosa	0.58	3.11	0.66	3.18	Rosa branca	1.13	3.87	1.46	4.20
Maragogipe	0.51	3.04	0.61	3.14	Gema ovo	1.00	3.75	1.30	4.05
Casca roxa	0.42	2.95	0.56	3.09	Cacau	0.93	3.68	1.21	3.96
UFLA 42	0.34	2.86	0.52	3.04	266	0.82	3.56	1.13	3.88
UFLA 22	0.31	2.84	0.48	3.01	Barro ver.	0.76	3.51	1.07	3.81
Barro ver.	0.31	2.83	0.46	2.98	347	0.67	3.42	1.01	3.76
266	0.26	2.79	0.43	2.96	Mocotó	0.65	3.40	0.97	3.71
Baiana	0.26	2.78	0.41	2.94	354	0.50	3.24	0.92	3.66
347	0.22	2.75	0.40	2.92	Maragogipe	0.42	3.17	0.87	3.61
Mean	3.05 m				Mean	3.92 Kg			
FRW					FWCR				
Clone	g	u + g	G. G.	N. M.	Clone	g	u + g	G. G.	N. M.
266	0.94	3.26	0.94	3.26	UFLA 42	0.86	2.69	0.86	2.69
UFLA 42	0.73	3.05	0.83	3.16	UFLA 10	0.52	2.35	0.69	2.52
Baiana	0.50	2.82	0.72	3.05	Saracura	0.51	2.34	0.63	2.46
118	0.49	2.81	0.66	2.99	Baiana	0.38	2.21	0.57	2.40
354	0.46	2.78	0.62	2.95	12818	0.38	2.21	0.53	2.36
Dona rosa	0.43	2.76	0.59	2.92	Manteiga	0.31	2.14	0.49	2.33
UFLA 10	0.39	2.72	0.56	2.89	Barro ver.	0.29	2.12	0.46	2.30
Saracura	0.38	2.70	0.54	2.86	Gema ovo	0.26	2.09	0.44	2.27
1418	0.33	2.66	0.51	2.84	Maragogipe	0.24	2.08	0.42	2.25
12818	0.33	2.65	0.50	2.82	118	0.23	2.07	0.40	2.23
Mean	2,97 Kg				Mean	2,38 Kg			
RL					RD				
Clone	g	u + g	G. G.	N. M.	Clone	g	u + g	G. G.	N. M.
347	5.31	36.86	5.31	36.86	Mantiqueira	0.76	5.35	0.76	5.35
Saracura	4.33	35.89	4.82	36.38	Saracura	0.53	5.12	0.65	5.24
Barro ver.	3.83	35.38	4.49	36.05	UFLA 42	0.40	4.99	0.56	5.15
Casca roxa	3.48	35.04	4.24	35.79	Baiana	0.26	4.85	0.49	5.08
12818	3.28	34.83	4.05	35.60	354	0.21	4.79	0.43	5.02
Gema ovo	3.09	34.65	3.89	35.44	UFLA 2	0.16	4.75	0.39	4.97
UFLA 42	2.88	34.44	3.74	35.30	Pinheirinha	0.16	4.75	0.36	4.94
Imbé	2.67	34.22	3.61	35.16	142	0.16	4.75	0.33	4.92
Umbaúba	2.49	34.04	3.48	35.04	Gema ovo	0.16	4.75	0.31	4.9
UFLA 22	2.31	33.86	3.37	34.92	Umbaúba	0.16	4.74	0.30	4.88
Mean	35.65 cm				Mean	5.05 cm			

¹PH = plant height, FWAP = fresh weight of aerial parts, FRW = fresh root weight, FWCR = fresh weight of commercial roots, RL = root length, RD = root diameter.

²g = predicted genotypic effect.

³u + g = predicted genotypic values

⁴G. G. = genotypic gain

⁵N. M. = new mean.

Table 4. Estimates of the direct and indirect effects of primary¹ and secondary² components on the basic variable fresh weight of commercial roots (FWCR) of cassava**Tabela 4.** Estimativas dos efeitos diretos e indiretos de componentes primários¹ e secundários² sobre a variável básica massa fresca de raízes comerciais (MFRCO) da mandioca

		Six months		Twelve months	
		Effect	Estimate	Effect	Estimate
RL	Direct on FWCR		0.33	Direct on FWCR	0.53
	Indirect via RD		0.02	Indirect via RD	0.04
	Total		0.35	Total	0.57
RD	Direct on FWCR		0.37	Direct on FWCR	0.25
	Indirect via RL		0.02	Indirect via RL	0.08
	Total		0.39	Total	0.32

¹RL = root length, RD = root diameter.²PH = plant height, FWAP = fresh weight of aerial parts.

When the effect of secondary components on FWCR was examined, a low correlation among traits was observed. However FWAP had the strongest total direct positive effect on FWCR at six months as

well as twelve months after planting (Table 5). Therefore, because the low correlation values, the selection for FWAP and PH would not be effective to obtain indirect gains FWCR via correlated response.

Table 5. Estimates of the direct and indirect effects of secondary components¹ on the basic variable fresh weight of commercial roots (FWCR) of cassava**Tabela 5.** Estimativas dos efeitos diretos e indiretos de componentes secundários¹ sobre a variável básica massa fresca de raízes comerciais (MFRCO) da mandioca

		Six months			Twelve months		
Effect		RL ²	RD ³	FWCR	RL	RD	FWCR
AP	Direct secondary	0.04	-0.03	0.01	0.13	0.05	0.18
	Indirect via FWAP	0.05	0.05	0.10	0.04	0.02	0.06
	Total	0.09	0.02	0.11	0.17	0.07	0.24
FWAP	Direct secondary	0.11	0.10	0.21	0.16	0.07	0.23
	Indirect via PH	0.02	-0.01	0.01	0.03	0.01	0.04
	Total	0.13	0.09	0.22	0.19	0.08	0.27

¹PH = plant height, FWAP = fresh weight of aerial parts.²RL = root length.³RD = root diameter.

4 Conclusions

The genotype UFLA 42 was among of the ten best clones for all traits evaluated as well as the most commercially productive. Gains in fresh weight of commercial roots via correlated response can be achieved based on the primary component root length at twelve months after planting. And the effect of plant height and fresh weight of aerial parts had little relevance as secondary components in path analysis.

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